(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
27 December 2002 (27.12.2002)

PCT

(10) International Publication Number
WO 02/102321 A2

(51) International Patent Classification^7: **A61K**

(21) International Application Number: PCT/US02/19522

(22) International Filing Date: 18 June 2002 (18.06.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/299,134	18 June 2001 (18.06.2001)	US
60/298,994	18 June 2001 (18.06.2001)	US
09/972,446	4 October 2001 (04.10.2001)	US
Not furnished	6 June 2002 (06.06.2002)	US
Not furnished	7 June 2002 (07.06.2002)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	60/299,134 (CIP)
Filed on	18 June 2001 (18.06.2001)
US	60/298,994 (CIP)
Filed on	18 June 2001 (18.06.2001)
US	09/972,446 (CIP)
Filed on	4 October 2001 (04.10.2001)
US	Not furnished (CIP)
Filed on	6 June 2002 (06.06.2002)
US	Not furnished (CIP)
Filed on	7 June 2002 (07.06.2002)

(71) Applicant *(for all designated States except US)*: **CURAGEN CORPORATION** [US/US]; 555 Long Wharf Drive, 11th floor, New Haven, CT 06511 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **ANDERSON, David, W.** [US/US]; 85 Montoya Drive, Branford, CT 06405 (US). **GUO, Xiaojia** [CN/US]; 713 Robert Frost Drive, Branford, CT 06405 (US). **GUSEV, Vladimir, Y.** [UA/US]; 1209 Durham Road, Madison, CT 06443 (US). **HERRMANN, John, L.** [US/US]; 78 Barnshed Lane, Guilford, CT 06437 (US). **LI, Li** [CN/US]; 56 Jerimoth Drive, Branford, CT 06405 (US). **MEZES, Peter, S.** [CA/US]; 7 Clark's Lane, Old Lyme, CT 06371 (US). **PENA, Carol, E., A.** [US/US]; 604 Orange Street, Number 2, New Haven, CT 06511 (US). **SPADERNA, Steven, K.** [US/US]; 261 Deerfield Drive, Berlin, CT 06037 (US). **ZHONG, Mei** [CA/US]; 45 Harrison Avenue, Apartment 1B, Branford, CT 06405 (US).

(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky, and Popeo, P., C., One Financial Center, Boston, MA 02111 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

---

(54) Title: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

(57) Abstract: Disclosed herein are nucleic acid sequences that encode G-coupled protein-receptor related polypeptides. Also disclosed are polypeptides encoded by these nucleic acid sequences, and antibodies, which immunospecifically bind to the polypeptide, as well as derivatives, variants, mutants, or fragments of the aforementioned polypeptide, polynucleotide, or antibody. The invention further discloses therapeutic, diagnostic and research methods for diagnosis, treatment, and prevention of disorders involving anyone of these novel human nucleic acids and proteins.

WO 02/102321 A2

NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

BACKGROUND OF THE INVENTION

The invention generally relates to nucleic acids and polypeptides. More particularly, the invention relates to nucleic acids encoding novel molecules (MOL) polypeptides, as well as vectors, host cells, antibodies, and recombinant methods for producing these nucleic acids and polypeptides.

SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of nucleic acid sequences encoding novel polypeptides. The novel nucleic acids and polypeptides are referred to herein as MOLX, or MOL1, MOL2, MOL3, MOL4, MOL5, MOL6, MOL7, MOL8, MOL9, MOL10, MOL11, MOL12, MOL13, MOL14, MOL15, MOL16, MOL17, MOL18, MOL19, MOL20, MOL21 or MOL22 nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be collectively designated as "MOLX" nucleic acid or polypeptide sequences.

In one aspect, the invention provides an isolated MOLX nucleic acid molecule encoding a MOLX polypeptide that includes a nucleic acid sequence that has identity to the nucleic acids disclosed in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205. In some embodiments, the MOLX nucleic acid molecule will hybridize under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule that includes a protein-coding sequence of a MOLX nucleic acid sequence. The invention also includes an isolated nucleic acid that encodes a MOLX polypeptide, or a fragment, homolog, analog or derivative thereof. For example, the nucleic acid can encode a polypeptide at least 80% identical to a polypeptide comprising the amino acid sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206. The nucleic acid can be, for example, a genomic DNA fragment or a cDNA molecule that includes the nucleic acid sequence of any of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205.

Also included in the invention is an oligonucleotide, *e.g.*, an oligonucleotide which includes at least 6 contiguous nucleotides of a MOLX nucleic acid (*e.g.,* SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205) or a complement of said oligonucleotide.

Also included in the invention are substantially purified MOLX polypeptides (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206). In certain embodiments, the MOLX polypeptides include an amino acid sequence that is substantially identical to the amino acid sequence of a human MOLX polypeptide.

The invention also features antibodies that immunoselectively bind to MOLX polypeptides, or fragments, homologs, analogs or derivatives thereof.

In another aspect, the invention includes pharmaceutical compositions that include therapeutically- or prophylactically-effective amounts of a therapeutic and a pharmaceutically-acceptable carrier. The therapeutic can be, *e.g.*, a MOLX nucleic acid, a MOLX polypeptide, or an antibody specific for a MOLX polypeptide. In a further aspect, the invention includes, in one or more containers, a therapeutically- or prophylactically-effective amount of this pharmaceutical composition.

In a further aspect, the invention includes a method of producing a polypeptide by culturing a cell that includes a MOLX nucleic acid, under conditions allowing for expression of the MOLX polypeptide encoded by the DNA. If desired, the MOLX polypeptide can then be recovered.

In another aspect, the invention includes a method of detecting the presence of a MOLX polypeptide in a sample. In the method, a sample is contacted with a compound that selectively binds to the polypeptide under conditions allowing for formation of a complex between the polypeptide and the compound. The complex is detected, if present, thereby identifying the MOLX polypeptide within the sample.

The invention also includes methods to identify specific cell or tissue types based on their expression of a MOLX.

Also included in the invention is a method of detecting the presence of a MOLX nucleic acid molecule in a sample by contacting the sample with a MOLX nucleic acid probe or primer, and detecting whether the nucleic acid probe or primer bound to a MOLX nucleic acid molecule in the sample.

In a further aspect, the invention provides a method for modulating the activity of a MOLX polypeptide by contacting a cell sample that includes the MOLX polypeptide with a compound that binds to the MOLX polypeptide in an amount sufficient to modulate the activity of said polypeptide. The compound can be, *e.g.*, a small molecule, such as a nucleic acid, peptide, polypeptide, peptidomimetic, carbohydrate, lipid or other organic (carbon containing) or inorganic molecule, as further described herein.

Also within the scope of the invention is the use of a therapeutic in the manufacture of a medicament for treating or preventing disorders or syndromes including, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, or other disorders related to cell signal processing and metabolic pathway modulation. The therapeutic can be, *e.g.*, a MOLX nucleic acid, a MOLX polypeptide, or a MOLX-specific antibody, or biologically-active derivatives or fragments thereof.

For example, the compositions of the present invention will have efficacy for treatment of patients suffering from: Cancer including pancreatic cancer, adenoma, brain tumor, colon cancer breast cancer, prostate cancer, testis cancer, neurological disorders including age-related disorders, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Behavioral disorders, Addiction, Anxiety, Pain, nephropathy, neurodegenerative disorders, Aneurysms, Fibromuscular dysplasia, metabolic disorders including. failure to thrive, nutritional edema, hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, Hypercholesterolemia, Obesity, Diabetes, cardiac disorders inclusing tachycardia, erythroderma, long QT syndrome, heart block, Ataxia-telangiectasia, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Larsen syndrome, night blindness, brugada syndrome, Von Hippel-Lindau (VHL) syndrome, Tuberous sclerosis, Hypercalceimia, Cirrhosis, angiogenesis and wound healing, blood pressure regulation, Trauma, Tuberous sclerosis, Fertility, Hirschsprung's disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, immune disorders including cell-mediated immunity disorders, Leukodystrophies, inflammation, Hyperthyroidism, Hypothyroidism, Lesch-Nyhan syndrome, Multiple sclerosis, Transplantation, lung diseases, including asthma, Emphysema, immundeficiencies, Crohn's disease, Scleroderma, Appendicitis, Autoimmune diseases, Systemic lupus erythematosus, developmental disorders, neural tube defects, modulation of apoptosis, viral, bacterial, and parasitic infections and/or other pathologies and disorders of the like.

The polypeptides can be used as immunogens to produce antibodies specific for the invention, and as vaccines. They can also be used to screen for potential agonist and antagonist compounds. For example, a cDNA encoding MOLX may be useful in gene therapy, and MOLX may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Cancer including pancreatic cancer, adenoma, brain tumor, colon cancer breast cancer, prostate cancer, testis cancer, neurological disorders including age-related disorders, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Behavioral disorders, Addiction, Anxiety, Pain, nephropathy, neurodegenerative disorders, Aneurysms, Fibromuscular dysplasia, metabolic disorders including. failure to thrive, nutritional edema, hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, Hypercholesterolemia, Obesity, Diabetes, cardiac disorders inclusing tachycardia, erythroderma, long QT syndrome, heart block, Ataxia-telangiectasia, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Larsen syndrome, night blindness, brugada syndrome, Von Hippel-Lindau (VHL) syndrome, Tuberous sclerosis, Hypercalceimia, Cirrhosis, angiogenesis and wound healing, blood pressure regulation, Trauma, Tuberous sclerosis, Fertility, Hirschsprung's disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, immune disorders including cell-mediated immunity disorders, Leukodystrophies, inflammation, Hyperthyroidism, Hypothyroidism, Lesch-Nyhan syndrome, Multiple sclerosis, Transplantation, lung diseases, including asthma, Emphysema, immundeficiencies, Crohn's disease, Scleroderma, Appendicitis, Autoimmune diseases, Systemic lupus erythematosus, developmental disorders, neural tube defects, modulation of apoptosis, viral, bacterial, and parasitic infections and/or other pathologies and disorders.

The invention further includes a method for screening for a modulator of disorders or syndromes including, *e.g.*, Cancer including pancreatic cancer, adenoma, brain tumor, colon cancer breast cancer, prostate cancer, testis cancer, neurological disorders including age-related disorders, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Behavioral disorders, Addiction, Anxiety, Pain, nephropathy, neurodegenerative disorders, Aneurysms, Fibromuscular dysplasia, metabolic disorders including. failure to thrive, nutritional edema, hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, Hypercholesterolemia, Obesity, Diabetes, cardiac disorders inclusing tachycardia, erythroderma, long QT syndrome, heart block, Ataxia-telangiectasia, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Larsen syndrome, night blindness, brugada syndrome, Von Hippel-Lindau (VHL) syndrome, Tuberous sclerosis, Hypercalceimia, Cirrhosis, angiogenesis and wound healing, blood pressure regulation, Trauma, Tuberous sclerosis, Fertility, Hirschsprung's disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, immune disorders including cell-mediated immunity disorders, Leukodystrophies, inflammation, Hyperthyroidism, Hypothyroidism, Lesch-Nyhan syndrome, Multiple sclerosis, Transplantation, lung diseases, including asthma, Emphysema, immundeficiencies, Crohn's disease, Scleroderma, Appendicitis, Autoimmune diseases, Systemic lupus erythematosus, developmental disorders, neural tube defects, modulation of apoptosis, viral, bacterial, and parasitic infections or other disorders related to cell signal processing and metabolic pathway modulation. The method includes contacting a test compound with a MOLX polypeptide and determining if the test compound binds to said MOLX polypeptide.

Binding of the test compound to the MOLX polypeptide indicates the test compound is a modulator of activity, or of latency or predisposition to the aforementioned disorders or syndromes.

Also within the scope of the invention is a method for screening for a modulator of activity, or of latency or predisposition to an disorders or syndromes including, *e.g.*, Cancer including pancreatic cancer, adenoma, brain tumor, colon cancer breast cancer, prostate cancer, testis cancer, neurological disorders including age-related disorders, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Behavioral disorders, Addiction, Anxiety, Pain, nephropathy, neurodegenerative disorders, Aneurysms, Fibromuscular dysplasia, metabolic disorders including. failure to thrive, nutritional edema, hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, Hypercholesterolemia, Obesity, Diabetes, cardiac disorders inclusing tachycardia, erythroderma, long QT syndrome, heart block, Ataxia-telangiectasia, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Larsen syndrome, night blindness, brugada syndrome, Von Hippel-Lindau (VHL) syndrome, Tuberous sclerosis, Hypercalceimia, Cirrhosis, angiogenesis and wound healing, blood pressure regulation, Trauma, Tuberous sclerosis, Fertility, Hirschsprung's disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, immune disorders including cell-mediated immunity disorders, Leukodystrophies, inflammation, Hyperthyroidism, Hypothyroidism, Lesch-Nyhan syndrome, Multiple sclerosis, Transplantation, lung diseases, including asthma, Emphysema, immundeficiencies, Crohn's disease, Scleroderma, Appendicitis, Autoimmune diseases, Systemic lupus erythematosus, developmental disorders, neural tube defects, modulation of apoptosis, viral, bacterial, and parasitic infections or other disorders related to cell signal processing and metabolic pathway modulation by administering a test compound to a test animal at increased risk for the aforementioned disorders or syndromes. The test animal expresses a recombinant polypeptide encoded by a MOLX nucleic acid. Expression or activity of MOLX polypeptide is then measured in the test animal, as is expression or activity of the protein in a control animal which recombinantly-expresses MOLX polypeptide and is not at increased risk for the disorder or syndrome. Next, the expression of MOLX polypeptide in both the test animal and the control animal is compared. A change in the activity of

MOLX polypeptide in the test animal relative to the control animal indicates the test compound is a modulator of latency of the disorder or syndrome.

In yet another aspect, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a MOLX polypeptide, a MOLX nucleic acid, or both, in a subject (*e.g.*, a human subject). The method includes measuring the amount of the MOLX polypeptide in a test sample from the subject and comparing the amount of the polypeptide in the test sample to the amount of the MOLX polypeptide present in a control sample. An alteration in the level of the MOLX polypeptide in the test sample as compared to the control sample indicates the presence of or predisposition to a disease in the subject. Preferably, the predisposition includes, *e.g.*, diabetes, metabolic disturbances associated with obesity, the metabolic syndrome X, anorexia, wasting disorders associated with chronic diseases, metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders. Also, the expression levels of the new polypeptides of the invention can be used in a method to screen for various cancers as well as to determine the stage of cancers.

In a further aspect, the invention includes a method of treating or preventing a pathological condition associated with a disorder in a mammal by administering to the subject a MOLX polypeptide, a MOLX nucleic acid, or a MOLX-specific antibody to a subject (*e.g.*, a human subject), in an amount sufficient to alleviate or prevent the pathological condition. In preferred embodiments, the disorder, includes, *e.g.*, Cancer including pancreatic cancer, adenoma, brain tumor, colon cancer breast cancer, prostate cancer, testis cancer, neurological disorders including age-related disorders, Alzheimer's disease, Stroke, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Behavioral disorders, Addiction, Anxiety, Pain, nephropathy, neurodegenerative disorders, Aneurysms, Fibromuscular dysplasia, metabolic disorders including. failure to thrive, nutritional edema, hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, Hypercholesterolemia, Obesity, Diabetes, cardiac disorders inclusing tachycardia, erythroderma, long QT syndrome, heart block, Ataxia-telangiectasia, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Larsen syndrome, night blindness, brugada syndrome, Von Hippel-Lindau

(VHL) syndrome, Tuberous sclerosis, Hypercalceimia, Cirrhosis, angiogenesis and wound healing, blood pressure regulation, Trauma, Tuberous sclerosis, Fertility, Hirschsprung's disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, immune disorders including cell-mediated immunity disorders, Leukodystrophies, inflammation, Hyperthyroidism, Hypothyroidism, Lesch-Nyhan syndrome, Multiple sclerosis, Transplantation, lung diseases, including asthma, Emphysema, immundeficiencies, Crohn's disease, Scleroderma, Appendicitis, Autoimmune diseases, Systemic lupus erythematosus, developmental disorders, neural tube defects, modulation of apoptosis, viral, bacterial, and parasitic infections.

In yet another aspect, the invention can be used in a method to identity the cellular receptors and downstream effectors of the invention by any one of a number of techniques commonly employed in the art. These include but are not limited to the two-hybrid system, affinity purification, co-precipitation with antibodies or other specific-interacting molecules.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention is based, in part, upon the discovery of novel nucleic acid sequences that encode novel polypeptides. The novel nucleic acids and their encoded polypeptides are referred to individually as MOL1, MOL2, MOL3, MOL4, MOL5, MOL6, MOL7, MOL8, MOL9, MOL10, MOL11, MOL12, MOL13, MOL14, MOL15, MOL16, MOL17, MOL18, MOL19, MOL20, MOL21 and MOL22. The nucleic acids, and their encoded polypeptides, are collectively designated herein as "MOLX".

The novel MOLX nucleic acids of the invention include the nucleic acids whose sequences are provided in Tables 1A, 2A, 3A, 4A, 5A, 6A, 6D, 7A, 8A, 8D, 9A, 9D, 9F, 10A, 11A, 12A, 13A, 14A, 15A, 16A, 17A, 18A, 19A, 20A, 21A and 22A. inclusive ("Tables 1A - 22A"), or a fragment, derivative, analog or homolog thereof. The novel MOLX proteins of the invention include the protein fragments whose sequences are provided in Tables 1B, 2B, 3B, 4B 5B, 6B, 6E, 7B, 8B, 8E, 9B, 9E, 9G, 10B, 11A, 12A, 13A, 14A, 15A, 16A, 17A, 18A, 19A, 20A, 21A and 22A, inclusive ("Tables 1B - 10B, 11A-22A"). The individual MOLX nucleic acids and proteins are described below. Within the scope of this invention is a method of using these nucleic acids and peptides in the treatment or prevention of a disorder related to cell signaling or metabolic pathway modulation.

MOL1

MOL1a

A disclosed interleukin-1 receptor/Toll-like nucleic acid of 1050 nucleotides, MOL1a, is shown in Table 1A. The disclosed MOL1a open reading frame ("ORF") begins at the ATG initiation codon at nucleotides 1-3, shown in bold in Table 1A. The encoded polypeptide is alternatively referred to herein as MOL1a or as GM_79960178. The disclosed MOL1a ORF terminates at a TGA codon at nucleotides 3043-3045. As shown in Table 1A the start and stop codons are in bold letters.

Table 1A. MOL1a nucleotide sequence (SEQ ID NO:1).
ATGCTGGCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGA ACTGCAACTGGCTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTC CTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTC AAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCT TGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCT CATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGC TTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCC TTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAG CCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTG CGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACT TCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTC CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAA TGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGA GGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGG CATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTG CAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGG ACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCA

GCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAAC TTCACCTTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGT GCCTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGT GCTAGACCTGTCCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTG GACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCA CCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCG GGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGC CTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCC CCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCC CAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGG CTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGC GAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCA AATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAG GCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGCATCTTTGCAC AGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTCGCTGCTGGCTGTGGCTCTGGG CCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTT CCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGC AGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGAGTGCCGTGGGCGCTGGGCACTCCG CCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAGAACCTGTGGGCCTCGGTCTATGGCAGC CGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGC AGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCCCTGACGGCCGCCGCTCCCGCTATGT GCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCAGTGGTCAGCGCAGCTTCTGG GCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAACTTCTGCCAGGGACCCACGGCCG AATAG

A disclosed encoded MOL1a protein has 346 amino acid residues, referred to as the MOL1a protein. The MOL1a protein was analyzed for signal peptide prediction and cellular localization. SignalP results predict that MOL1a is cleaved between position 41 and 42 of SEQ ID NO:2. Psort and Hydropathy profiles also predict that MOL1a contains a signal peptide and is likely to be localized in the plasma membrane (Certainty=0.4600). The disclosed MOL1a polypeptide sequence is presented in Table 1B using the one-letter amino acid code.

Table 1B. Encoded MOL1a protein sequence (SEQ ID NO:2).
MLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLK WNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFL FMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVL DVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKCITK TKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFI NQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQ PFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLD LSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCN SISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRV KCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSGRDE DALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDR VSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHH FYNRNFCQGPTAE

MOL1a was initially identified on chromosome 3 with a TblastN analysis of a proprietary sequence file for a G-protein coupled receptor probe or homolog, which was run against the Genomic Daily Files made available by GenBank. A proprietary software program (GenScan™) was used to further predict the nucleic acid sequence and the selection of exons. The resulting sequences were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein.

A region of the MOL1a nucleic acid sequence has 690 of 1203 bases (57 %) identical to a *Homo sapiens* Toll Receptor mRNA (GENBANK-ID: AL137451), with an E-value of 5.7×10^{-8}. In all BLAST alignments herein, the "E-value" or "Expect" value is a numeric indication of the probability that the aligned sequences could have achieved their similarity to the BLAST query sequence by chance alone, within the database that was searched. For example, the probability that the subject ("Sbjct") retrieved from the MOL1a BLAST analysis, *e.g.*, the *Homo sapiens* MOL, matched the Query MOL1a sequence purely by chance is 5.7×10^{-8}.

A BLASTX search was performed against public protein databases. The full amino acid sequence of the protein of the invention was found to have 342 of 900 amino acid residues (38%) identical to, and 493 of 900 residues (54%) positive with, the 1049 amino acid residue Toll-like Receptor 7 protein from *Homo sapiens* (ptnr:SPTREMBL-ACC:AAF60188).

MOL1b

A disclosed Toll receptor 9-like nucleic acid of 3118 nucleotides, MOL1b, is shown in Table 1C. The disclosed MOL1b open reading frame ("ORF") begins at the ATG initiation codon at nucleotides 18-20, shown in bold in Table 1C. The encoded polypeptide is alternatively referred to herein as MOL1b or as CG54674-02. The disclosed MOL1b ORF terminates at a TAG codon at nucleotides 3114-3116. As shown in Table 1C the start and stop codons are in bold letters.

Table 1C. MOL1b nucleotide sequence (SEQ ID NO:114).
CCCCTCGCACCCCCAGCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTG
GCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAA
CTGGCTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCT
CCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAAC
TGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCC
CACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGT
CCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATG
GACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAA
CCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGC
TGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTG
GGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCC
CGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTT
GGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAG

GCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCT
GTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCG
ATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAG
GCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTC
GGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCC
CAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCGCCTTGGATCTGTCACGGAAC
AACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCAT
CTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGG
ACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTT
GGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAA
CAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGG
GCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCC
CAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGA
CAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACC
AGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATC
AGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGAC
AGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCG
CCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGT
GGCAGTCCGGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTG
GGACTGTTTCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGG
ACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCC
CTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGG
GCAGCTGGAGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCC
TCTTTGAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGT
GGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGAT
CCTGAGCCCTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGC
CCCACCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTAT
AACCGGAACTTCTGCCAGGGACCCACGGCCGAATAGCC

A disclosed encoded MOL1b protein has 1032 amino acid residues, referred to as the MOL1b protein. The disclosed MOL1b polypeptide sequence is presented in Table 1D using the one-letter amino acid code.

Table 1D. Encoded MOL1b protein sequence (SEQ ID NO:115).
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHH
LHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTN
ILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNR
IVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLG
NLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLR
PLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPS
SEDFRPNCSTLNFALDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEH
SFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAE
GDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALT
NGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAF
MDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCF
HLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLW
ASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSG
QRSFWAQLGMALTRDNHHFYNRNFCQGPTAE*

MOL1c

A disclosed Toll receptor 9-like nucleic acid of 3034 nucleotides, MOL1c, is shown in Table 1E. The disclosed MOL1c open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 2-4, shown in bold in Table 1E. The encoded polypeptide is alternatively referred to herein as MOL1c or as 248587042. The disclosed MOL1c ORF terminates at a GAG codon at nucleotides 3032-3034. As shown in Table

1E the start and stop codons are in bold letters. Because MOL1c does not start or stop at traditional initiation and termination codons, MOL1c could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1E. MOL1c nucleotide sequence (SEQ ID NO:116).
TGGATCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGTTCC TGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCAC CACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCGGTTGGCCT CAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACC TGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTG ATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCC CTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACA ACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCG CCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAA CCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGG TGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGT GAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTT CAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGG ACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTG CGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTC GGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGC CTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACC TTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCT GAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCC ACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGC CAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGC CCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCAC TGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCC CAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAA TTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGA AGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTG GCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTC CTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCT TTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCCGCCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTC CAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTCGCT GCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTTCCACCTGT GCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTC GACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGAGTGCCGTGGGCGCTGGGC ACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAGAACCTGTGGGCCTCGGTCTATGGCA GCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGCAG CGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCCCTGACGGCCGCCGCTCCCGCTACGTGCGGCT GCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGG GCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAACTTCTGCCAGGGACCCACGGCCGAACTCGAG

A disclosed encoded MOL1c protein has 1011amino acid residues, referred to as the MOL1c protein. The disclosed MOL1c polypeptide sequence is presented in Table 1F using the one-letter amino acid code.

Table 1F. Encoded MOL1c protein sequence (SEQ ID NO:117).
GSLGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPP VGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGN CYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGN CRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAFQ GLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQL GIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLV

TVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQ
GVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNR
LHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFV
APGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGPPSRVKCGSP
GQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSGRDEDALPY
DAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLL
RASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRN
FCQGPTAELE*

MOL1d

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1d, is shown in Table 1G. The disclosed MOL1d open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1G. The encoded polypeptide is alternatively referred to herein as MOL1d or as 248651580. The disclosed MOL1d ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1G the start and stop codons are in bold letters. Because MOL1d does not start or stop at traditional initiation and termination codons, MOL1d could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1G. MOL1d nucleotide sequence (SEQ ID NO:118).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC
CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT
TCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC
ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC
GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGG
AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC
CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA
CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC
ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC
TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA
TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT
TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT
GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA
GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG
CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC
ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT
CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA
CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC
ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT
GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG
CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCTGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC
CACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA
GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC
ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG
TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG
CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC
TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAG
GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT
GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC
ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGG
GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCC
GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT
TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG
TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA
CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG

AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG
AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT
GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC
CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG
CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA
CTTCTGCCAGGGACCCACGGCCGAACTCGAG

A disclosed encoded MOL1d protein has 1037 amino acid residues, referred to as the MOL1d protein. The disclosed MOL1d polypeptide sequence is presented in Table 1H using the one-letter amino acid code.

Table 1H. Encoded MOL1d protein sequence (SEQ ID NO:119).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR
IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLS
HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS
YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR
GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET
TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD
TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTCLQVLDLSHNKLDLY
HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM
WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK
ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACG
AAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW
YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE
NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ
PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

MOL1e

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1e, is shown in Table 1I. The disclosed MOL1e open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1G. The encoded polypeptide is alternatively referred to herein as MOL1e or as 255304731. The disclosed MOL1e ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1I the start and stop codons are in bold letters. Because MOL1e does not start or stop at traditional initiation and termination codons, MOL1e could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1I. MOL1e nucleotide sequence (SEQ ID NO:120).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC
CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT
TCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC
ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC
GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGG
AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC
CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA
CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC
ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC
TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA
TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT
TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT

GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC CACGAGCACTCATTCACGGAGCTACCGCGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAATCAGCTGAAG GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGG GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCC GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA CTTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement of MOL1e is shown below in Table 1J.

Table 1J. MOL1e nucleotide sequence (SEQ ID NO:121).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCAGACCGGGCACGGCAGCCT GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG CTCCTTGGCCTTGGAAAAGAAGCCGGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGATTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGACGCAGCACCTGTAGGCTCTTGGGGAGGTT GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGGTTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG AGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA GTCGCGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGGAAGTGACGAGGGCACTCCATGCA GGGGTTGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC

ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT GCCATGGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG TAGGAAGGCAGGCAAGGTACCCAGGGCCAGGGTCATGGCCAGCATGATGGCCTGCACCAGGAGAGACAGCGGGTGCA GGGCGCTGCGGCAGAAACCCATGGTGGATCC

A disclosed encoded MOL1e protein has 1037 amino acid residues, referred to as the MOL1e protein. The disclosed MOL1e polypeptide sequence is presented in Table 1K using the one-letter amino acid code.

Table 1K. Encoded MOL1e protein sequence (SEQ ID NO:122).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLS HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLY HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACG AAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

MOL1f

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1f, is shown in Table 1L. The disclosed MOL1f open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1G. The encoded polypeptide is alternatively referred to herein as MOL1f or as 255304783. The disclosed MOL1f ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1L the start and stop codons are in bold letters. Because MOL1f does not start or stop at traditional initiation and termination codons, MOL1f could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1L. MOL1f nucleotide sequence (SEQ ID NO:123).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT TCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCATCCTGG AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC

TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC CACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAG GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCCACCCTCTGCACTGCGCCTGTGGG GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCCGCCCAGCCGGGTGAAGTGTGGCAGTCC GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA CTTCTGCCAGGGACCCACGGCCGAACTCGAG

A disclosed encoded MOL1f protein has 1037 amino acid residues, referred to as the MOL1f protein. The disclosed MOL1f polypeptide sequence is presented in Table 1M using the one-letter amino acid code.

Table 1M. Encoded MOL1f protein sequence (SEQ ID NO:124).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPILEELNLSYNNIMTVPALPKSLISLSLS HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLY HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSAHPLHCACG AAFMDFLLEVQAAVPGPPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

MOL1g

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1g, is shown in Table 1N. The disclosed MOL1g open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1G. The encoded polypeptide is alternatively referred to herein as MOL1g or as 255341675. The disclosed MOL1g ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1N the start and stop codons are in bold letters. Because MOL1g does not start or stop at traditional initiation and termination codons, MOL1g could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1N. MOL1g nucleotide sequence (SEQ ID NO:125).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC
CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT
TCCTGAAGTCTGTGCCCCACTTCTCTATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC
ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC
GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGG
AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC
CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA
CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC
ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC
TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA
TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT
TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT
GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA
GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG
CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC
ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT
CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA
CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC
ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT
GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG
CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC
CACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA
GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC
ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG
TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG
CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC
TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAG
GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT
GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC
ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGG
GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCCGCCCAGCCGGGTGAAGTGTGGCAGTCC
GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT
TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG
TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA
CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG
AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG
AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT
GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC
CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG
CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA
CTTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement of MOL1g is shown below in Table 1O.

Table 1O. MOL1g nucleotide sequence (SEQ ID NO:126).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA
GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC
AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG
GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT
TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC
AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT
CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG

```
GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG
CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG
TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCGGACCGGGCACGGCAGCCT
GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC
AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG
CTCCTTGGCCTTGGAAAAGAAGCCGGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG
TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGGTTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG
AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGACGCAGCACCTGTAGGCTCTTGGGGAGGTT
GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGGTTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA
AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC
GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG
AGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA
GTCGTGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG
GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA
GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC
AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC
TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA
GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA
GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC
TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA
CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC
TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC
ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGAAGTGACGAGGGCACTCCATGCA
GGGGTTGGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT
CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC
ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG
TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC
TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC
ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG
GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT
GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT
GCCATAGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG
TAGGAAGGCAGGCAAGGTACCCAGGGCCAGGGTCATGGCCAGCATGATGGCCTGCACCAGGAGAGACAGCGGGTGCA
GGGCGCTGCGGCAGAAACCCATGGTGGATCC
```

A disclosed encoded MOL1g protein has 1037 amino acid residues, referred to as the MOL1g protein. The disclosed MOL1g polypeptide sequence is presented in Table 1P using the one-letter amino acid code.

Table 1P. Encoded MOL1g protein sequence (SEQ ID NO:127).

```
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR
IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLS
HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS
YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR
GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET
TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD
TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLY
HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM
WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK
ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACG
AAFMDFLLEVQAAVPGPPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW
YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE
NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ
PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE
```

MOL1h

A disclosed Toll receptor 9-like nucleic acid of 2145 nucleotides, MOL1h, is shown in Table 1Q. The disclosed MOL1h open reading frame ("ORF") begins at the

GGA initiation codon at nucleotides 1-3, shown in bold in Table 1Q. The encoded polypeptide is alternatively referred to herein as MOL1h or as 248210503. The disclosed MOL1h ORF terminates at a GAG codon at nucleotides 2143-2145. As shown in Table 1Q the start and stop codons are in bold letters. Because MOL1h does not start or stop at traditional initiation and termination codons, MOL1h could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1Q. MOL1h nucleotide sequence (SEQ ID NO:128).
GGATCCAATGTCACCAGCCTTTTCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCC
CAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGA
CCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTG
CCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGC
CGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGG
TGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCC
CGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGC
CAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGG
AGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAG
GACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAA
CTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCA
ATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTG
GACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGAC
TCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGG
ACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTC
TGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACC
TGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTG
CAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGC
CCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGC
GCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG
CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGG
CCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCC
CCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCC
AAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCT
CCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAG
AGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATA
CTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTCGAG

A disclosed encoded MOL1h protein has 715 amino acid residues, referred to as the MOL1h protein. The disclosed MOL1h polypeptide sequence is presented in Table 1R using the one-letter amino acid code.

Table 1R. Encoded MOL1h protein sequence (SEQ ID NO:129).
GSNVTSLFLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTV
PALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVP
RNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLK
DSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKEL
DMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKV
WLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGL
QVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLP
KLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQI
LDVSANPLHCACGAAFMDFLLE

MOL1i

A disclosed Toll receptor 9-like nucleic acid of 2145 nucleotides, MOL1i, is shown in Table 1S. The disclosed MOL1i open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1S. The encoded polypeptide is alternatively referred to herein as MOL1i or as 248210481. The disclosed MOL1i ORF terminates at a GAG codon at nucleotides 2143-2145. As shown in Table 1S the start and stop codons are in bold letters. Because MOL1i does not start or stop at traditional initiation and termination codons, MOL1i could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1S. MOL1i nucleotide sequence (SEQ ID NO:130).
GGATCCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCC CAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGA CCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTG CCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGC CGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGG TGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCC CGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGC CAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGG AGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAG GACAGTTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAA CTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCA ATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTG GACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGAC TCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGG ACCTGTCGGACAACCACATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTC TGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC CCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACC TGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTG CAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGC CCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGC GCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGG CCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCC CCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCC AAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCT CCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAG AGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATA CTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTCGAG

A disclosed encoded MOL1i protein has 715 amino acid residues, referred to as the MOL1i protein. The disclosed MOL1i polypeptide sequence is presented in Table 1T using the one-letter amino acid code.

Table 1T. Encoded MOL1i protein sequence (SEQ ID NO:131).
GSNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTV PALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVP RNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLK DSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKEL DMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNHISGASELTATMGEADGGEKV

WLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGL QVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSL RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLP KLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQI LDVSANPLHCACGAAFMDFLLE

MOL1j

A disclosed Toll receptor 9-like nucleic acid of 2145 nucleotides, MOL1j, is shown in Table 1U. The disclosed MOL1j open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1U. The encoded polypeptide is alternatively referred to herein as MOL1j or as 248210473. The disclosed MOL1j ORF terminates at a GAG codon at nucleotides 2143-2145. As shown in Table 1U the start and stop codons are in bold letters. Because MOL1j does not start or stop at traditional initiation and termination codons, MOL1j could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1U. MOL1j nucleotide sequence (SEQ ID NO:132).
GGATCCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCC CAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGA CCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTG CCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGC CGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGG TGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCC CGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGC CAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGG AGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAG GACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAA CTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCA ATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTG GACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGAC TCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGG ACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTC TGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC CCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACC TGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTG CAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGC CCTGGACCTCAACTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGC GCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGG CCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCC CCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCC AAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCT CCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAG AGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATA CTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTCGAG

A disclosed encoded MOL1j protein has 715 amino acid residues, referred to as the MOL1j protein. The disclosed MOL1j polypeptide sequence is presented in Table 1V using the one-letter amino acid code.

Table 1V. Encoded MOL1j protein sequence (SEQ ID NO:133).
GSNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTV
PALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVP
RNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLK
DSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKEL
DMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKV
WLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGL
QVLDLSHNKLDLYHEHSFTELPRLEALDLNYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLP
KLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQI
LDVSANPLHCACGAAFMDFLLE

MOL1k

A disclosed Toll receptor 9-like nucleic acid of 2145 nucleotides, MOL1k, is shown in Table 1W. The disclosed MOL1k open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1W. The encoded polypeptide is alternatively referred to herein as MOL1k or as 248210474. The disclosed MOL1k ORF terminates at a GAG codon at nucleotides 2143-2145. As shown in Table 1W the start and stop codons are in bold letters. Because MOL1k does not start or stop at traditional initiation and termination codons, MOL1k could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1W. MOL1k nucleotide sequence (SEQ ID NO:134).
GGATCCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCC
CAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGA
CCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTG
CCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGC
CGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGG
TGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCC
CGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGC
CAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGG
AGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAG
GACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAA
CTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCA
ATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTG
GACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGAC
TCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGG
ACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTC
TGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACC
TGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTG
CAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGC
CCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGC
GCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG
CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGG
CCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCC
CCAAGAGCCTACAGGTGCTGCGTCTCCGTAACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCC
AAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCT
CCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAG
AGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATA
CTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTCGAG

A disclosed encoded MOL1k protein has 715 amino acid residues, referred to as the MOL1k protein. The disclosed MOL1k polypeptide sequence is presented in Table 1X using the one-letter amino acid code.

Table 1X. Encoded MOL1k protein sequence (SEQ ID NO:135).
GSNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTV
PALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVP
RNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLK
DSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKEL
DMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKV
WLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGL
QVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRNNYLAFFKWWSLHFLP
KLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQI
LDVSANPLHCACGAAFMDFLLE

MOL1l

A disclosed Toll receptor 9-like nucleic acid of 2145 nucleotides, MOL1l, is shown in Table 1Y. The disclosed MOL1l open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1Y. The encoded polypeptide is alternatively referred to herein as MOL1l or as 246484229. The disclosed MOL1l ORF terminates at a GAG codon at nucleotides 2143-2145. As shown in Table 1Y the start and stop codons are in bold letters. Because MOL1l does not start or stop at traditional initiation and termination codons, MOL1l could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1Y. MOL1l nucleotide sequence (SEQ ID NO:136).
GGATCCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCC
CAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGA
CCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTG
CCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGC
CGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGG
TGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCC
CGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGC
CAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGG
AGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAG
GACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAA
CTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCA
ATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTG
GACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGAC
TCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGG
ACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTC
TGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACC
TGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTG
CAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGC
CCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGC
GCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG
CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGG
CCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCC
CCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAACTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCC

AAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCT CCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAG AGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATA CTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTCGAG

A disclosed encoded MOL1l protein has 715 amino acid residues, referred to as the MOL1l protein. The disclosed MOL1l polypeptide sequence is presented in Table 1Z using the one-letter amino acid code.

MOL1m

A disclosed Toll receptor 9-like nucleic acid of 3033 nucleotides, MOL1m, is shown in Table 1AAA. The disclosed MOL1m open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAA. The encoded polypeptide is alternatively referred to herein as MOL1m or as 258065840. The disclosed MOL1m ORF terminates at a GAG codon at nucleotides 3031-3033. As shown in Table 1AAA the start and stop codons are in bold letters. Because MOL1m does not start or stop at traditional initiation and termination codons, MOL1m could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAA. MOL1m nucleotide sequence (SEQ ID NO:158).
GGATCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGTT CCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCA TCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCG GTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGGA AGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGCC ATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAAC TGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCCA CCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCCT ACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAAT TGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTT CAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGTG GGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCAG GGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGC CCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACCA CGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCTC GGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGAC AGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACA CTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGTG ACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGGC AGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTACC ACGAGCACTCATTCACGGAGCTACCGCGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAG GGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCCA CAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGT GGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGC CTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCT GGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAGG CCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTG GCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCA CTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGGG CGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCCG GGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTT

CGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGT ACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTAC GATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGA GGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAGA ACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTTG CGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCCC TGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGC CCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAAC TTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement of MOL1m is shown in Table 1AAB.

Table 1AAB. MOL1m reverse complement nucleotide sequence (SEQ ID NO:178).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCAGACCGGGCACGGCAGCCT GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG CTCCTTGGCCTTGGAAAAGAAGCCGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGGTTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGACGCAGCACCTGTAGGCTCTTGGGGAGGTT GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGGTTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG AGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA GTCGCGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGGAAGTGACGAGGGCACTCCATGCA GGGGTTGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT GCCATGGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG TAGGAAGGCAGGCAAGGTACCCAGGATCC

A disclosed encoded MOL1m protein has 1011 amino acid residues, referred to as the MOL1m protein. The disclosed MOL1m polypeptide sequence is presented in Table 1AAC using the one-letter amino acid code.

Table 1AAC. Encoded MOL1m protein sequence (SEQ ID NO:159).
GSLGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPP VGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDGN CYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGN CRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAFQ GLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQL GIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNLV TVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQ GVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNR LHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFV APGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRVKCGSP GQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSGRDEDALPY DAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLL RASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRN FCQGPTAELE

MOL1n

A disclosed Toll receptor 9-like nucleic acid of 2389 nucleotides, MOL1n, is shown in Table 1AAD. The disclosed MOL1n open reading frame ("ORF") begins at the AAC initiation codon at nucleotides 2-4, shown in bold in Table 1AAD. The encoded polypeptide is alternatively referred to herein as MOL1n or as 263483006. The disclosed MOL1n ORF terminates at a GGC codon at nucleotides 2387-2389. As shown in Table 1AAD the start and stop codons are in bold letters. Because MOL1n does not start or stop at traditional initiation and termination codons, MOL1n could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAD. MOL1n nucleotide sequence (SEQ ID NO:160).
CACCGGATCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGG CTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCA ACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTG CCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCC ACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGT CCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCAT GGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGC AACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATC TGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGA TGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTA CATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATG CCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAA AACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTT GCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCC GCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTT CATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATC AGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGACC TTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGA TCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTG AGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGT CCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTA CAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCAC CTCAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACT TCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTT GATCTGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTA CAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAG

TCCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCT
GGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAAC
CTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATG
TAAGCGCCAACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCC
CGGTCCGCCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGC
CTCTGCCTGGATGAGGCCCTCTCCCTCGAGGGC

A disclosed encoded MOL1n protein has 796 amino acid residues, referred to as the MOL1n protein. The disclosed MOL1n polypeptide sequence is presented in Table 1AAE using the one-letter amino acid code.

Table 1AAE. Encoded MOL1n protein sequence (SEQ ID NO:161).
TGSLGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCP
PVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFLFMDG
NCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGG
NCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKCITKTKAF
QGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQ
LGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLSRNNL
VTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQPFGM
QGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQN
RLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISF
VAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGPPSRVKCGS
PGQLQGLSIFAQDLRLCLDEALSLEG

MOL1o

A disclosed Toll receptor 9-like nucleic acid of 3049 nucleotides, MOL1o, is shown in Table 1AAF. The disclosed MOL1o open reading frame ("ORF") begins at the ATG initiation codon at nucleotides 1-3, shown in bold in Table 1AAF. The encoded polypeptide is alternatively referred to herein as MOL1o or as CG54674-01. The disclosed MOL1o ORF terminates at a TAG codon at nucleotides 3043-3045. As shown in Table 1AAF the start and stop codons are in bold letters. Because MOL1o does not stop at a traditional termination codon, MOL1o could be a partial open reading frame which extends further in the 3' direction.

Table 1AAF. MOL1o nucleotide sequence (SEQ ID NO:162).
ATGCTGGCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAA
CTGCAACTGGCTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCT
TGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAG
TGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGC
TGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATAT
CCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTA
TTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCT
GGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGT
ATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTC
GATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCT
ACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATG
CCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAA
ACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGC
CCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCT
CACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATC

AACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGG AGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTC CGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCA CGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAA CTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATA AGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAG CCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGC CCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATG CACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGAC TTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCT CCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAG GAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAAC AGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCT CAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGC ACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTG AAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCT CTCCTGGGACTGTTTCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTG GCTGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAG GATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCT TCGGGGGCAGCTGGAGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCA AAACCCTCTTTGAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGG GTCAGTGGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCT GGTGATCCTGAGCCCTGACGGCCGCCGCTCCCGCTATGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCC TCTGGCCCCACCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCAC TTCTATAACCGGAACTTCTGCCAGGGACCCACGGCCGAATAGACTG

A disclosed encoded MOL1o protein has 1014 amino acid residues, referred to as the MOL1o protein. The disclosed MOL1o polypeptide sequence is presented in Table 1AAG using the one-letter amino acid code.

Table 1AAG. Encoded MOL1o protein sequence (SEQ ID NO:163).
MLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLK WNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHALRFL FMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVL DVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKCITK TKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFI NQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSYNSQ PFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLD LSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCN SISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLPSRV KCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSGRDE DALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDR VSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHH FYNRNFCQGPTAE

MOL1p

A disclosed Toll receptor 9-like nucleic acid of 3057 nucleotides, MOL1p, is shown in Table 1AAH. The disclosed MOL1p open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAH. The encoded polypeptide is alternatively referred to herein as MOL1p or as 263676346. The disclosed MOL1p ORF terminates at a GAG codon at nucleotides 3055-3057. As shown in Table 1AAH the start and stop codons are in bold letters. Because MOL1p does not start or stop at traditional initiation and termination codons, MOL1p could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAH. MOL1p nucleotide sequence (SEQ ID NO:164).
GGATCCACCATGCTGGCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGG
CCTGGTGAACTGCAACTGGCTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCA
GCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTC
AACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCAC
CTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAAT
CCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTG
CGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCT
CCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCA
GCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTG
CGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
CCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCT
GGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGC
ATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGT
GTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCT
TCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATG
AACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCG
CATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGG
ACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTG
GATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCT
GAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGT
CCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTAC
AACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCCCACCTGCGCACCCTGCGCCACCT
CAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCA
GCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATC
TGGCTGGACTTGTCCCAGAATCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGT
GCTGCATCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCG
ACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTC
AGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGC
CAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCA
ACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCC
AGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGA
TGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATC
ACCTCTGTGGCTGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGG
CGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTA
CAACGAGCTTCGGGGGCAGCTGGAGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGC
TGCCTGGCAAAACCCTCTTTGAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCAC
ACGGACCGGGTCAGTGGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGT
CGTGGTGCTGGTGATCCTGAGCCCTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGA
GTGTCCTCCTCTGGCCCCACCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGAC
AACCACCACTTCTATAACCGGAACTTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement to MOL1p is shown in Table 1AAI.

Table 1AAI. MOL1p reverse complement nucleotide sequence (SEQ ID NO:179).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA
GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC
AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG
GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT
TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC
AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT
CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG
GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG
CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG
TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCAGACCGGGCACGGCAGCCT
GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC
AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG
CTCCTTGGCCTTGGAAAAGAAGCCGGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG
TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGGTTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG

AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGATGCAGCACCTGTAGGCTCTTGGGGAGGTT GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGATTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG GGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA GTCGTGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGGAAGTGACGAGGGCACTCCATGCA GGGGTTGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT GCCATGGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG TAGGAAGGCAGGCAAGGTACCCAGGGCCAGGTCATGGCCAGCATGGTGGATCC

A disclosed encoded MOL1p protein has 1019 amino acid residues, referred to as the MOL1p protein. The disclosed MOL1p polypeptide sequence is presented in Table 1AAJ using the one-letter amino acid code.

Table 1AAJ. Encoded MOL1p protein sequence (SEQ ID NO:165).
GSTMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHL NLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHAL RFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTAL RVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKC ITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQM NFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTL DLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSY NSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLI WLDLSQNRLHTLLPQTLRNLPKSLQVLHLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDV SCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLP SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSG RDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAH TDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRD NHHFYNRNFCQGPTAELE

MOL1q

A disclosed Toll receptor 9-like nucleic acid of 3057 nucleotides, MOL1q, is shown in Table 1AAK. The disclosed MOL1q open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAK. The encoded polypeptide is alternatively referred to herein as MOL1q or as 264289162. The disclosed MOL1q ORF terminates at a GAG codon at nucleotides 3055-3057. As shown in Table 1AAK the start and stop codons are in bold letters. Because MOL1q does not start or stop at traditional initiation and termination codons, MOL1q could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAK. MOL1q nucleotide sequence (SEQ ID NO:166).
GGATCCACCATGCTGGCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGG
CCTGGTGAACTGCAACTGGCTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCA
GCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTC
AACCTCAAGTGGAACTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCAC
CTTCTTGGCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAAT
CCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTG
CGCTTCCTATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCT
CCTTGGCCTGGGCAACCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCA
GCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTG
CGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
CCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCT
GGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGC
ATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGT
GTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCT
TCTTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATG
AACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCG
CATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGG
ACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTG
GATCTGTCACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCT
GAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGT
CCCACAATAAGCTGGACCTCTACCACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTAC
AACAGCCAGCCCTTTGGCATGCAGGGCGTGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCT
CAGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCA
GCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATC
TGGCTGGACTTGTCCCAGAACCGCCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGT
GCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCG
ACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTC
AGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGC
CAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCA
ACCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCC
AGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGA
TGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATC
ACCTCTGTGGCTGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGG
CGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTA
CAACGAGCTTCGGGGGCAGCTGGAGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGC
TGCCTGGCAAAACCCTCTTTGAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCAC
ACGGACCGGGTCAGTGGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGT
CGTGGTGCTGGTGATCCTGAGCCCTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGA
GTGTCCTCCTCTGGCCCCACCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGAC
AACCACCACTTCTATAACCGGAACTTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement to MOL1q is shown in Table 1AAL.

Table 1AAL. MOL1q reverse complement nucleotide sequence (SEQ ID NO:180).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA
GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC
AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG
GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT
TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC
AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT
CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG
GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG
CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG
TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCAGACCGGGCACGGCAGCCT
GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC
AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG
CTCCTTGGCCTTGGAAAAGAAGCCGGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG
TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGGTTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG

AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGACGCAGCACCTGTAGGCTCTTGGGGAGGTT
GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGGTTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA
AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC
GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG
AGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA
GTCGTGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG
GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA
GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC
AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC
TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA
GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA
GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC
TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA
CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC
TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC
ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGGAAGTGACGAGGGCACTCCATGCA
GGGGTTGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT
CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC
ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG
TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC
TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC
ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG
GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT
GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT
GCCATGGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG
TAGGAAGGCAGGCAAGGTACCCAGGGCCAGGGTCATGGCCAGCATGGTGGATCC

A disclosed encoded MOL1q protein has 1019 amino acid residues, referred to as the MOL1q protein. The disclosed MOL1q polypeptide sequence is presented in Table 1AAM using the one-letter amino acid code.

Table 1AAM. Encoded MOL1q protein sequence (SEQ ID NO:167).
GSTMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHL
NLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNILMLDSASLAGLHAL
RFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTAL
RVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFRGLGNLRVLDLSENFLYKC
ITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQM
NFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTL
DLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHSFTELPRLEALDLSY
NSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMWAEGDLYLHFFQGLSGLI
WLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDV
SCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAAVPGLP
SRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPWRGRQSG
RDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAH
TDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRD
NHHFYNRNFCQGPTAELE

MOL1r

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1r, is shown in Table 1AAN. The disclosed MOL1r open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAN. The encoded polypeptide is alternatively referred to herein as MOL1r or as 248651580. The disclosed MOL1r ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1AAN the start and stop codons are in bold letters. Because MOL1r does not start or stop at traditional initiation or termination codons, MOL1r could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAN. MOL1r nucleotide sequence (SEQ ID NO:168).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT TCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGG AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCTGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC CACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAG GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGG GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCC GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA CTTCTGCCAGGGACCCACGGCCGAACTCGAG

A disclosed encoded MOL1r protein has 1037 amino acid residues, referred to as the MOL1r protein. The disclosed MOL1r polypeptide sequence is presented in Table 1AAO using the one-letter amino acid code.

Table 1AAO. Encoded MOL1r protein sequence (SEQ ID NO:169).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLS HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTCLQVLDLSHNKLDLY

HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM
WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK
ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACG
AAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW
YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE
NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ
PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

MOL1s

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1s, is shown in Table 1AAP. The disclosed MOL1s open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAP. The encoded polypeptide is alternatively referred to herein as MOL1s or as 255304731. The disclosed MOL1s ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1AAP the start and stop codons are in bold letters. Because MOL1s does not start or stop at traditional initiation or termination codons, MOL1s could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAP. MOL1s nucleotide sequence (SEQ ID NO:170).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC
CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT
TCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC
ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC
GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGG
AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC
CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA
CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC
ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC
TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA
TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT
TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT
GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA
GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG
CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC
ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT
CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA
CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC
ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT
GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG
CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC
CACGAGCACTCATTCACGGAGCTACCGCGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA
GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC
ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG
TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG
CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC
TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAATCAGCTGAAG
GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT
GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC
ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGG
GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCC
GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT
TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG
TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA
CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG
AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG
AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT
GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC

CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG
CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA
CTTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement of MOL1s is shown in Table 1AAQ.

Table 1AAQ. MOL1s reverse complement nucleotide sequence (SEQ ID NO:181).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA
GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC
AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG
GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT
TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC
AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT
CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG
GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG
CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG
TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCAGACCGGGCACGGCAGCCT
GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC
AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG
CTCCTTGGCCTTGGAAAAGAAGCCGGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG
TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGATTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG
AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGACGCAGCACCTGTAGGCTCTTGGGGAGGTT
GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGGTTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA
AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC
GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG
AGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA
GTCGCGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG
GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA
GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC
AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC
TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA
GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA
GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC
TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA
CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC
TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC
ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGGAAGTGACGAGGGCACTCCATGCA
GGGGTTGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT
CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC
ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG
TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC
TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC
ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG
GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT
GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT
GCCATGGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG
TAGGAAGGCAGGCAAGGTACCCAGGGCCAGGGTCATGGCCAGCATGATGGCCTGCACCAGGAGAGACAGCGGGTGCA
GGGCGCTGCGGCAGAAACCCATGGTGGATCC

A disclosed encoded MOL1s protein has 1037 amino acid residues, referred to as the MOL1s protein. The disclosed MOL1s polypeptide sequence is presented in Table 1AAR using the one-letter amino acid code.

Table 1AAR. Encoded MOL1s protein sequence (SEQ ID NO:171).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR
IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLS
HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS
YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR

GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET
TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD
TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLY
HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM
WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK
ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACG
AAFMDFLLEVQAAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW
YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE
NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ
PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

MOL1t

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1t, is shown in Table 1AAS. The disclosed MOL1t open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAS. The encoded polypeptide is alternatively referred to herein as MOL1t or as 255304783. The disclosed MOL1t ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1AAS the start and stop codons are in bold letters. Because MOL1t does not start or stop at traditional initiation or termination codons, MOL1t could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAS. MOL1t nucleotide sequence (SEQ ID NO:172).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC
CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT
TCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC
ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC
GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCATCCTGG
AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC
CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA
CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC
ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC
TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA
TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT
TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT
GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA
GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG
CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC
ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT
CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA
CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC
ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT
GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG
CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC
CACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA
GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC
ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG
TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG
CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC
TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAG
GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT
GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC
ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCCACCCTCTGCACTGCGCCTGTGGG
GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCCGCCCAGCCGGGTGAAGTGTGGCAGTCC
GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT
TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG
TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA
CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG

AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA CTTCTGCCAGGGACCCACGGCCGAACTCGAG

A disclosed encoded MOL1t protein has 1037 amino acid residues, referred to as the MOL1t protein. The disclosed MOL1t polypeptide sequence is presented in Table 1AAT using the one-letter amino acid code.

Table 1AAT. Encoded MOL1t protein sequence (SEQ ID NO:173).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPILEELNLSYNNIMTVPALPKSLISLSLS HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLY HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSAHPLHCACG AAFMDFLLEVQAAVPGPPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

MOL1u

A disclosed Toll receptor 9-like nucleic acid of 3111 nucleotides, MOL1u, is shown in Table 1AAU. The disclosed MOL1u open reading frame ("ORF") begins at the GGA initiation codon at nucleotides 1-3, shown in bold in Table 1AAU. The encoded polypeptide is alternatively referred to herein as MOL1u or as 255341675. The disclosed MOL1u ORF terminates at a GAG codon at nucleotides 3109-3111. As shown in Table 1AAU the start and stop codons are in bold letters. Because MOL1u does not start or stop at traditional initiation or termination codons, MOL1u could be a partial open reading frame which extends further in the 5' and/or 3' directions.

Table 1AAU. MOL1u nucleotide sequence (SEQ ID NO:174).
GGATCCACCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCATGAC CCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAACTGCAACTGGCTGT TCCTGAAGTCTGTGCCCCACTTCTCTATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGC ATCCACCACCTCCATGATTCTGACTTTGCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCC GGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGTGCCCACCCTGG AAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATCCCTGTCCCTCAGC CATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAA CTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAACCTCACCC ACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCCAGCCTGGAGTATCTGCTGTTGTCC TACAACCGCATCGTCAAACTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAA TTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCT TCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAATGCCAGTTGGTTCCGT

GGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTCTACAAATGCATCACTAAAACCAAGGCCTTCCA
GGGCCTAACACAGCTGCGCAAGCTTAACCTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGG
CCCCTTCCTTCGGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGATGAGACC
ACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATGAACTTCATCAACCAGGCCCAGCT
CGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGA
CAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGAC
ACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCACGGAACAACCTGGT
GACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGCCTGCGCCTGAGCCACAACTGCATCTCGCAGG
CAGTCAATGGCTCCCAGTTCCTGCCGCTGACCGGTCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTCTAC
CACGAGCACTCATTCACGGAGCTACCACGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCA
GGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTCAGCCTGGCCCACAACAACATCC
ACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATG
TGGGCCGAGGGAGACCTCTATCTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCG
CCTGCACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACC
TGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAAGTCCTCGACCTGGCAGGAAACCAGCTGAAG
GCCCTGACCAATGGCAGCCTGCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGT
GGCCCCCGGCTTCTTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACC
ACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCTCTGCACTGCGCCTGTGGG
GCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCCGCCCAGCCGGGTGAAGTGTGGCAGTCC
GGGCCAGCTCCAGGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTT
TCGCCCTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGG
TACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTA
CGATGCCTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGG
AGGAGTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTTGAG
AACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACGGACCGGGTCAGTGGTCTCTT
GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCC
CTGACGGCCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAG
CCCAGTGGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAACCGGAA
CTTCTGCCAGGGACCCACGGCCGAACTCGAG

The reverse complement of MOL1u is shown in Table 1AAV.

Table 1AAV. MOL1u reverse complement nucleotide sequence (SEQ ID NO:182).
CTCGAGTTCGGCCGTGGGTCCCTGGCAGAAGTTCCGGTTATAGAAGTGGTGGTTGTCCCTGGTCAGGGCCATGCCCA
GCTGGGCCCAGAAGCTGCGCTGACCACTGGGCTGGTGGGGCCAGAGGAGGACACTCTGGCGGCAGAGGCGCTGGCGC
AGCCGCACGTAGCGGGAGCGGCGGCCGTCAGGGCTCAGGATCACCAGCACCACGACGTCCTTGCGGTCCTCCAGCAG
GCGCTGCTGGGCCAGCAGGAAGCTGGCGCGCAAGAGACCACTGACCCGGTCCGTGTGGGCCAGCACAAACAGCGTCT
TGCGGCTGCCATAGACCGAGGCCCACAGGTTCTCAAAGAGGGTTTTGCCAGGCAGCCAGTCGCGTTCCTCCAGGCAC
AGGCGGAGTGCCCAGCGCCCACGGCACTCCTCCAGCTGCCCCCGAAGCTCGTTGTACACCCAGTCTGCCACTGCGCT
CTGCGTTTTGTCGAAGACCACGAAGGCATCGTAGGGCAGGGCATCCTCATCTCGCCCACTTTGCCGCCCCCGCCAGG
GAAGCCAGGCCAGGCACAGGTGGAAGCAGTACCAGAGGTCCCAGCCACAGAGGTGATGCAGCATGGGCACACCCAGG
CCCAGAGCCACAGCCAGCAGCGAGAGGGCGAAACAGTCCCAGGAGAGGGCCTCATCCAGGCAGAGGCGCAGGTCCTG
TGCAAAGATGCTGAGGCCCTGGAGCTGGCCCGGACTGCCACACTTCACCCGGCTGGGCGGACCGGGCACGGCAGCCT
GCACCTCCAGCAGGAAGTCCATAAAGGCCGCCCCACAGGCGCAGTGCAGAGGGTTGGCGCTTACATCTAGTATTTGC
AGGGCACTCGCCAGGGGCCCAAACCAGGAGTGGTCCACTGTCTTGAGGGCGTTGGCGCTAAGGTTGAGCTCTCGCAG
CTCCTTGGCCTTGGAAAAGAAGCCGGGGGCCACGAAGCTGATGCTGTTGCAGCTGACATCCAGCCTCCGGAGCCGGG
TGCCAGCAGGCAGGCTGCCATTGGTCAGGGCCTTCAGCTGGTTTCCTGCCAGGTCGAGGACTTCCAGTTTGGGCAGG
AAGTGGAGGCTCCACCACTTAAAGAAGGCCAGGTAATTGTCACGGAGACGCAGCACCTGTAGGCTCTTGGGGAGGTT
GCGCAGGGTTTGGGGCAGGAGGGTGTGCAGGCGGTTCTGGGACAAGTCCAGCCAGATCAAACCGCTCAGGCCTTGGA
AGAAGTGCAGATAGAGGTCTCCCTCGGCCCACATATGGCCCAGTGCATTGCCGCTGAAGTCCAGGGCCCGCAGCGAC
GTACTGCAGAGCTGCTGGGACACTTGGCTGTGGATGTTGTTGTGGGCCAGGCTGAGGTGGCGCAGGGTGCGCAGGTG
AGCCACGAAGCTGAAGTTGTGGCCCACGCCCTGCATGCCAAAGGGCTGGCTGTTGTAGCTGAGGTCCAGGGCCTCCA
GTCGTGGTAGCTCCGTGAATGAGTGCTCGTGGTAGAGGTCCAGCTTATTGTGGGACAGGTCTAGCACCTGCAGACCG
GTCAGCGGCAGGAACTGGGAGCCATTGACTGCCTGCGAGATGCAGTTGTGGCTCAGGCGCAGGCACTGCAGGTGCGA
GAGCTGGGCAAACATCTCCGGCTGCACGGTCACCAGGTTGTTCCGTGACAGATCCAAGGTGAAGTTGAGGGTGCTGC
AGTTGGGCCTGAAGTCTTCAGAGCTGGGAGTGTCCACTGGGGCCGGAGCAAGGTCCCCAGGCTGCAGCCAGACCTTC
TCCCCTCCATCTGCCTCCCCCATGGTGGCTGTCAGCTCCGAAGCTCCGCTGATGCGGTTGTCCGACAGGTCCACGTA
GCGCAGGCCAGGGAAGGCCCTGAAGATGCCGAGCTGGGCCTGGTTGATGAAGTTCATCTGCAGACGCAGAGTCTGGA
GCATGGGCAGGCGGGCCAGTGGCCGGAGCGTGGTCTCATCGAGTGAGCGGAAGAAGATGCCGTGCATGTCCAGCTCC
TTCAGGGCGACCAGGCTCCCGAAGGAAGGGGCCAGAGACAGGTGGGCAAAGGACACCCTCTTTTGGTAATTGAAGGA
CAGGTTAAGCTTGCGCAGCTGTGTTAGGCCCTGGAAGGCCTTGGTTTTAGTGATGCATTTGTAGAGGAAGTTCTCAC
TCAGGTCCAGCACTCGGAGGTTTCCCAGCCCACGGAACCAACTGGCATTCAGCCAGGAGAGAGAACTGTCCTTCAAC
ACCAGGCCTTCAAGACGGCTCAGGTGGCTGAAGGTATCGGGATGTAGCTGGGGGAAGTGACGAGGGCACTCCATGCA

GGGGTTGGGAGCGTGGTCGCAGCGGCGGCAATTTCCGCCCACATCGAGCACACGCAGGGCGGTCAGATTGGCCAGGT
CCTCAGGCGCCAGTTTGACGATGCGGTTGTAGGACAACAGCAGATACTCCAGGCTGGAAGGCAGGTTGCGGGGCACC
ACAGTGAGGTTGTTGTACTTGAGTGACAGGTGGGTGAGGTTGCCCAGGCCAAGGAGGGCACCCGGGGCCACCTCCAG
TGCCTGCCTGCAGGGGTTCTTGTAATAACAGTTGCCGTCCATGAATAGGAAGCGCAGGGCATGCAGGCCGGCGAGGC
TGGCAGAGTCTAGCATCAGGATGTTGGTATGGCTGAGGGACAGGGATATGAGGGATTTGGGCAGCGCAGGCACAGTC
ATGATGTTGTTGTAGCTCAGGTTTAGCTCTTCCAGGGTGGGCACAGCCAAGAAGGTGCTGGGCTCGATGGTCATGTG
GCAGGGGAAGTGCATGGGGCTGAGGCCAACCGGCGGGCAGTTCCACTTGAGGTTGAGATGCCGCAGGCTGGGCAGGT
GGGCAAAGTCAGAATCATGGAGGTGGTGGATGCGGTTGGAGGACAAGGAAAGGCTGGTGACATTGCCACGGGGTGCT
GCCATAGAGAAGTGGGGCACAGACTTCAGGAACAGCCAGTTGCAGTTCACCAGGCCGTGGGGCTGGAGCTCACAGGG
TAGGAAGGCAGGCAAGGTACCCAGGGCCAGGGTCATGGCCAGCATGATGGCCTGCACCAGGAGAGACAGCGGGTGCA
GGGCGCTGCGGCAGAAACCCATGGTGGATCC

A disclosed encoded MOL1u protein has 1037 amino acid residues, referred to as the MOL1u protein. The disclosed MOL1u polypeptide sequence is presented in Table 1AAW using the one-letter amino acid code.

Table 1AAW. Encoded MOL1u protein sequence (SEQ ID NO:175).
GSTMGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMAAPRGNVTSLSLSSNR
IHHLHDSDFAHLPSLRHLNLKWNCPPVGLSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLS
HTNILMLDSASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNLPSSLEYLLLS
YNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLNASWFR
GLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSLAPSFGSLVALKELDMHGIFFRSLDET
TLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYVDLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVD
TPSSEDFRPNCSTLNFTLDLSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLY
HEHSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHM
WAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVLRLRDNYLAFFKWWSLHFLPKLEVLDLAGNQLK
ALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACG
AAFMDFLLEVQAAVPGPPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLW
YCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWLPGKTLFE
NLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQ
PSGQRSFWAQLGMALTRDNHHFYNRNFCQGPTAELE

The amino acid sequence of MOL1a also had high homology to other proteins as shown in table 1AA.

Table 1AA. BLAST results for MOL1a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
Patp:W86365	DNAX toll-like receptor DTLR-10 [Homo sapiens]	336	335/336 (99%)	335/336 (99%)	0.0
gi|8394456|ref|NP_059138.1|	toll-like receptor 9 [Homo sapiens]	1032	960/1014 (94%)	960/1014 (94%)	0.0
gi|13648665|ref|XP_003236.2|	toll-like receptor 9 [Homo sapiens]	1014	960/1014 (94%)	960/1014 (94%)	0.0
gi|8099654|gb|AAF72190.1|AF259263_1	toll-like receptor 9 form B [Homo sapiens]	975	921/975 (94%)	921/975 (94%)	0.0

gi|13507173|gb|AAK28488.1|AF314224_1	toll-like receptor 9 [Mus musculus]	1032	720/1015 (70%)	799/1015 (77%)	0.0

A ClustalW analysis comparing disclosed proteins of the invention with related OR protein sequences is given in Table 1BB, with MOL1a shown on line 1.

In the ClustalW alignment of the MOL1a protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (*i.e.*, regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be mutated to a much broader extent without altering protein structure or function. Residue differences between any MOLX variant sequences herein are written to show the residue in the "a" variant and the residue position with respect to the "a" variant. MOL residues in all following sequence alignments that differ between the individual MOL variants are highlighted with a box and marked with the (o) symbol above the variant residue in all alignments herein.

Table 1BB. ClustalW Analysis of MOL1a

1) Novel MOL1a (SEQ ID NO:2)
2) gi|8394456|ref|NP_059138.1| toll-like receptor 9 [Homo sapiens] (SEQ ID NO:31)
3) gi|13648665|ref|XP_003236.2| toll-like receptor 9 [Homo sapiens] (SEQ ID NO:32)
4) gi|8099654|gb|AAF72190.1|AF259263_1 toll-like receptor 9 form B [Homo sapiens] (SEQ ID NO:33)
5) gi|13507173|gb|AAK28488.1|AF314224_1 toll-like receptor 9 [Mus musculus] (SEQ ID NO:34)

```
                      10         20         30         40         50         60
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          ---------- --------ML AMTLALGTLP AFLPCELQPH GLVNCNWLFL KSVPHFSMAA  42
NP_059138.    MGFCRSALHP LSLLVQAIML AMTLALGTLP AFLPCELQPH GLVNCNWLFL KSVPHFSMAA  60
XP_003236.    ---------- --------ML AMTLALGTLP AFLPCELQPH GLVNCNWLFL KSVPHFSMAA  42
AF259263_1    ---------- ---------- ---------- ---------- ---------- -------MAA  3
AF314224_1    MVLRRRTLHP LSLLVQAAVL AETLALGTLP AFLPCELKPH GLVDCNWLFL KSVPRFSAAA  60

                      70         80         90        100        110        120
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          PRGNVTSLSL SSNRIHHLHD SDFAHLPSLR HLNLKWNCPP VGLSPMHFPC HMTIEPSTFL  102
NP_059138.    PRGNVTSLSL SSNRIHHLHD SDFAHLPSLR HLNLKWNCPP VGLSPMHFPC HMTIEPSTFL  120
XP_003236.    PRGNVTSLSL SSNRIHHLHD SDFAHLPSLR HLNLKWNCPP VGLSPMHFPC HMTIEPSTFL  102
AF259263_1    PRGNVTSLSL SSNRIHHLHD SDFAHLPSLR HLNLKWNCPP VGLSPMHFPC HMTIEPSTFL  63
AF314224_1    SCSNITRLSL ISNRIHHLHN SDFVHLSNLR QLNLKWNCPP TGLSPLHFSC HMTIEPRTFL  120

                     130        140        150        160        170        180
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          AVPTLEELNL SYNNIMTVPA LPKSLISLSL SHTNILMLDS ASLAGLHALR FLFMDGNCYY  162
NP_059138.    AVPTLEELNL SYNNIMTVPA LPKSLISLSL SHTNILMLDS ASLAGLHALR FLFMDGNCYY  180
XP_003236.    AVPTLEELNL SYNNIMTVPA LPKSLISLSL SHTNILMLDS ASLAGLHALR FLFMDGNCYY  162
AF259263_1    AVPTLEELNL SYNNIMTVPA LPKSLISLSL SHTNILMLDS ASLAGLHALR FLFMDGNCYY  123
AF314224_1    AMRTLEELNL SYNGITTVPR LPSSLVNLSL SHTNILVLDA NSLAGLYSLR VLFMDGNCYY  180

                     190        200        210        220        230        240
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          KNPCRQALEV APGALLGLGN LTHLSLKYNN LTVVPRNLPS SLEYLLLSYN RIVKLAPEDL  222
```

```
NP_059138.    KNPCRQALEV APGALLGLGN LTHLSLKYNN LTVVPRNLPS SLEYLLLSYN RIVKLAPEDL  240
XP_003236.    KNPCRQALEV APGALLGLGN LTHLSLKYNN LTVVPRNLPS SLEYLLLSYN RIVKLAPEDL  222
AF259263_1    KNPCRQALEV APGALLGLGN LTHLSLKYNN LTVVPRNLPS SLEYLLLSYN RIVKLAPEDL  183
AF314224_1    KNPCTGAVKV TPGALLGLSN LTHLSLKYNN LTKVPRQLPP SLEYLLVSYN LIVKLGPEDL  240

                     250        260        270        280        290        300
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          ANLTALRVLD VGGNCRRCDH APNPCMECPR HFPQLHPDTF SHLSRLEGLV LKDSSLSWLN  282
NP_059138.    ANLTALRVLD VGGNCRRCDH APNPCMECPR HFPQLHPDTF SHLSRLEGLV LKDSSLSWLN  300
XP_003236.    ANLTALRVLD VGGNCRRCDH APNPCMECPR HFPQLHPDTF SHLSRLEGLV LKDSSLSWLN  282
AF259263_1    ANLTALRVLD VGGNCRRCDH APNPCMECPR HFPQLHPDTF SHLSRLEGLV LKDSSLSWLN  243
AF314224_1    ANLTSLRVLD VGGNCRRCDH APNPCIECGQ KSLHLHPETF HHLSHLEGLV LKDSSLHTLN  300

                     310        320        330        340        350        360
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          ASWFRGLGNL RVLDLSENFL YKCITKTKAF QGLTQLRKLN LSFNYQKRVS FAHLSLAPSF  342
NP_059138.    ASWFRGLGNL RVLDLSENFL YKCITKTKAF QGLTQLRKLN LSFNYQKRVS FAHLSLAPSF  360
XP_003236.    ASWFRGLGNL RVLDLSENFL YKCITKTKAF QGLTQLRKLN LSFNYQKRVS FAHLSLAPSF  342
AF259263_1    ASWFRGLGNL RVLDLSENFL YKCITKTKAF QGLTQLRKLN LSFNYQKRVS FAHLSLAPSF  303
AF314224_1    SSWFQGLVNL SVLDLSENFL YESINHINAF QNLTRLRKLN LSFNYRKKVS FARLHLASSF  360

                     370        380        390        400        410        420
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          GSLVALKELD MHGIFFRSLD ETTLRPLARL PMLQTLRLQM NFINQAQLGI FRAFPGLRYV  402
NP_059138.    GSLVALKELD MHGIFFRSLD ETTLRPLARL PMLQTLRLQM NFINQAQLGI FRAFPGLRYV  420
XP_003236.    GSLVALKELD MHGIFFRSLD ETTLRPLARL PMLQTLRLQM NFINQAQLGI FRAFPGLRYV  402
AF259263_1    GSLVALKELD MHGIFFRSLD ETTLRPLARL PMLQTLRLQM NFINQAQLGI FRAFPGLRYV  363
AF314224_1    KNLVSLQELN MNGIFFRSLN KYTLRWLADL PKLHTLHLQM NFINQAQLSI FGTFRALRFV  420

                     430        440        450        460        470        480
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          DLSDNRISGA SELT-ATMGE ADGGEKVWLQ PGDLAPAPVD TPSSEDFRPN CSTLNFTLDL  461
NP_059138.    DLSDNRISGA SELT-ATMGE ADGGEKVWLQ PGDLAPAPVD TPSSEDFRPN CSTLNFTLDL  479
XP_003236.    DLSDNRISGA SELT-ATMGE ADGGEKVWLQ PGDLAPAPVD TPSSEDFRPN CSTLNFTLDL  461
AF259263_1    DLSDNRISGA SELT-ATMGE ADGGEKVWLQ PGDLAPAPVD TPSSEDFRPN CSTLNFTLDL  422
AF314224_1    DLSDNRISGP STLSEATPEE ADDAEQEELL SADPHPAPLS TPASKNFMDR CKNFKFTMDL  480

                     490        500        510        520        530        540
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          SRNNLVTVQP EMFAQLSHLQ CLRLSHNCIS QAVNGSQFLP LTGLQVLDLS HNKLDLYHEH  521
NP_059138.    SRNNLVTVQP EMFAQLSHLQ CLRLSHNCIS QAVNGSQFLP LTGLQVLDLS HNKLDLYHEH  539
XP_003236.    SRNNLVTVQP EMFAQLSHLQ CLRLSHNCIS QAVNGSQFLP LTGLQVLDLS HNKLDLYHEH  521
AF259263_1    SRNNLVTVQP EMFAQLSHLQ CLRLSHNCIS QAVNGSQFLP LTGLQVLDLS HNKLDLYHEH  482
AF314224_1    SRNNLVTIKP EMFVNLSRLQ CLSLSHNSIA QAVNGSQFLP LTNLQVLDLS HNKLDLYHWK  540

                     550        560        570        580        590        600
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          SFTELPRLEA LDLSYNSQPF GMQGVGHNFS FVAHLRTLRH LSLAHNNIHS QVSQQLCSTS  581
NP_059138.    SFTELPRLEA LDLSYNSQPF GMQGVGHNFS FVAHLRTLRH LSLAHNNIHS QVSQQLCSTS  599
XP_003236.    SFTELPRLEA LDLSYNSQPF GMQGVGHNFS FVAHLRTLRH LSLAHNNIHS QVSQQLCSTS  581
AF259263_1    SFTELPRLEA LDLSYNSQPF GMQGVGHNFS FVAHLRTLRH LSLAHNNIHS QVSQQLCSTS  542
AF314224_1    SFSELPQLQA LDLGYNSQPF SIKGIGHNFS FVAHLSMLHS LSLAHNDIHT RVSSHLNSNS  600

                     610        620        630        640        650        660
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          LRALDFSGNA LGHMWAEGDL YLHFFQGLSG LIWLDLSQNR LHTLLPQTLR NLPKSLQVLR  641
NP_059138.    LRALDFSGNA LGHMWAEGDL YLHFFQGLSG LIWLDLSQNR LHTLLPQTLR NLPKSLQVLR  659
XP_003236.    LRALDFSGNA LGHMWAEGDL YLHFFQGLSG LIWLDLSQNR LHTLLPQTLR NLPKSLQVLR  641
AF259263_1    LRALDFSGNA LGHMWAEGDL YLHFFQGLSG LIWLDLSQNR LHTLLPQTLR NLPKSLQVLR  602
AF314224_1    VRFLDFSGNG MGRMWDEGGL YLHFFQGLSG LLKLDLSQNN LHILRPQNLD NLPKSLKLLS  660

                     670        680        690        700        710        720
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          LRDNYLAFFK WWSLHFLPKL EVLDLAGNQL KALTNGSLPA GTRLRRLDVS CNSISFVAPG  701
NP_059138.    LRDNYLAFFK WWSLHFLPKL EVLDLAGNQL KALTNGSLPA GTRLRRLDVS CNSISFVAPG  719
XP_003236.    LRDNYLAFFK WWSLHFLPKL EVLDLAGNQL KALTNGSLPA GTRLRRLDVS CNSISFVAPG  701
AF259263_1    LRDNYLAFFK WWSLHFLPKL EVLDLAGNQL KALTNGSLPA GTRLRRLDVS CNSISFVAPG  662
AF314224_1    LRDNYLSFFN WTSLSFLPNL EVLDLAGNQL KALTNGTLPN GTLLQKLDVS SNSIVSVVPA  720

                     730        740        750        760        770        780
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1          FFSKAKELRE LNLSANALKT VDHSWFGPLA SALQILDVSA NPLHCACGAA FMDFLLEVQA  761
NP_059138.    FFSKAKELRE LNLSANALKT VDHSWFGPLA SALQILDVSA NPLHCACGAA FMDFLLEVQA  779
XP_003236.    FFSKAKELRE LNLSANALKT VDHSWFGPLA SALQILDVSA NPLHCACGAA FMDFLLEVQA  761
AF259263_1    FFSKAKELRE LNLSANALKT VDHSWFGPLA SALQILDVSA NPLHCACGAA FMDFLLEVQA  722
AF314224_1    FFALAVELKE VNLSHNILKT VDRSWFGPIV MNLTVLDVRS NPLHCACGAA FVDLLLEVQT  780
```

```
                      790        800        810        820        830        840
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1            AVPGLPSRVK CGSPGQLQGL SIFAQDLRLC LDEALSWDCF ALSLLAVALG LGVPMLHHLC  821
NP_059138.      AVPGLPSRVK CGSPGQLQGL SIFAQDLRLC LDEALSWDCF ALSLLAVALG LGVPMLHHLC  839
XP_003236.      AVPGLPSRVK CGSPGQLQGL SIFAQDLRLC LDEALSWDCF ALSLLAVALG LGVPMLHHLC  821
AF259263_1      AVPGLPSRVK CGSPGQLQGL SIFAQDLRLC LDEALSWDCF ALSLLAVALG LGVPMLHHLC  782
AF314224_1      KVPGLANGVK CGSPGQLQGR SIFAQDLRLC LDEVLSWDCF GLSLLAVAVG MVVPILHHLC  840


                      850        860        870        880        890        900
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1            GWDLWYCFHL CLAWLPWRGR QSGRDEDALP YDAFVVFDKT QSAVADWVYN ELRGQLEECR  881
NP_059138.      GWDLWYCFHL CLAWLPWRGR QSGRDEDALP YDAFVVFDKT QSAVADWVYN ELRGQLEECR  899
XP_003236.      GWDLWYCFHL CLAWLPWRGR QSGRDEDALP YDAFVVFDKT QSAVADWVYN ELRGQLEECR  881
AF259263_1      GWDLWYCFHL CLAWLPWRGR QSGRDEDALP YDAFVVFDKT QSAVADWVYN ELRGQLEECR  842
AF314224_1      GWDVWYCFHL CLAWLPLLAR -SRRSAQALP YDAFVVFDKA QSAVADWVYN ELRVRLEGRR  899

                      910        920        930        940        950        960
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1            GRWALRLCLE ERDWLPGKTL FENLWASVYG SRKTLFVLAH TDRVSGLLRA SFLLAQQRLL  941
NP_059138.      GRWALRLCLE ERDWLPGKTL FENLWASVYG SRKTLFVLAH TDRVSGLLRA SFLLAQQRLL  959
XP_003236.      GRWALRLCLE ERDWLPGKTL FENLWASVYG SRKTLFVLAH TDRVSGLLRA SFLLAQQRLL  941
AF259263_1      GRWALRLCLE ERDWLPGKTL FENLWASVYG SRKTLFVLAH TDRVSGLLRA SFLLAQQRLL  902
AF314224_1      GRRALRLCLE DRDWLPGQTL FENLWASIYG SRKTLFVLAH TDRVSGLLRT SFLLAQQRLL  959

                      970        980        990       1000       1010       1020
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
PRO1            EDRKDVVVLV ILSPDGRRSR YVRLRQRLCR QSVLLWPHQP SGQRSFWAQL GMALTRDNHH  1001
NP_059138.      EDRKDVVVLV ILSPDGRRSR YVRLRQRLCR QSVLLWPHQP SGQRSFWAQL GMALTRDNHH  1019
XP_003236.      EDRKDVVVLV ILSPDGRRSR YVRLRQRLCR QSVLLWPHQP SGQRSFWAQL GMALTRDNHH  1001
AF259263_1      EDRKDVVVLV ILSPDGRRSR YVRLRQRLCR QSVLLWPHQP SGQRSFWAQL GMALTRDNHH  962
AF314224_1      EDRKDVVVLV ILRPDAHRSR YVRLRQRLCR QSVLFWPQQP NGQGGFWAQL STALTRDNRH  1019

                     1030
                ....|....| ...
PRO1            FYNRNFCQGP TAE  1014
NP_059138.      FYNRNFCQGP TAE  1032
XP_003236.      FYNRNFCQGP TAE  1014
AF259263_1      FYNRNFCQGP TAE  975
AF314224_1      FYNQNFCRGP TAE  1032
```

The interleukin-1 (IL-1) receptor/Toll-like receptor (TLR) superfamily is a recently defined and expanding group of receptors that participate in host responses to injury and infection. The superfamily is defined by the Toll/IL-1 receptor (TIR) domain, which occurs in the cytosolic region of family members, and is further subdivided into two groups based on homology to either the Type I IL-1 receptor or Drosophila Toll receptor extracellular domain. The former group includes the receptor for the important Th1 cytokine IL-18, and T1/ST2, which may have a role in Th2 cell function. The latter group includes six mammalian TLRs, including TLR2 and TLR4, that largely mediate the host response to gram-positive and gram-negative bacteria, respectively. Whether bacterial products are actual ligands for TLRs, or whether they generate ligands via as yet unidentified pattern recognition receptors, has yet to be determined. Signaling pathways activated via the TIR domain trigger the activation of downstream kinases, and transcription factors such as NF-kappaB, and involve the adaptor protein MyD88, which itself contains a TIR domain.

As our primary interface with the environment, the skin is constantly subjected to injury and invasion by pathogens. The fundamental force driving the evolution of the immune system has been the need to protect the host against overwhelming infection. The ability of T and B cells to recombine antigen receptor genes during development provides an efficient, flexible, and powerful immune system with nearly unlimited specificity for antigen. The capacity to expand subsets of antigen-specific lymphocytes that become activated by environmental antigens (memory response) is termed "acquired" immunity. Immunologic memory, although a fundamental aspect of mammalian biology, is a relatively recent evolutionary event that permits organisms to live for years to decades. "Innate" immunity, mediated by genes that remain in germ line conformation and encode for proteins that recognize conserved structural patterns on microorganisms, is a much more ancient system of host defense. Defensins and other antimicrobial peptides, complement and opsonins, and endocytic receptors are all considered components of the innate immune system. None of these, however, are signal-transducing receptors. Most recently, a large family of cell surface receptors that mediate signaling through the NF-kappaB transcription factor has been identified. This family of proteins shares striking homology with plant and Drosophila genes that mediate innate immunity. In mammals, this family includes the type I interleukin-1 receptor, the interleukin-18 receptor, and a growing family of Toll-like receptors, two of which were recently identified as signal-transducing receptors for bacterial endotoxin. In this review, we discuss how interleukin-1 links the innate and acquired immune systems to provide synergistic host defense activities in skin.

In *Drosophila* the Toll protein is involved in establishment of dorso-ventral polarity in the embryo. In addition, members of the Toll family play a key role in innate antibacterial and antifungal immunity in insects as well as in mammals. These proteins are type-I transmembrane receptors that share an intracellular 200 residue domain with the interleukin-1 receptor (IL-1R), the Toll/IL-1R homologous region (TIR). The similarity between Toll-like receptors (LTRs) and IL-1R is not restricted to sequence homology since these proteins also share a similar signaling pathway. They both induce the activation of a Rel type transcription factor via an adaptor protein and a protein kinase. Interestingly, MyD88, a cytoplasmic adaptor protein found in mammals, contains a TIR domain associated to a DEATH domain (see IPR000488). Besides the mammalian and

Drosophila proteins, a TIR domain is also found in a number of plant proteins implicated in host defense. As MyD88, these proteins are cytoplasmic. Site directed mutagenesis and deletion analysis have shown that the TIR domain is essential for Toll and IL-1R activities. Sequence analysis have revealed the presence of three highly conserved regions among the different members of the family: box 1 (FDAFISY), box 2 (GYKLC-RD-PG), and box 3 (a conserved W surrounded by basic residues). It has been proposed that boxes 1 and 2 are involved in the binding of proteins involved in signaling, whereas box 3 is primarily involved in directing localization of receptor, perhaps through interactions with cytoskeletal elements

Toll is a *Drosophila* gene essential for ontogenesis and antimicrobial resistance. Several hortologues of Toll have been identified and cloned in vertebrates, namely Toll-like receptors (TLR). Human TLR are a growing family of molecules involved in innate immunity. TLR are structurally characterized by a cytoplasmic Toll/interleukin-1R (TIR) domain and by extracellular leucine-rich repeats. TLR characterized so far activate the MyD88/IRAK signaling cascade, which bifurcates and leads to NF-kappaB and c-Jun/ATF2/TCF activation. Genetic, gene transfer, and dominant-negative approaches have involved TLR family members (TLR2 and TLR4) in lipopolysaccharide recognition and signaling. Accumulating evidence suggests that some TLR molecules are also involved in signaling receptor complexes that recognize components of gram-positive bacteria and mycobacteria. However, the definitive role of other TLR is still lacking. A systematic approach has been used to determine whether different human leukocyte populations selectively or specifically expressed TLR mRNA. Based on expression pattern, TLR can be classified as ubiquitous (TLR1), restricted (TLR2, TLR4, and TLR5), and specific (TLR3). Expression and regulation of distinct though overlapping ligand recognition patterns may underlie the existence of a numerous, seemingly redundant, TLR family. Alternately, the expression of a TLR in a single cell type may indicate a specific role for this molecule in a restricted setting.

The amino acids differences between the three MOL1 proteins are shown in Table 1H. Deletions are marked by a delta (Δ). The differences between the three proteins appear to be localized to a few distinct regions. Thus, these proteins may have similar functions, such as serving as olfactory or chemokine receptors.

Uses of the Compositions of the Invention

The above defined information for this invention suggests that this Toll Receptor-like protein may function as a member of a "Toll Receptor family". Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in pancreatic cancer, adenoma, and other cancers, Larsen syndrome, tachycardia, erythroderma, night blindness, long QT syndrome, brugada syndrome, heart block, cell-mediated immunity, and applications as a mediator in inflammation and/or other pathologies and disorders. For example, a cDNA encoding the Toll Receptor-like protein may be useful in gene therapy, and the Toll Receptor-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from pancreatic cancer, adenoma, and other cancers, Larsen syndrome, tachycardia, erythroderma, night blindness, long QT syndrome, brugada syndrome, heart block, cell-mediated immunity, and applications as a mediator in inflammation. The novel nucleic acid encoding Toll Receptor-like protein, and the Toll Receptor-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL2

MOL2a

An additional murine GNC2 eIFK -like protein of the invention, referred to herein as MOL2a, is an Olfactory Receptor ("OR")-like protein. The novel nucleic acid of 4989 nucleotides, (20466828_EXT1, SEQ ID NO:3) encoding a novel GNC2 eIFK-like protein is shown in Table 2A.

Table 2A. MOL2a Nucleotide Sequence (SEQ ID NO:3)
ATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGAGCCTCCGGAGAGCTACCCGCAACGACAGGACCACGA GCTACAGGCCCTGGAGGCCATCTACGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTTAAGGTCA AAGAGCCCCCTGAAATCAATTTAGTTTTGTACCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTG AGGGTTAAATGCCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAATGCCAAAGGTCTATCAAATGA AAGTGTCAATTTGTTAAAATCTCGCCTAGAAGAACTGGCCAAGAAACACTGTGGGGAGGTAGTGATGATCTTTGAAC TGGCTTACCACGTGCAGTCATTTCTCAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAA AGGCGGGCTCAAGAGGAGCAACAGAGGCTGTTGGAGGCCCAAGCGGAAAGAAGAGCACAGCAACGTGAAATCCTGCA TGAGATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAAGGAAAGAAATGGCTAAGCAGGAACGTTTGGAAA TTGCTAGTTTGTCAAACCAAGATCATACCTCTAAGAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGA GGCTCTCCTGACTTTGTAGGAAATGGTAAACATCGGGCAAACTCCTCAGGAAGGTCTAGGTTAAGGCGAGAACGTCA GTATTCTGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAGTCCTGATCAGC TCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGGAAAATTAGTCTACAATGCTTTGGAAACAGCC ACTGGTGGCTTTGTCTTGTTGTATGAGTGGGTCCTTCAGTGGCAGAAAAAAATGGGTCCATTCCTTACCAGTCAAGA AAAAGAGAAGATTGATAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAGCC ATCCAAATGTAGTACGCTACCTTGCAATGAATTCAAAGAGCAAGACGACTCCATTCGTGGTGGACATTTTAGTGGAG CACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTCAGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACAC AGCTCAGCTCCTGTCAGGCCTTGATTATCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATCTAATGTCT TGGTGGATGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTGCAAGGAGGAT GTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAAAACGGGGAAGAAAGGAGATGTTTGGCG TCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGGACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTAC CAGCTGACTTTCAAGATTTTCTAAAGAAGAGATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTG TTGAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCCTGAATCTGAAGGACAAGATTA TGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGCCTTCTTTAGTGAGACACAGAGACAGTTTTCCCGAT ACTTCATTGAGTTTGAAGAATTACAACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTG GACGGCTGCTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAAGGGCGAAGT GACACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAGCGGCACGAGCGGCCGG CGGGACCGGGGACGCCGCCCCCGGACTCCGGGCCCCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGC GACACAGACGGCCTGGACAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGAGGACGACGACGAGGACG AGCACGGTGGCGTCTTCTCCCAGTCCTTCCTGCCTGCTTCAGATTCTGAAAGTGATATTATCTTTGACAATGAAGAT GAGAACAGTAAAAGTCAGAATCAGGATGAAGATTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGAC GACTGAGGCTGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCATTGACCAGG GACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTCGAGAGATTCTGGATGGATTAGCTTATATCCATGAGAAA GGAATGATTCACCGGGATTTGAAGCCTGTCAACATTTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGG TTTGGCGACAGACCATCTAGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACC CTTCAGGTCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGGAAGCACCAAATCTGCA TACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTCCTATCACCCCATGGTCACGGCTTC AGAAAGGATCTTTGTTCTCAACCAACTCAGAGATCCCACTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGC ATGCAAAGCAGAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAAACGGCCCACAGCCACAGAACTGCTC AAGAGTGAGCTGCTGCCCCCACCCCAGATGGAGGAGTCAGAGCTGCATGAAGTGCTGCACCACACGCTGACCAACGT GGATGGGAAGGCCTACCGCACCATGATGGCCCAGATCTTCTCGCAGCGCATCTCCCCTGCCATCGATTACACCTATG ACAGCGACATACTGAAGGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGC ATCTTTAAAAGACATGGTGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACAAATATATGAGCACAA CGAAGCTGCCCTATTCATGGACCACAGCGGGATGCTGGTGATGCTTCCTTTTGACCTGCGGGTGCCTTTTGCAAGAT ATGTGGCAAGAAATAATATATTGAATTTAAAACGGTACTGCATAGAACGTGTGTTCACGCCGCGCAAGTTAGATCGA TTTCATCCCAAAGAACTTCTGGAGTGTGCCTTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCACTGCTGA AATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAAGAAAGAAATTACAGTATTTATTTGAACC ATACCATGTTATTGAAAGCAATACTCTTACACTGTGGGATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTG TATGATGCTGTGACAGAGAAGCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTCTAATAG TCTGTGTCGACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATTCATTAATAG AACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAAGAAA CTCGGCATCAAGTTACAGGTTTGGGTCTTGATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCAT CTTCCAGTTTGTGGCTATCATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACC TGCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGTCAGCATAGCTATAGAC AAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTAAGTTCTGTTACAATAGGCTCTGGGGACCTCCTGGTTGT AAGTGTGGGCCAGATGTCTATGTCCAGGGCCATAAACCTAACCCAGAAACTCTGGACAGCAGGCATCACAGCAGAAA TCATGTACGACTGGTCACAGTTTCAGTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTG GCCCTTGTCTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGAGAAGCGTGT GCTGGAGACTGAACTTGTGGACCATGTACTGCAGAAACTGAGGACTAAAGTCACTGATGAAAGGAATTTTAGAGAAG

CTTCCGATAATCTTGCAGTGCAAAATCTGAAGGGGTCATTTTCTAATGCTTCAGGTTTGTTTGAAATCCATGGAGCA ACAGTGGTTCCCATTGTGAGTGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT ACAAACTCGACTTCAGACCTCCCTTGCCAACTTACATCAGAAAAGCAGTGAAATTGAAATTCTGGCTGTAGTGGATC TACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTTAACACAACTGTGAAG CAGCTGCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAA AAAGGTGTCTGTGCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAA

An open reading frame (ORF) for MOL2a was identified from nucleotides 1 to 4986. The disclosed MOL2a polypeptide (SEQ ID NO:4) encoded by SEQ ID NO:3 is 1662 amino acid residues, has a molecular weight of 188250.1 and is presented using the one-letter code in Table 2B. The SignalP, Psort and or Hydropathy profile of MOL2a indicate that this sequence does not have a signal peptide and is likely to be localized to the nucleus. Therefore it is likely that MOL2a is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 2B. Encoded MOL2a protein sequence (SEQ ID NO:4).
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKVKEPPEINLVLYPQGLTGEEVYVKVDL RVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGEVVMIFELAYHVQSFLSEHNKPPPKSFHEEMLE RRAQEEQQRLLEAQAERRAQQREILHEIQRRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHG GSPDFVGNGKHRANSSGRSRLRRERQYSVCNSEDSPGSCEILYFNMGSPDQLMVHKGKCIGSDEQLGKLVYNALETA TGGFVLLYEWVLQWQKKMGPFLTSQEKEKIDKCKKQIQGTETEFNSLVKLSHPNVVRYLAMNSKSKTTPFVVDILVE HISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLHSNSVVHKVLSASNVLVDAEGTVKITDYSISKRLADICKED VFEQTRVRFSDNALPYKTGKKGDVWRLGLLLLSLSQGQECGEYPVTIPSDLPADFQDFLKKRCVCLDDKERWSPQQL LKHSFINPQPKMPLVEQSPESEGQDYVETVIPSNRLPSAAFFSETQRQFSRYFIEFEELQLLGKGAFGAVIKVQNKL DGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHENIVRYYNAWIERHERPAGPGTPPPDSGPLAKDDRAARGQPAS DTDGLDSVEAAAPPPILSSSVEWSTSGERSASARFPATGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDIIFDNED ENSKSQNQDEDCNEKNGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIHEK GMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTGMVGTALYVSPEVQGSTKSA YNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSPKFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELL KSELLPPPQMEESELHEVLHHTLTNVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIR IFKRHGAVQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRVPFARYVARNNILNLKRYCIERVFTPRKLDR FHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIYLNHTMLLKAILLHCGIPEDKLSQVYIIL YDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKFIEQKGDLQDLMPTINSLIEQKTGIAQLVKYGLKDLEEVVGLLKK LGIKLQVWVLINLGLVYKVQQHNGIIFQFVAIIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIAID KISAAVLNMEESVSSVTIGSGDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQFQSQEELQEYCRHHEITYV ALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNFREASDNLAVQNLKGSFSNASGLFEIHGA TVVPIVSVLAPEKLSASTRRRYETQVQTRLQTSLANLHQKSSEIEILAVVDLPKETILQFLSLEWDADEQAFNTTVK QLLSRLPKQRYLKLVCDEIYNIKVEKKVSVLFLYSYRDDYYRILF

The MOL2a nucleic acid sequence has 3119 of 3723 bases (83 %) identical to a *Mus musculus* GCN2 EIF2alpha kinase mRNA (GENBANK-ID: MMU243533\|acc:AJ243533)

The full amino acid sequence of the protein of the invention was found to have 479 of 1662 bases (88 %) amino acid residues (88 %) identical to, and 1554 of 1662 residues (93 %) similar to, the 1648 amino acid residue CAB58363 GCN2 EIF2alpha kinase protein from *Mus musculus* (ptnr: TREMBLNEW-ACC: CAB58363).

MOL2b

An additional murine GNC2 eIFK -like nucleic acid of the invention, referred to herein as MOL2b, encodes an Olfactory Receptor ("OR")-like protein. The novel nucleic acid of 5094 nucleotides is disclosed in Table 2C. The disclosed MOL2b open reading frame ("ORF") begins at the ATG initiation codon at nucleotides 20-22, shown in bold in Table 2C. The encoded polypeptide is alternatively referred to herein as MOL2b or as CG51424-02. The disclosed MOL2b ORF terminates at a TGA codon at nucleotides 4898-4900. As shown in Table 2C the start and stop codons are in bold letters and the 5' and 3' untranslated regions are underlined.

Table 2C. MOL2b Nucleotide Sequence (SEQ ID NO:138)
GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGAGCCTCCGGA
GAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTACGGCGCGGACTTCCAAGA
CCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGAAATCAATTTAGTTTTGTACCCTCAAGG
CCTAACTGGTGAAGAAGTATATGTAAAAGTGGATTTGAGGGTTAAATGCCCACCTACCTATCCAGATGT
AGTTCCTGAAATAGAGTTAAAAAATGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAAATCTCG
CCTAGAAGAACTGGCCAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTC
ATTTCTCAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGCTCA
GGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGAAATCCTGCATGA
GATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAAGGAAAGAAATGGCTAAGCAGGAACGTTT
GGAAATTGCTAGTTTGTCAAACCAAGATCATACCTCTAAGAAGGACCCAGGAGGACACAGAACGGCTGC
CATTCTACATGGAGGCTCTCCTGACTTTGTAGGAAATGGTAAACATCGGGCAAACTCCTCAGGAAGGTC
TAGGCGAGAACGTCAGTATTCTGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTT
CAATATGGGGAGTCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGG
AAAATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTATGAGTGGGTCCTTCA
GTGGCAGAAAAAAATGGGTCCATTCCTTACCAGTCAAGAAAAAGAGAAGATTGATAAGTGCAAAAAGCA
GATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAGCCATCCAAATGTAGTACGCTACCT
TGCAATGAATCTCAAAGAGCAAGACGACTCCATCGTGGTGGACATTTTAGTGGAGCACATTAGTGGGGT
CTCTCTTGCTGCACACCTGAGCCACTCAGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCA
GCTCCTGTCAGGCCTTGATTATCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATCTAATGT
CTTGGTGGATGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAAAACGGGGAA
GAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGGACAGGAATGTGGAGAGTA
CCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGATTTTCTAAAGAAATGTGTGTGCTTGGA
TGACAAGGAAAGATGGAGTCCCCAGCAGTTGTTGAAACACAGCTTTATAAATCCCCAGCCAAAAATGCC
TCTAGTGGAACAAAGTCCTGAAGATTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCG
GCTACCCAGTGCTGCCTTCTTTAGTGAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGA
ATTACAACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCATCAAGGTGCAGAACAAGTTGGACGGCTGCTG
CTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAAGGGCGAAGTGAC
ACTGCTGTCACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGCCTGGATCGAGCGGCACGAGCG
GCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCCCCTGGCCAAGGATGACCGAGCTGCACGCGG
GCAGCCGGCGAGCGACACAGACGGCCTGGACAGCGTAGAGGCCGCCGCGCCGCCACCCATCCTCAGCAG
CTCGGTGGAGTGGAGCACTTCGGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTC
CAGCGATGACGAGGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCCAGTCCTTCCTGCCTGCTTC
AGATTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGATGAAGA
TTGCAATGAAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGCTGTGCACTACCTATA
CATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCATTGACCAGGGACTGTATCGAGACAC
CGTCAGACTCTGGAGGCTTTTTCGAGAGATTCTGGATGGATTAGCTTATATCCATGAGAAAGGAATGAT
TCACCGGGATTTGAAGCCTGTCAACATTTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGG
TTTGGCGACAGACCATCTAGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAA
GTCAGACCCTTCAGGTCACTTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG

```
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTTTGAGATGTC
CTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACTCAGAGATCCCACTTCGCC
TAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCAGAAATCAGTCATCTCCTGGCTGTTGAA
CCACGATCCAGCAAAACGGCCCACAGCCACAGAGCTGCTCAAGAGTGAGCTGCTGCCCCCACCCCAGAT
GGAGGAGTCAGAGCTGCATGAAGTGCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCTACCGCAC
CATGATGGCCCAGATCTTCTCGCAGCGCATCTCCCCTGCCATCGATTACACCTATGACAGCGACATACT
GAAGGGCAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCATCTT
TAAAAGACATGGAGCTGTTCAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACAAATATATGAGCA
CAACGAAGCTGCCCTATTCATGGACCACAGCGGGATGCTGGTGATGCTTCCTTTTGACCTGCGGATCCC
TTTTGCAAGATATGTGGCAAGAAATAATATATTGAATTTAAAACGATACTGCATAGAACGTGTGTTCAG
GCCGCGCAAGTTAGATCGATTTCATCCCAAAGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTAC
CACCAACAGCTTTCTGCCCACTGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGC
ACTTCAGGAAAGAAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTG
TGGGATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAAGCTGAC
GAGGAGAGAAGTGGAAGCTAAATTTTGTAATCTGTCTTTGTCTTCTAATAGTCTGTGTCGACTCTACAA
GTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAATAAATTCATTAATAAAACAGAAAAC
AGGTATTGCACAGTTGGTGAAGTATGGCTTAAAAGACCTAGAGGAGGTTGTTGGACTGTTGAAGAAACT
CGGCATCAAGTTACAGGTCTTGATCAATTTGGGCTTGGTTTACAAGGTGCAGCAGCACAATGGAATCAT
CTTCCAGTTTGTGGCTTTCATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAG
ATATGACCTGCTGATTCCCCAGTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTTACAATAAGCTCTTG
TGACCTCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAACCTAACCCAGAAACTCTG
GACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACAGTCCCAAGAGGAATTACAAGAGTACTG
CAGACATCATGAAATCACCTATGTGGCCCTTGTCTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTC
TTTCGAGAAGGAAAGGCAGACAGAGAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAA
ACTGAGGACTAAAGTCACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAGTGCAAAATCT
GAAGGGGTCATTTTCTAATGCTTCAGGTTTGTTTGAATTCCATGGAGCAACAGTGGTTCCCATTGTGAG
TGTGCTAGCCCCGGAGAAGCTGTCAGCCAGCACTAGGAGGCGCTATGAAACTCTGGTGGATCTACCCAA
AGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGCTGATGAACAGGCATTTAACACAACTGTGAA
GCAGCTGCTGTCACGCCTGCCAAAGCAAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAA
AGTAGAAAAAAAGGTGTCTGTGCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTA
ACCCTAAAGAACTGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTA
CATTCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAATCCCAG
CACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAAACCAGGAGTTTGAGACCAGCCT
```

The disclosed nucleic acid MOL2b sequence, localized to chromosome 15, has 4678 of 4680 bases (99%) identical to a gb:GENBANK-ID:AX056426|acc:AX056426.1 mRNA from *Homo sapiens* (Sequence 70 from Patent WO0073469) (E = 0.0).

The disclosed MOL2b polypeptide (SEQ ID NO:139) encoded by SEQ ID NO:138 is 1626 amino acid residues and is presented using the one-letter code in Table 2D. The SignalP, Psort and or Hydropathy profile of MOL2b indicate that this sequence does not have a signal peptide In one embodiment, MOL2b is likely to be located to the nucleus with a certainty of 0.9800. In other embodiments, MOL2b couild also be located to the microbody (peroxisome), with a certainty of 0.3000, the mitochondrial matrix space with a certainty of 0.1000, or to the lysosome (lumen) with a certainty of 0.1000. Therefore it is likely that MOL2b is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 2D. Encoded MOL2b protein sequence (SEQ ID NO:139).
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACGPVKEPPEINLVLYPQGLTGEEV YVKVDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGEVMIFELAYHVQSFLSEHN KPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQRRKEEIKEEKKRKEMAKQERLEIASLS NQDHTSKKDPGGHRTAAILHGGSPDFVGNGKHRANSSGRSRRERQYSVCNSEDSPGSCEILYFNMGSPD QLMVHKGKCIGSDEQLGKLVYNALETATGGFVLLYEWVLQWQKKMGPFLTSQEKEKIDKCKKQIQGTET EFNSLVKLSHPNVVRYLAMNLKEQDDSIVVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLD YLHSNSVVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGDVWR LGLLLLSLSQGQECGEYPVTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFINPQPKMPLVEQSP EDSGGQDYVETVIPSNRLPSAAFFSETQRQFSRYFIEFEELQLLGKGAFGAVIKVQNKLDGCCYAVKRI PINPASRQFRRIKGEVTLLSRLHHENIVRYYNAWIERHERPAGPGTPPPDSGPLAKDDRAARGQPASDT DGLDSVEAAAPPPILSSSVEWSTSGERSASARFPATGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDI IFDNEDENSKSQNQDEDCNEKNGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRL FREILDGLAYIHEKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGH LTGMVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSPKFPEDF DDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPQMEESELHEVLHHTLTNVDGKAYRTMMAQIF SQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGAVQLCTPLLLPRNRQIYEHNEAALF MDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIERVFRPRKLDRFHPKELLECAFDIVTSTTNSFLP TAEIIYTIYEIIQEFPALQERNYSIYLNHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEA KFCNLSLSSNSLCRLYKFIEQKGDLQDLMPTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQV LINLGLVYKVQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIAIDK ISAAVLNMEESVTISSCDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQEYCRHHEIT YVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNGREASDNLAVQNLKGSFSN ASGLFEFHGATVVPIVSVLAPEKLSASTRRRYETLVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRL PKQRYLKLVCDEIYNIKVEKKVSVLFLYSYRDDYYRILF

The full amino acid sequence of the protein of the invention was found to have 1448 of 1473 amino acid residues (98%) identical to, and 1448 of 1473 amino acid residues (98%) similar to, the 1495 amino acid residue ptnr:SPTREMBL-ACC:Q9P2K8 protein from *Homo sapiens* (Human) (KIAA1338 PROTEIN).

MOL2b is expressed in at least Aorta, Brain, Colon, Heart, Kidney, Lung, Prostate, Thyroid, Uterus, Whole embryo, Bladder, Bone, Eye, Liver, Muscle, Pancreas, Salivary Gland, and Skin. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of CuraGen Acc. No. CG51424-02. The sequence is predicted to be expressed in the following tissues because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AX056426|acc:AX056426.1) a closely related Sequence 70 from Patent WO0073469 homolog in species *Homo sapiens* :Bone, and Prostate.

Other BLAST results including the sequences used for ClustalW analysis are presented in Table 2E.

Table 2E. BLAST results for MOL2					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
PatP:B65663	Protein kinase [Homo sapiens]	1649	1626/1662 (97%)	1632/1662 (98%)	0.0
PatP:B43581	Cancer associated protein [Homo sapiens]	604	592/609 (97%)	594/609 (97%)	6.5e-306
PatP:B42761	ORF2525 polypeptide	619	585/624 (93%)	596/624 (95%)	1.3e-300
gi|10764165|gb|AAG22591.1| (AF193344)	GCN2gamma [Mus musculus]	1570	1313/1577 (83%)	1375/1577 (86%)	0.0
gi|11360320|pir||T46924	probable translation initiation factor eIF-2alpha kinase (EC 2.7.1.-) [similarity] - human (fragment)	938	887/946 (93%)	889/946 (93%)	0.0
gi|7305017|ref|NP_038747.1|	GCN2 eIF2alpha kinase [Mus musculus]	1648	1374/1647 (83%)	1442/1647 (87%)	0.0
gi|10764161|gb|AAG22589.1|	GCN2alpha [Mus musculus]	1370	1189/1381 (86%)	1241/1381 (89%)	0.0
gi|7243057|dbj|BAA92576.1| (AB037759)	KIAA1338 protein [Homo sapiens]	1495	1377/1460 (94%)	1380/1460 (94%)	0.0
gi|10764163|gb|AAG22590.1| (AF193343)	GCN2beta [Mus musculus]	1648	1373/1647 (83%)	1440/1647 (87%)	0.0
gi|6065914|emb|CAB58360.1| (AJ243428)	putative eIF2 alpha kinase [Homo sapiens]	548	505/556 (90%)	507/556 (90%)	0.0

This information is presented graphically in the multiple sequence alignment given in Table 2F (with MOL2 being shown on line 1) as a ClustalW analysis comparing MOL2 with related protein sequences.

Table 2F. Information for the ClustalW proteins:

1) Novel MOL2 (SEQ ID NO:4)
2) gi|10764165|gb|AAG22591.1| (AF193344) GCN2gamma [Mus musculus] (SEQ ID NO:35)
3) gi|11360320|pir||T46924 probable translation initiation factor eIF-2alpha kinase (EC 2.7.1.-) [similarity] - human (fragment) (SEQ ID NO:36)
4) gi|7305017|ref|NP_038747.1| GCN2 eIF2alpha kinase [Mus musculus] (SEQ ID NO:37)
5) gi|7243057|dbj|BAA92576.1| (AB037759) KIAA1338 protein [Homo sapiens] (SEQ ID NO:38)
6) gi|10764163|gb|AAG22590.1| (AF193343) GCN2beta [Mus musculus] (SEQ ID NO:39)

7) gi|6065914|emb|CAB58360.1| (AJ243428) putative eIF2 alpha kinase [Homo sapiens] (SEQ ID NO:40)

```
                     10         20         30         40         50         60
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   MAGGRGAPGR GRDEPPESYP QRQDHELQAL EAIYGADFQD LRPDACGPVK VKEPPEINLV  60
AF193344     ---------- ---------- ---------- ---------- ---------- MRTQRAL---  7
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   MAGGRGASGR GRAEPQESYS QRQDHELQAL EAIYGSDFQD LRPDARG--R VREPPEINLV  58
AAG22589.1   ---------- ---------- ---------- ---------- ---------- ----------  1
AB037759     ---------- ---------- ---------- ---------- ---------- -------LLL  3
AF193343     MAGGRGASGR GRAEPQESYS QRQDHELQAL EAIYGSDFQD LRPDARG--R VREPPEINLV  58
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                     70         80         90        100        110        120
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LYPQGLTGEE VYVKVDLRVK CPPTYPDVVP EIELKNAKGL SNESVNLLKS RLEELAKKHC  120
AF193344     ---------- ---------- -------LVP EIELKNAKGL SNESVNLLKS HLEELAKKQC  40
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   LYPQGLAGEE VYVQVELQVK CPPTYPDVVP EIELKNAKGL SNESVNLLKS HLEELAKKQC  118
AAG22589.1   ---------- ---------- ---------- ---------- ---------- ----------  1
AB037759     FFPLGLQ--- ---------- ---------- ---------- --QPLLLLLS ----------  18
AF193343     LYPQGLAGEE VYVQVELQVK CPPTYPDVVP EIELKNAKGL SNESVNLLKS HLEELAKKQC  118
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    130        140        150        160        170        180
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   GEVVMIFELA YHVQSFLSEH NKPPPKSFHE EMLERRAQEE QQRLLEAQAE RRAQQREILH  180
AF193344     G-EVMIFELA HHVQSFLSEH NKPPPKSFHE EMLERQAQEK QQRLLEARRK EEQEQREILH  99
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   G-EVMIFELA HHVQSFLSEH NKPPPKSFHE EMLERQAQEK QQRLLEARRK EEQEQREILH  177
AAG22589.1   ---------- ---------- ---------- ---------- ---------- ----------  1
AB037759     ---------- ---------- --PP------ ---------- ---------- -------FQH  23
AF193343     G-EVMIFELA HHVQSFLSEH NKPPPKSFHE EMLERQAQEK QQRLLEARRK EEQEQREILH  177
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    190        200        210        220        230        240
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   EIQRRKEEIK EEKKRKEMAK QERLEIASLS NQDHTSKKDP GGHRTAAILH GGSPDFVGNG  240
AF193344     EIQRRKEEIK EEKKRKEMAK QERLEITSLT NQDYASKRDP AGHRAAAILH GGSPDFVGNG  159
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   EIQRRKEEIK EEKKRKEMAK QERLEITSLT NQDYASKRDP AGHRAAAILH GGSPDFVGNG  237
AAG22589.1   ---------- ---------- ---------- ---------- ---------- ----------  1
AB037759     EIQRRKEEIK EEKKRKEMAK QERLEIASLS NQDHTSKKDP GGHRTAAILH GGSPDFVGNG  83
AF193343     EIQRRKEEIK EEKKRKEMAK QERLEITSLT NQDYASKRDP AGHRAAAILH GGSPDFVGNG  237
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    250        260        270        280        290        300
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   KHRANSSGRS RLRRERQYSV CNSEDSPGSC EILYFNMGSP DQLMVHKGKC IGSDEQLGKL  300
AF193344     KARTYSSGRS --RRERQYSV CSGEPSPGSC DILHFSVGSP DQLMVHKGRC VGSDEQLGKV  217
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   KARTYSSGRS --RRERQYSV CSGEPSPGSC DILHFSVGSP DQLMVHKGRC VGSDEQLGKV  295
AAG22589.1   ---------- ---------- ---------- ---------- ---MVHKGRC VGSDEQLGKV  17
AB037759     KHRANSSGRS --RRERQYSV CNSEDSPGSC EILYFNMGSP DQLMVHKGKC IGSDEQLGKL  141
AF193343     KARTYSSGRS --RRERQYSV CSGEPSPGSC DILHFSVGSP DQLMVHKGRC VGSDEQLGKV  295
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    310        320        330        340        350        360
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   VYNALETATG GFVLLYEWVL QWQKKMGPFL TSQEKEKIDK CKKQIQGTET EFNSLVKLSH  360
AF193344     VYNALETATG SFVLLHEWVL QWQK-MGPCL TSQEKEKIDK CKRQIQGAET EFSSLVKLSH  276
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   VYNALETATG SFVLLHEWVL QWQK-MGPCL TSQEKEKIDK CKRQIQGAET EFSSLVKLSH  354
AAG22589.1   VYNALETATG SFVLLHEWVL QWQK-MGPCL TSQEKEKIDK CKRQIQGAET EFSSLVKLSH  76
AB037759     VYNALETATG GFVLLYEWVL QWQKKMGPFL TSQEKEKIDK CKKQIQGTET EFNSLVKLSH  201
AF193343     VYNALETATG SFVLLHEWVL QWQK-MGPCL TSQEKEKIDK CKRQIQGAET EFSSLVKLSH  354
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    370        380        390        400        410        420
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   PNVVRYLAMN SKSKTTPFVV DILVEHISGV SLAAHLSHSG PIPVHQLRRY TAQLLSGLDY  420
AF193344     PNIVRYFAMN SREEEDSIVI DILAEHVSGI SLATHLSHSG PVPAHQLRKY TAQLLAGLDY  336
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   PNIVRYFAMN SREEEDSIVI DILAEHVSGI SLATHLSHSG PVPAHQLRKY TAQLLAGLDY  414
AAG22589.1   PNIVRYFAMN SREEEDSIVI DILAEHVSGI SLATHLSHSG PVPAHQLRKY TAQLLAGLDY  136
```

```
AB037759     PNVVRYLAMN LKEQDDSIVV DILVEHISGV SLAAHLSHSG PIPVHQLRRY TAQLLSGLDY  261
AF193343     PNIVRYFAMN SREEEDSIVI DILAEHVSGI SLATHLSHSG PVPAHQLRKY TAQLLAGLDY  414
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    430        440        450        460        470        480
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LHSNSVVHKV LSASNVLVDA EGTVKITDYS ISKRLADICK EDVFEQTRVR FSDNALPYKT  480
AF193344     LHSNSVVHKV LSASSVLVDA EGTVKITDYS ISKRLADICK EDVFEQARVR FSDSALPYKT  396
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   LHSNSVVHKV LSASSVLVDA EGTVKITDYS ISKRLADICK EDVFEQARVR FSDSALPYKT  474
AAG22589.1   LHSNSVVHKV LSASSVLVDA EGTVKITDYS ISKRLADICK EDVFEQARVR FSDSALPYKT  196
AB037759     LHSNSVVHKV LSASNVLVDA EGTVKITDYS ISKRLADICK EDVFEQTRVR FSDNALPYKT  321
AF193343     LHSNSVVHKV LSASSVLVDA EGTVKITDYS ISKRLADICK EDVFEQARVR FSDSALPYKT  474
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    490        500        510        520        530        540
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   GKKGDVWRLG LLLLSLSQGQ ECGEYPVTIP SDLPADFQDF LKKRCVCLDD KERWSPQQLL  540
AF193344     GKKGDVWRLG LLLLSLSQGQ ECGEYPVTIP SDLPADFQDF LKK-CVCLDD KERWSPQQLL  455
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   GKKGDVWRLG LLLLSLSQGQ ECGEYPVTIP SDLPADFQDF LKK-CVCLDD KERWSPQQLL  533
AAG22589.1   GKKGDVWRLG LLLLSLSQGQ ECGEYPVTIP SDLPADFQDF LKK-CVCLDD KERWSPQQLL  255
AB037759     GKKGDVWRLG LLLLSLSQGQ ECGEYPVTIP SDLPADFQDF LKK-CVCLDD KERWSPQQLL  380
AF193343     GKKGDVWRLG LLLLSLSQGQ ECGEYPVTIP SDLPADFQDF LKK-CVCLDD KERWSPQQLL  533
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    550        560        570        580        590        600
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   KHSFINPQPK MPLVEQSPE- SEGQDYVETV IPSNRLPSAA FFSETQRQFS RYFIEFEELQ  599
AF193344     KHSFINPQPK LPLVEQSPED SGGQDYIETV IPSNQLPSAA FFSETQKQFS RYFIEFEELQ  515
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   KHSFINPQPK LPLVEQSPED SGGQDYIETV IPSNQLPSAA FFSETQKQFS RYFIEFEELQ  593
AAG22589.1   KHSFINPQPK LPLVEQSPED SGGQDYIETV IPSNQLPSAA FFSETQKQFS RYFIEFEELQ  315
AB037759     KHSFINPQPK MPLVEQSPED SGGQDYVETV IPSNRLPSAA FFSETQRQFS RYFIEFEELQ  440
AF193343     KHSFINPQPK LPLVEQSPED SGGQDYIETV IPSNQLPSAA FFSETQKQFS RYFIEFEELQ  593
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    610        620        630        640        650        660
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LLGKGAFGAV IKVQNKLDGC CYAVKRIPIN PASRQFRRIK GEVTLLSRLH HENIVRYYNA  659
AF193344     LLGKGAFGAV IKVQNKLDGC CYAVKRIPIN PASRHFRRIK GEVTLLSRLH HENIVRYYNA  575
T46924       ---------- ---------- ---------- ---------- ---------- ----------  1
NP_038747.   LLGKGAFGAV IKVQNKLDGC CYAVKRIPIN PASRHFRRIK GEVTLLSRLH HENIVRYYNA  653
AAG22589.1   LLGKGAFGAV IKVQNKLDGC CYAVKRIPIN PASRHFRRIK GEVTLLSRLH HENIVRYYNA  375
AB037759     LLGKGAFGAV IKVQNKLDGC CYAVKRIPIN PASRQFRRIK GEVTLLSRLH HENIVRYYNA  500
AF193343     LLGKGAFGAV IKVQNKLDGC CYAVKRIPIN PASRHFRRIK GEVTLLSRLH HENIVRYYNA  653
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    670        680        690        700        710        720
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   WIERHERPAG PGTPPPDSGP LAKDDRAARG QPASDTDGLD SVEAAAPPPI LSSSVEWSTS  719
AF193344     WIERHERPAV PGTPPPDCTP QAQDSPATYG KTSGDTEELG SVEAAAPPPI LSSSVEWSTS  635
T46924       ---------- ---------- ---------- ---------- ---------- -------STS  3
NP_038747.   WIERHERPAV PGTPPPDCTP QAQDSPATCG KTSGDTEELG SVEAAAPPPI LSSSVEWSTS  713
AAG22589.1   WIERHERPAV PGTPPPDCTP QAQDSPATYG KTSGDTEELG SVEAAAPPPI LSSSVEWSTS  435
AB037759     WIERHERPAG PGTPPPDSGP LAKDDRAARG QPASDTDGLD SVEAAAPPPI LSSSVEWSTS  560
AF193343     WIERHERPAV PGTPPPDCTP QAQDSPATYG KTSGDTEELG SVEAAAPPPI LSSSVEWSTS  713
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    730        740        750        760        770        780
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   GERSASARFP ATGPGSSDDE DDDEDEHGGV FSQSFLPASD SESDIIFDNE DENSKSQNQD  779
AF193344     AERSTSTRFP VTGQDSSSDE ED-EDERDGV FSQSFLPASD SDSDIIFDNE DENSKSQNQD  694
T46924       GERSASARFP ATGPGSSDDE DDDEDEHGGV FSQSFLPASD SESDIIFDNE DENSKSQNQD  63
NP_038747.   AERSTSTRFP VTGQDSSSDE ED-EDERDGV FSQSFLPASD SDSDIIFDNE DENSKSQNQD  772
AAG22589.1   AERSTSTRFP VTGQDSSSDE ED-EDERDGV FSQSFLPASD SDSDIIFDNE DENSKSQNQD  494
AB037759     GERSASARFP ATGPGSSDDE DDDEDEHGGV FSQSFLPASD SESDIIFDNE DENSKSQNQD  620
AF193343     AERSTSTRFP VTGQDSSSDE ED-EDERDGV FSQSFLPASD SDSDIIFDNE DENSKSQNQD  772
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------  1

                    790        800        810        820        830        840
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   EDCNEKNGCH ESEPSVTTEA VHYLYIQMEY CEKSTLRDTI DQGLYRDTVR LWRLFREILD  839
AF193344     EDCNQKDGSH EVEPSVTAEA VHYLYIQMEY CEKSTLRDTI DQGLFRDTSR LWRLFREILD  754
T46924       EDCNEKNGCH ESEPSVTTEA VHYLYIQMEY CEKSTLRDTI DQGLYRDTVR LWRLFREILD  123
NP_038747.   EDCNQKDGSH EIEPSVTAEA VHYLYIQMEY CEKSTLRDTI DQGLFRDTSR LWRLFREILD  832
```

```
AAG22589.1   EDCNQKDGSH EVEPSVTAEA VHYLYIQMEY CEKSTLRDTI DQGLFRDTSR LWRLFREILD   554
AB037759     EDCNEKNGCH ESEPSVTTEA VHYLYIQMEY CEKSTLRDTI DQGLYRDTVR LWRLFREILD   680
AF193343     EDCNQKDGSH EVEPSVTAEA VHYLYIQMEY CEKSTLRDTI DQGLFRDTSR LWRLFREILD   832
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------   1

                    850        860        870        880        890        900
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFSADSKQDD QTGD-LIKSD   898
AF193344     GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFTAEGKQDG QAGDRVIKSD   814
T46924       GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFSADSKQDD QTGD-LIKSD   182
NP_038747.   GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFTAEGKQDD QAGDGVIKSD   892
AAG22589.1   GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFTAEGKQDG QAGDRVIKSD   614
AB037759     GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFSADSKQDD QTGD-LIKSD   739
AF193343     GLAYIHEKGM IHRDLKPVNI FLDSDDHVKI GDFGLATDHL AFTAEGKQDG QAGDRVIKSD   892
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------   1

                    910        920        930        940        950        960
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   958
AF193344     PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   874
T46924       PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   242
NP_038747.   PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   952
AAG22589.1   PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   674
AB037759     PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   799
AF193343     PSGHLTGMVG TALYVSPEVQ GSTKSAYNQK VDLFSLGIIF FEMSYHPMVT ASERIFVLNQ   952
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------   1

                    970        980        990       1000       1010       1020
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LRDPTSPKFP EDFDDGEHAK QKSVISWLLN HDPAKRPTAT ELLKSELLPP PQMEESELHE   1018
AF193344     LRDPTSPKFP DDFDDGEHTK QKSVISWLLN HDPAKRPTAM ELLKSELLPP PQMEESELHE   934
T46924       LRDPTSPKFP EDFDDGEHAK QKSVISWLLN HDPAKRPTAT ELLKSELLPP PQMEESELHE   302
NP_038747.   LRDPTSPKFP DDFDDGEHTK QKSVISWLLN HDPAKRPTAM ELLKSELLPP PQMEESELHE   1012
AAG22589.1   LRDPTSPKFP DDFDDGEHTK QKSVISWLLN HDPAKRPTAM ELLKSELLPP PQMEESELHE   734
AB037759     LRDPTSPKFP EDFDDGEHAK QKSVISWLLN HDPAKRPTAT ELLKSELLPP PQMEESELHE   859
AF193343     LRDPTSPKFP DDFDDGEHTK QKSVISWLLN HDPAKRPTAM ELLKSELLPP PQMEESELHE   1012
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------   1

                   1030       1040       1050       1060       1070       1080
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   VLHHTLTNVD GKAYRTMMAQ IFSQRISPAI DYTYDSDILK GNFSIRTAKM QQHVCETIIR   1078
AF193344     VLHHTLANTD GKAYRTMMSQ LFCQHSSPAI DYTYDSDILK GNFLIRTAKI QQLVCETIVR   994
T46924       VLHHTLTNVD GKAYRTMMAQ IFSQRISPAI DYTYDSDILK GNFSIRTAKM QQHVCETIIR   362
NP_038747.   VLHHTLANID GKAYRTMMSQ IFCQHISPAI DYTYDSDILK GNFLIRTAKI QQLVCETIVR   1072
AAG22589.1   VLHHTLANTD GKAYRTMMSQ LFCQHSSPAI DYTYDSDILK GNFLIRTAKI QQLVCETIVR   794
AB037759     VLHHTLTNVD GKAYRTMMAQ IFSQRISPAI DYTYDSDILK GNFSIRTAKM QQHVCETIIR   919
AF193343     VLHHTLANTD GKAYRTMMSQ LFCQHSSPAI DYTYDSDILK GNFLIRTAKI QQLVCETIVR   1072
AJ243428     ---------- ---------- ---------- ---------- ---------- ----------   1

                   1090       1100       1110       1120       1130       1140
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   IFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRVPFA RYVARNNILN   1138
AF193344     VFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRVPFA RYVARNNILN   1054
T46924       IFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRIPFA RYVARNNILN   422
NP_038747.   VFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRVPFA RYVARNNILN   1132
AAG22589.1   VFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRVPFA RYVARNNILN   854
AB037759     IFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRIPFA RYVARNNILN   979
AF193343     VFKRHGAVQL CTPLLLPRNR QIYEHNEAAL FMDHSGMLVM LPFDLRVPFA RYVARNNILN   1132
AJ243428     ---------- ---------- --------AL FMDHSGMLVM LPFDLRIPFA RYVARNNILI   32

                   1150       1160       1170       1180       1190       1200
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LKRYCIERVF TPRKLDRFHP KELLECAFDI VTSTTNSFLP TAEIIYTIYE IIQEFPALQE   1198
AF193344     LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTANSSLP TAETIYTIYE VIQEFPALQE   1114
T46924       LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTTNSFLP TAEIIYTIYE IIQEFPALQE   482
NP_038747.   LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTTNSSLP TAETIYTIYE IIQEFPALQE   1192
AAG22589.1   LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTANSSLP TAETIYTIYE VIQEFPALQE   914
AB037759     LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTTNSFLP TAEIIYTIYE IIQEFPALQE   1039
AF193343     LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTANSSLP TAETIYTIYE VIQEFPALQE   1192
AJ243428     LKRYCIERVF RPRKLDRFHP KELLECAFDI VTSTTNSFLP TAEIIYTIYE IIQEFPALQE   92

                   1210       1220       1230       1240       1250       1260
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YIILYDAVTE KLTRREVEAK FCNLSLSSNS   1258
AF193344     RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YVILYDAVTE KLTRREVEAK FCNLSLSSNS   1174
T46924       RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YIILYDAVTE KLTRREVEAK FCNLSLSSNS   542
```

```
NP_038747.   RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YVILYDAVTE KLTRREVEAK FCNLSLSSNS 1252
AAG22589.1   RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YVILYDAVTE KLTRREVEAK FCNLSLSSNS 974
AB037759     RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YIILYDAVTE KLTRREVEAK FCNLSLSSNS 1099
AF193343     RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YVILYDAVTE KLTRREVEAK FCNLSLSSNS 1252
AJ243428     RNYSIYLNHT MLLKAILLHC GIPEDKLSQV YIILYDAVTE KLTRREVEAK FCNLSLSSNS 152

                   1270       1280       1290       1300       1310       1320
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LCRLYKFIEQ KGDLQDLMPT INSLIEQKTG IAQLVKYGLK DLEEVVGLLK KLGIKLQVWV 1318
AF193344     LCRLYKFIEQ KGDLQDLTPT INSLIKQKTG IAQLVKYSLK DLEEVVGLLK KLGVKLQ--V 1232
T46924       LCRLYKFIEQ KGDLQDLMPT INSLIKQKTG IAQLVKYGLK DLEEVVGLLK KLGIKLQ--V 600
NP_038747.   LCRLYKFIEQ KGDLQDLTPT INSLIKQKTG VAQLVKYSLK DLEDVVGLLK KLGVKLQ--V 1310
AAG22589.1   LCRLYKFIEQ KGDLQDLTPT INSLIKQKTG IAQLVKYSLK DLEEVVGLLK KLGVKLQ--V 1032
AB037759     LCRLYKFIEQ KGDLQDLMPT INSLIKQKTG IAQLVKYGLK DLEEVVGLLK KLGIKLQ--V 1157
AF193343     LCRLYKFIEQ KGDLQDLTPT INSLIKQKTG IAQLVKYSLK DLEEVVGLLK KLGVKLQ--V 1310
AJ243428     LCRLYKFIEQ KGDLQDLMPT INSLIKQKTG IAQLVKYGLK DLEEVVGLLK KLGIKLQ--V 210

                   1330       1340       1350       1360       1370       1380
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LINLGLVYKV QQHNGIIFQF VAIIKRRQRA VPEILAAGGR YDLLIPQFRG PQALGPVPTA 1378
AF193344     SINLGLVYKV QQHNGIIFQF LAFSKRRQRV VPEILAAGGR YDLLIPKFRG PQALGPVPTA 1292
T46924       LINLGLVYKV QQHNGIIFQF VAFIKRRQRA VPEILAAGGR YDLLIPQFRG PQALGPVPTA 660
NP_038747.   SINLGLVYKV QQHTGIIFQF LAFSKRRQRV VPEILAAGGR YDLLIPKFRG PQTVGPVPTA 1370
AAG22589.1   SINLGLVYKV QQHNGIIFQF LAFSKRRQRV VPEILAAGGR YDLLIPKFRG PQALGPVPTA 1092
AB037759     LINLGLVYKV QQHNGIIFQF VAFIKRRQRA VPEILAAGGR YDLLIPQFRG PQALGPVPTA 1217
AF193343     SINLGLVYKV QQHNGIIFQF LAFSKRRQRV VPEILAAGGR YDLLIPKFRG PQALGPVPTA 1370
AJ243428     LINLGLVYKV QQHNGIIFQF VAFIKRRQRA VPEILAAGGR YDLLIPQFRG PQALGPVPTA 270

                   1390       1400       1410       1420       1430       1440
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   IGVSIAIDKI SAAVLNMEES VSSVTIGSGD LLVVSVGQMS MSRAINLTQK LWTAGITAEI 1438
AF193344     VGVSIAIDKI FAAVLNMGEP VT---VSSCD LLVVSAGQMS MSRAINLTQK LWTAGITAEI 1349
T46924       IGVSIAIDKI SAAVLNMEES VT---ISSCD LLVVSVGQMS MSRAINLTQK LWTAGITAEI 717
NP_038747.   VGVSIAIDKI FAVVLNMEEP VT---VSSCD LLVVSVGQMS MSRAINLTQK LWTAGITAEI 1427
AAG22589.1   VGVSIAIDKI FAAVLNMGEP VT---VSSCD LLVVSAGQMS MSRAINLTQK LWTAGITAEI 1149
AB037759     IGVSIAIDKI SAAVLNMEES VT---ISSCD LLVVSVGQMS MSRAINLTQK LWTAGITAEI 1274
AF193343     VGVSIAIDKI FAAVLNMGEP VT---VSSCD LLVVSAGQMS MSRAINLTQK LWTAGITAEI 1427
AJ243428     IGVSIAIDKI SAAVLNMEES VT---ISSCD LLVVSVGQMS MSRAINLTQK LWTAGITAEI 327

                   1450       1460       1470       1480       1490       1500
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   MYDWSQFQSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLETELVDHV 1498
AF193344     MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLESDLVDHV 1407
T46924       MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLETELVDHV 775
NP_038747.   MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLESDLVDHV 1485
AAG22589.1   MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLESDLVDHV 1207
AB037759     MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLETELVDHV 1332
AF193343     MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLESDLVDHV 1485
AJ243428     MYDWS--QSQ EELQEYCRHH EITYVALVSD KEGSHVKVKS FEKERQTEKR VLETELVDHV 385

                   1510       1520       1530       1540       1550       1560
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   LQKLRTKVTD ERNFREASDN LAVQNLKGSF SNASGLFEIH GATVVPIVSV LAPEKLSAST 1558
AF193344     MQKLRTKVGD ERNFRDASDN LAVQTLKGSF SNASGLFEIH GTTVVPTVSV ISPEKLSAST 1467
T46924       LQKLRTKVTD ERNGREASDN LAVQNLKGSF SNASGLFEIH GATVVPIVSV LAPEKLSAST 835
NP_038747.   MQKLRTKVGD ERNFRDASDN LAVQTLKGSF SNASGLFEIH GTTVVPNVIV LAPEKLSAST 1545
AAG22589.1   MQKLRTKVGD ERNFRDASDN LAVQTLKGSF SNASGLFEIH GTTVVPTVSV ISPEKLSAST 1267
AB037759     LQKLRTKVTD ERNGREASDN LAVQNLKGSF SNASGLFEIH GATVVPIVSV LAPEKLSAST 1392
AF193343     MQKLRTKVGD ERNFRDASDN LAVQTLKGSF SNASGLFEIH GTTVVPTVSV ISPEKLSAST 1545
AJ243428     LQKLRTKVTD ERNGREASDN LAVQNLKGSF SNASGLFEIH GATVVPIVSV LAPEKLSAST 445

                   1570       1580       1590       1600       1610       1620
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL2 Prote   RRRYETQVQT RLQTSLANLH QKSSEIEILA VVDLPKETIL QFLSLEWDAD EQAFNTTVKQ 1618
AF193344     RRRHEIQVQT RLQTTLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 1526
T46924       RRRYETQVQT RLQTSLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 894
NP_038747.   RRRHEIQVQT RLQTTLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 1604
AAG22589.1   RRRHEIQVQT RLQTTLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 1326
AB037759     RRRYETQVQT RLQTSLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 1451
AF193343     RRRHEIQVQT RLQTTLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 1604
AJ243428     RRRYETQVQT RLQTSLANLH QKSSEIEILA -VDLPKETIL QFLSLEWDAD EQAFNTTVKQ 504

                   1630       1640       1650       1660
             ....|....| ....|....| ....|....| ....|....| ....
MOL2 Prote   LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 1662
AF193344     LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 1570
```

```
T46924       LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 938
NP_038747.   LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 1648
AAG22589.1   LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 1370
AB037759     LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 1495
AF193343     LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 1648
AJ243428     LLSRLPKQRY LKLVCDEIYN IKVEKKVSVL FLYSYRDDYY RILF 548
```

Domain Analysis

The presence of identifiable domains in the protein disclosed herein was determined by searches versus domain databases such as Pfam, PROSITE, ProDom, Blocks or Prints and then identified by the Interpro domain accession number. Significant domains are summarized in Table 2G.

Table 2G. Domain Analysis of MOL2b

MODEL	DESCRIPTION	SCORE	E-VALUE	N
pkinase	Protein kinase domain	282.0	7.8e-81	4
Ribosomal_L23	Ribosomal protein L23	5.0	4.1	1
GalP_UDP_transf	Galactose-1-phosphate uridyl transfer	2.7	6.5	1
mRNA_cap_enzyme	mRNA capping enzyme	-181.3	9.6	1

IPR000719; (Euk_pkinase)
Eukaryotic protein kinase
PROSITE: PS00107 PROTEIN_KINASE_ATP
PROFILE: PS50011 PROTEIN_KINASE_DOM
PFAM: PF00069 pkinase
SMART: SM00221 STYKc
IPR002290 Serine/Threonine protein kinase family active site
IPR001245 Tyrosine kinase catalytic domain
GO Hierarchy:
Molecular Function:
protein kinase (GO:0004672)
ATP binding (GO:0005524)
Biological Process:
protein phosphorylation (GO:0006468)

Eukaryotic protein kinases are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common with both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. In the N-terminal extremity of the catalytic domain there is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. In the central part of the catalytic domain there is a conserved aspartic acid residue which is important for the catalytic activity of the enzyme.

This indicates that the sequence of the invention has properties similar to those of other proteins known to contain this/these domain(s) and similar to the properties of these domains.

Chromosomal information

MOL2 belongs to genomic DNA [Acc.NO.: AC025168 from GenbankNEW]. Within this GenbankNew entry was a note showing that the sequence was from Chromosome 15q14. Therefore we assign the chromosomal locus of this invention as Chromosome 15q14.

Tissue expression

MOL2 is expressed in at least the following tissues: brain and liver (derived from literature sources) and thyroid (derived from 20466828_EXT1).

Based on information available on expression of SWISSPROT-ACC:P29089 TYPE-1B ANGIOTENSIN II RECEPTOR (AT1B) (AT3) - *Rattus norvegicus* (Rat), the closest G-protein coupled receptor family member it is likely that MOL2 is expressed in cardiac tissue, renal tissue, and vascular tissue as angiotensin is expressed in these tissues.MOL2 has similarity to the murine GNC2 eIFK protein, a possible GNC2 eIFK and other GNC2 eIFKs and their functions as described in but not limited to the references below: In eukaryotic cells, protein synthesis is regulated in response to various environmental stresses by phosphorylating the alpha subunit of the eukaryotic initiation factor 2 (eIF2alpha) (Berlanga, et.al., Eur J Biochem; 265(2):754-62; Oct,1999). Three different eIF2alpha kinases have been identified in mammalian cells, the heme-regulated inhibitor (HRI), the interferon-inducible RNA-dependent kinase (PKR) and the endoplasmic reticulum-resident kinase (PERK). A fourth eIF2alpha kinase, termed GCN2, was previously characterized from Saccharomyces cerevisiae, Drosophila melanogaster and Neurospora crassa. Berlanga et al. 1999 describe the cloning of a mouse GCN2 cDNA (MGCN2), which represents the first mammalian GCN2 homolog. MGCN2 has a conserved motif, N-terminal to the kinase subdomain V, and a large insert of 139 amino acids located between subdomains IV and V that are characteristic of the known eIF2alpha kinases. Furthermore, MGCN2 contains a class II aminoacyl-tRNA synthetase domain and a degenerate kinase segment, downstream and upstream of the eIF2alpha kinase domain, respectively, and both are singular features of GCN2 protein kinases. MGCN2 mRNA is expressed as a single message of approximately 5.5 kb in a wide range of different tissues, with the highest levels in the liver and the brain. Specific polyclonal anti-(MGCN2) immunoprecipitated an eIF2alpha kinase activity and recognized a 190 kDa phosphoprotein in Western blots from either mouse liver or MGCN2-transfected 293 cell extracts. Interestingly, serum starvation increased eIF2alpha phosphorylation in MGCN2-transfected human 293T cells. This finding provides evidence that GCN2 is the unique eIF2alpha kinase present in all eukaryotes from yeast to mammals and underscores the role of MGCN2 kinase in translational control and its potential physiological significance.

A family of protein kinases regulates translation in response to different cellular stresses byphosphorylation of the alpha subunit of eukaryotic initiation factor-2 (eIF-2alpha). In yeast, an eIF-2alpha kinase, GCN2, functions in translational control in response to amino acid starvation. It is thought that uncharged tRNA that accumulates during amino acid limitation binds to sequences in GCN2 homologous to histidyl-tRNA synthetase (HisRS) enzymes, leading to enhanced kinase catalytic activity. Given that starvation for amino acids also stimulates phosphorylation of eIF-2alpha in mammalian cells, we searched for and identified a GCN2 homologue in mice. Sood et.al., 2000 cloned three different cDNAs encoding mouse GCN2 isoforms, derived from a single gene, that vary in their amino-terminal sequences. Like their yeast counterpart, the mouse GCN2 isoforms contain HisRS-related sequences juxtaposed to the kinase catalytic domain. While GCN2 mRNA was found in all mouse tissues examined, the isoforms appear to be differentially expressed. Mouse GCN2 expressed in yeast was found to inhibit growth by hyperphosphorylation of eIF-2alpha, requiring both the kinase catalytic domain and the HisRS-related sequences. Additionally, lysates prepared from yeast expressing mGCN2 were found to phosphorylate recombinant eIF-2alpha substrate. Mouse GCN2 activity in both the in vivo and in vitro assays required the presence of serine-51, the known regulatory phosphorylation site in eIF-2alpha. Together, those studies identify a new mammalian eIF-2alpha kinase, GCN2, that can mediate translational control.Phosphorylation of the alpha subunit of eukaryotic initiation factor 2 (eIF-2alpha) is a well-characterized mechanism regulating protein synthesis in response to environmental stresses (Yang et al., Mol Cell Biol; 20(8):2706-17; Apr, 2000). In the yeast Saccharomyces cerevisiae, starvation for amino acids induces phosphorylation of eIF-2alpha by Gcn2 protein kinase, leading to elevated translation of GCN4, a transcriptional activator of more than 50 genes. Uncharged tRNA that accumulates during amino acid limitation is proposed to activate Gcn2p by associating with Gcn2p sequences homologous to histidyl-tRNA synthetase (HisRS) enzymes. Given that eIF-2alpha phosphorylation in mammals is induced in response to both carbohydrate and amino acid limitations, we addressed whether activation of Gcn2p in yeast is also controlled by different nutrient deprivations. It was found that starvation for glucose induces Gcn2p phosphorylation of eIF-2alpha and stimulates GCN4 translation. Induction of eIF-2alpha phosphorylation by Gcn2p during glucose limitation requires the function of the HisRS-related domain but is largely independent of the ribosome binding sequences of Gcn2p. Furthermore, Gcn20p, a factor required for Gcn2 protein kinase stimulation of GCN4 expression in response to amino acid starvation, is not essential for GCN4 translational control in response to limitation for carbohydrates. These results indicate there are differences between the mechanisms regulating Gcn2p activity in response to amino acid and carbohydrate deficiency. Gcn2p induction of GCN4 translation during carbohydrate limitation enhances storage of amino acids in the vacuoles and facilitates entry into exponential growth during a shift from low-glucose to high-glucose medium. Gcn2p function also contributes to maintenance of glycogen levels during prolonged glucose starvation, suggesting a linkage between amino acid control and glycogen metabolism.

Uses of the Compositions of the Invention

The expression pattern, map location and protein similarity information for MOL2 suggest that it may function like a member of the GCN2 eIFαK family. Therefore, the nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated, for example but not limited to, in various pathologies /disorders as described below:

- Hyperthyroidism
- Hypothyroidism
- Von Hippel-Lindau (VHL) syndrome
- Alzheimer's disease
- Stroke
- Tuberous sclerosis
- Hypercalceimia
- Parkinson's disease
- Huntington's disease
- Cerebral palsy

- Epilepsy
- Lesch-Nyhan syndrome
- Multiple sclerosis
- Ataxia-telangiectasia
- Leukodystrophies
- Behavioral disorders
- Addiction
- Anxiety
- Pain
- Cirrhosis
- Transplantation
- and/or other pathologies/disorders.

Potential therapeutic uses for the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues).

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies and disorders. For example, but not limited to, a cDNA encoding the GCN2 eIFαK -like protein may be useful in gene therapy, and the GCN2 eIFαK -like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Hyperthyroidism, Hypothyroidism, Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, Hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection Cirrhosis, Transplantation and/or other pathologies/disorders. The novel nucleic acid encoding the GCN2 eIFαK-like protein, and the GCN2 eIFαK -like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL3

An additional protein of the invention, referred to herein as MOL3, is a human complement C3-like protein. The novel nucleic acid was identified by TblastN using CuraGen Corporation's sequence file for MOL probe or homolog, run against the Genomic Daily Files made available by GenBank. The nucleic acid was further predicted by the program GenScan™, including selection of exons. These were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. The novel nucleic acid of 4894 nucleotides (82254077.0.1, SEQ ID NO:5) encoding a novel olfactory receptor-like protein is shown in Table 3A. An open reading frame (ORF) was identified beginning with an ATG initiation codon at nucleotides 1-3 and ending with a TGA codon at nucleotides 4837-4839. Putative untranslated regions downstream from the termination codon are underlined in Table 3A, and the start and stop codons are in bold letters.

Table 3A. MOL3 Nucleotide Sequence (SEQ ID NO:5)
ATGTCCCCGTCTCTCCCTTTCTCTGCCATCTCCCTATGTCTCTCCCATCTCCCTATGCCTCTCCCATCTCCAAGG TACATCCTGGTGACCCCCCGAGTTCTGAGGGTTGGCAGTCCGGAGAGCATTCACATTCAGGCCCACTCAGACTCC AGACAGCCCCTCACAAGGACCCTCAAGGTGAACCTCACAGTGTGGGACTTCCCCATGAGGAAGACAGTGTTGGCA AGGAGCCAGCTCATTCTCTCACCAGGAAACAACTTTATGGACCAGGCACCTGTGACGGTTCCCGAGAGCCTGATG TACCTCCCAAAACCAGGGCAGCAATATGTCATCATCCGGGCAACTTGGGCACCCACCTCGGCTCCTCATTCATG GAGAAGATGGTGCTGGTGGCTCTTCATGCTGGCTACATCTTTATCCAGACGGAGAAGACCATCTACACCCCTTCT CCCCTAGTTCACTACCGGGTGTTCACTGTGAACCACAAGATGGACCCTGTGACCAGGACATTCACTCTGGACATC AAGAATCCTGATGGGTCCCCAGCTTCCAGAGTCCTTGTCCACTCCCAAGACCAACCTGGGGTGCTTGCACTGTCT TGGGGCCCTGAAAAGTCCCTGTGCCTCAGTTTGGGGACCTGGACCATCGAAGCCAGCTACCAAAGTACACCCAAG CAGAAGTTCGAGGCTGCCTTTGATGTGAAGGAATATGTCCTCCCATCTTTTGAGGTCCAGCTGGTCCCAAATAAG ACTTTCTTTTACCTCAAGGATGAGGCTCTGGGCGTTGACATCCAGGCTCGGTATATATTTAACAAGCCAGTGGAC GGACATGCTTTGGTCATCTTTGGGGTGAAATTGGACTCCTGCCGGATCCCTATCCAAAGCTCCCTGCAGAGGGTG GAGGTGACTGAAACAGGGGGTGAGATGGTGCAAGCTGAGACCTCAGGGGTGAAGATCATCCAGAGCCCATACAAC ATCAAGTTCACCAGGACACCCCAGTATTTCAAGCCAGGAATGCCCTTCCACTTTCGGGTCAGAGTCGTACAAAGC AGTCCTATTCAGATCATATTCCAGTCTCACCTCTCACACCAGGCCACTGCAGGCTTTTCCTTCACCTTACCCCAG ATTCCACCTCAGGTCTTCATCTCAAATCCTGATGGGTCCCCAGCTTCCAGAGTCCTTGTCCACTCCCAAGACCAA AAAGTGTACACCTCAGCTGAGGGGTTGGCCACTCTGACCATCAACACAGATGCAAATCTGGACAAGCTCCCCATC GAGGTGAAAACTGAGGAATCTCTTCAGCCAGAGGAGCAGGCTTCAGCCAAGATGACAGCTTGGCCTTACTTGACT CAGGATGGGTCAGGAAACTTCCTACACATCGAAGTAAAGACATTGGGCACAGAGGTTGGCAGCAGCATCCAGCTG AGCCTCAACACAAGGCATCAGGACCCTAAAACCAAGGACAAGATTACTCACTTCACCATCCTGGTGGTCAGGGAG GGTAAGGCCCGGCAGCTTGGGAGGCAGGTGGCGCAGGTGGGGGTACCCTCCTTCCGCATTCTGGCCTTTTATTTA CTTCCCAGAGGAGCAAGCCAAGACCCTGAGTTGGTGGCTGATTCCATATGGATTGATGTGAATGACAGATGCATA GGGCTGAAAGTTGGCTTGAAGAATGATAGATTCTTCCAGTCTTTGGAGCCCAACAGCCAAGTCGAACTGAAGGTG ACAGGTGATGCAGAAGCCACAGTGGGGCTGGTGGCTGTGGACAAGGCTGTCTATGTCTTGAACAGCAAACACAAG CTCACTCAGAAGAAGGTATGGAATGTGGTGGAGGAACATGACATTGGCTGCACAGGAGGAAGTGGGAAAGACAGA

TTTGCTGTGTTCAAGGATGCTGGATTGGACCTGAAAATCAGCACAGGAATGGATAGCGGCCACCAGCAAAGTCAC AGCTGCCAGGAGGCTGAGGTGGGAGAATCACTTGAACCCGGGAGGCAGAGGTTGCGGTCAGCCGAGATTGCGCCA CTGCACTCCAGCGTGAACAAGTTTAAGACAGAGCTGGAGCAAAAGTGCTGTGAGGCTGGGCTCCGGGAGAGCCCA GTGGGGCTGTCTTGTGAGGAGAGGACCTGGCATGTCCGCCATGGTCCAGCCTGTGTGGCTGCTTTCCTGGACTGC TGCTCACACCTGCTCCCTCCAGCGGATGAAGAAGAGGACTTCGATGACCTCTTCTTGGATGACATGCCTGTGCGG ACCTTGTTCCCCGAGAGTTGGCTCTGGAACAGCATCTCCCATTACCCCATCTCTGTGAAGGTGCCAGATTCCATC ACCACGTGGCAGTTTGTGGTGGTCAGCCTCAAGGCTGGACAAGGTGGTCTCTGTGTCTCGGACCCCTTTGAGCTG ACAGTTATGAAATCGTTCTTTGTGGACCTTAAGTTGCCCTCCTCCGTGATCAGGAATGAGCAGGTCCAGATCCAA GCCATGTTGTACAATTTCAGGGATCGCCAGGCCAAGGTCCGAGTGGAGTTCCCCCACAAGGAGACACTGTGCAGT GCGTCAAAGCCAGGAGCACCATCCCACCAGGTAGTGGTCGTGCCCCCCACCTCCTCCAAGATAGTACACTTTGTG CTTCTCCCTCTGGAGACAGGCAAAGTGGACGTGGAGGTCAAGGCTGTGGGCTACGGGGTCCAGGACCATGTGAAG AAGACACTCTTGGTCGAAGGTTGTGGTTATTCAGGTCAGACCCAGACAAAACTGGTGCCAAGACAGGAGTTCTTG AACATGGTACCCGACACGGAGGCGGAAGTGTTTATCAGTGTTCAAGGTGACATCCTTGGTGAGACAATTGTGGGC AGCCTGACACCCAGTGAGATTCAGCAGCTGCTGCGGGTCCCCACGGGCTGCCCTGAGCAGACGCTGAGCTCCCTG ACGCCCGTCATCATCCTGTCCCGCTATTTGGATACCACCGGCCAGTGGGGCAAGGTCGGGGTGGAGCACAGGGAC CAGGTGATGAAGAATATTGGCTACACTCAGATGCTGACCCACCGGAGTTCAGACGGCACCTACCACACCTCCAAG GGGAACCCAGGAAGCACTTGGCTCACAAGCTATGTGTTCCGCGTCTTTGCCCTGGCCTACTCTATGATGACGACC CAAGTGCTTAGCCTGTCCTCTCTCTGTGACATGGCCAACTGGATCATCATCGACAGGCAGGCAGAGGATGGGCAC TTCCTGGAGAAGGGCCCTGTGGTCATGACATCCATGTCCGAGGAGGATGTATCCCTCACAGCTCTTGTCCTAATA GCCCTGAATGAGGGAAAGGAGTTGTGCAGACAGAAGGTAGGACCCAATTTGATGGCCAGCATCGAGAAGGCCGGA GGATTGCTTGAGCTCAGGAGGTTGAGGCTGCAGCGGAGCTATGCCGTAGCCATAGCCTCCTATGCACTGGCCGAC AAAACCCACTGGCCAGTGGATGAGCAGAATCTGGGCTCCCTGTACACCATTGAGGCCACAGCCTATGGGCTCATG CAGAAGCTGGAGCTGGGCCGGTACAATGAGACACACGCCATAGCCAAGTGGCTACTAGAGAAGCAGGAGCTGGGA GGAGGCTTCAGGTCCACCCAGCCAGGCAGGAGCAGTCGCCTTTCCCACCCACAGCGCTGGCCACAGGGCTCCCTG NTGGCCCTTGAAGCTCTGACCCGCTTCCGCGAAGCTGTCCCCTTCAAGGGCATCCAGGATCTCCACGTCCAGATC AGAGCCCCCAAGACAGCCCTGAATGTGAATTGGTACATTGATCACAGCAATGCCTACCAACAGCGGTCAGCAAAG TTCCTTGCCCAGGACGACCTAGAGATCAAAGCCAGTGGCAACGGAGAGGCACCATCTCGATCCTGACAATGTAT CACAAGTCCCCAGAGTCCCGGGAGGACAACTGCAACCTGTACCACCTGAATGCGACTCTCCACAGTGCCCTAGAA GAAAATAAAAAGGGAGGTGAGACTTTTCGGCTCCGGATGGAAACAAGGTTCCAGAACAATGGAGAGGCCACAATG ACTATCATGGAGGTCTCCCTGCTCACGGGCTTCTACCCCAACCAGGATGACCTCAAACAGCTCACGAGTGATGTG GAGAGGTACGCCTTTCAGTACAAAACCAAGACAAGTACCAGCGACAGCACTGTTGTCCTCTACCTGGAAAAGCTC TCCCATGAGAAGAACACGGTGCTGGGCTTTCGGGTTCACAGGATGCTGCAGGCGGAGTTCCTGCAGGCCGCCCTG GTCACCATCTACGACTACTACGAGCCTTCCCGGAGGTGCAGCACTTTCTACAACCTGCCCACAGAGCAATCTTCC CTGAGAAAGATCTGCCACAAAGACATCTGCAGATGTGCAGAGGGACAGTGCCCATCCCTGCAGAAGCCCAGTGGC CAATTGAGGCAGGAGGAGCTCCAGACAACAGCATGTGAGGCAGGCGTGGATTTTGTGTACAAGACAAAGCTGGAA TCTGTGGAGGTCTCTGCCTCCAACCCTTACGTCTATTACAACACGCAGCTCGAAGACATCATTAAGAGTGGTACG GACCCTGCCAAACCCCTGGCCATGAAGAAATTCGTCTCCCATGCCACTTGCCATGACTCCCTGGGGTTGCAAGAA CAGGAATCGTACCTCATCATGGGCCAGACGTCAGACCTGTGGAGAATCAAATCTGATTACAGCTATGTTCTGGGC AAGGAGACGTTCCTCATCCTTTGGCCAGCAGATGGAGATGCCAGCAAGAAAGAATTGCGGACCAACTGGAGGAA TTTTTGGAATATATGCGCACCCACGGCTGCCAGTCCTGAGCCTCTTCTGCTTTCAGGGAGGTGTCATCAGGGCAG CTCTGGGCCACGTGGGTTT

The disclosed MOL3 polypeptide (SEQ ID NO:6) encoded by SEQ ID NO:5 is 1612 amino acid residues, and is presented using the one-letter code in Table 3B. The MOL3 protein were analyzed for signal peptide prediction and cellular localization. SignalP results predict that MOL3 is cleaved between position 20 and 21 of SEQ ID NO:6. Psort and Hydropathy profiles also predict that MOL3 contains a signal peptide and is likely to be localized at the endoplasmic reticulum (certainty of 0.5500).

Table 3B. Encoded MOL3 protein sequence (SEQ ID NO:6).
MSPSLPFSAISLCLSHLPMPLPSPRYILVTPRVLRVGSPESIHIQAHSDSRQPLTRTLKVNLTVWDFPMRKTVLA RSQLILSPGNNFMDQAPVTVPESLMYLPKPGQQYVIIRATWAPTSGSSFMEKMVLVALHAGYIFIQTEKTIYTPS PLVHYRVFTVNHKMDPVTRTFTLDIKNPDGSPASRVLVHSQDQPGVLALSWGPEKSLCLSLGTWTIEASYQSTPK QKFEAAFDVKEYVLPSFEVQLVPNKTFFYLKDEALGVDIQARYIFNKPVDGHALVIFGVKLDSCRIPIQSSLQRV EVTETGGEMVQAETSGVKIIQSPYNIKFTRTPQYFKPGMPFHFRVRVVQSSPIQIIFQSHLSHQATAGFSFTLPQ IPPQVFISNPDGSPASRVLVHSQDQKVYTSAEGLATLTINTDANLDKLPIEVKTEESLQPEEQASAKMTAWPYLT QDGSGNFLHIEVKTLGTEVGSSIQLSLNTRHQDPKTKDKITHFTILVVREGKARQLGRQVAQVGVPSFRILAFYL LPRGASQDPELVADSIWIDVNDRCIGLKVGLKNDRFFQSLEPNSQVELKVTGDAEATVGLVAVDKAVYVLNSKHK LTQKKVWNVVEEHDIGCTGGSGKDRFAVFKDAGLDLKISTGMDSGHQQSHSCQEAEVGESLEPGRQRLRSAEIAP LHSSVNKFKTELEQKCCEAGLRESPVGLSCEERTWHVRHGPACVAAFLDCCSHLLPPADEEEDFDDLFLDDMPVR

```
TLFPESWLWNSISHYPISVKVPDSITTWQFVVVSLKAGQGGLCVSDPFELTVMKSFFVDLKLPSSVIRNEQVQIQ
AMLYNFRDRQAKVRVEFPHKETLCSASKPGAPSHQVVVVPPTSSKIVHFVLLPLETGKVDVEVKAVGYGVQDHVK
KTLLVEGCGYSGQTQTKLVPRQEFLNMVPDTEAEVFISVQGDILGETIVGSLTPSEIQQLLRVPTGCPEQTLSSL
TPVIILSRYLDTTGQWGKVGVEHRDQVMKNIGYTQMLTHRSSDGTYHTSKGNPGSTWLTSYVFRVFALAYSMMTT
QVLSLSSLCDMANWIIIDRQAEDGHFLEKGPVVMTSMSEEDVSLTALVLIALNEGKELCRQKVGPNLMASIEKAG
GLLELRRLRLQRSYAVAIASYALADKTHWPVDEQNLGSLYTIEATAYGLMQKLELGRYNETHAIAKWLLEKQELG
GGFRSTQPGRSSRLSHPQRWPQGSLXALEALTRFREAVPFKGIQDLHVQIRAPKTALNVNWYIDHSNAYQQRSAK
FLAQDDLEIKASGNGRGTISILTMYHKSPESREDNCNLYHLNATLHSALEENKKGGETFRLRMETRFQNNGEATM
TIMEVSLLTGFYPNQDDLKQLTSDVERYAFQYKTKTSTSDSTVVLYLEKLSHEKNTVLGFRVHRMLQAEFLQAAL
VTIYDYYEPSRRCSTFYNLPTEQSSLRKICHKDICRCAEGQCPSLQKPSGQLRQEELQTTACEAGVDFVYKTKLE
SVEVSASNPYVYYNTQLEDIIKSGTDPAKPLAMKKFVSHATCHDSLGLQEQESYLIMGQTSDLWRIKSDYSYVLG
KETFLILWPADGDASKKELRDQLEEFLEYMRTHGCQS
```

The full amino acid sequence of the protein of the invention was found to have 257 of 734 amino acids (35 %) identical and 403 of 734 (54%) homolog to a *Cavia porcellus* (guinea pig) complement C3 precursor (contains: C3A anaphylatoxin) (ACC:P12387; 1666 aa), and 255 of 717 amino acid residues (35 %) identical to, and 401 of 717 residues (55 %) similar to, the 1663 amino acid residue complement C3 precursor (contains: C3A anaphylatoxin) from *Homo sapiens* (human) (ACC:P01024).

The disclosed MOL3 protein (SEQ ID NO:6) also has good identity with a number of complement compontent proteins, as shown in Table 3C.

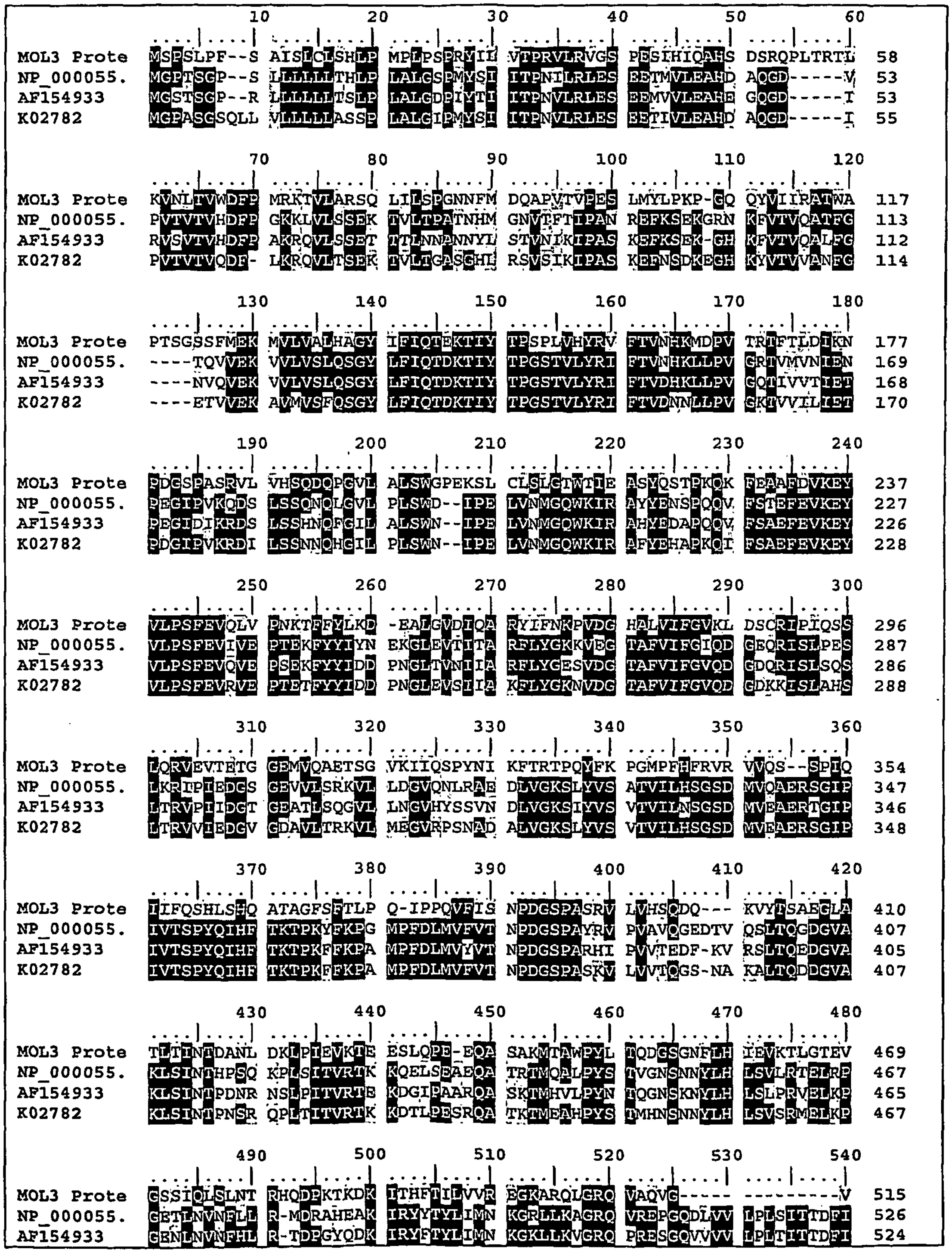
Table 3C. BLAST results for MOL3

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi|4557385|ref|NP _000055.1|	complement component 3 precursor [Homo sapiens]	1663	633/1750 (36%)	938/1750 (53%)	0.0
gi|11869931|gb|AA G40565.1|AF154933 _1 (AF154933)	complement component C3 [Sus scrofa]	1661	617/1733 (35%)	935/1733 (53%)	0.0
gi|309122|gb|AAC4 2013.1| (K02782)	preprocomplement component C3 [Mus musculus]	1663	606/1734 (34%)	915/1734 (51%)	0.0

This information is presented graphically in the multiple sequence alignment given in Table 3D (with MOL3 being shown on line 1) as a ClustalW analysis comparing MOL3 with related protein sequences.

Table 3D. Information for the ClustalW proteins:

1) Novel MOL3 (SEQ ID NO:6)
2) gi|4557385|ref|NP_000055.1| complement component 3 precursor [Homo sapiens] (SEQ ID NO:41)
3) gi|11869931|gb|AAG40565.1|AF154933_1 (AF154933) complement component C3 [Sus scrofa] (SEQ ID NO:42)
4) gi|309122|gb|AAC42013.1| (K02782) preprocomplement component C3 [Mus musculus] (SEQ ID NO:43)



```
                     10         20         30         40         50         60
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   MSPSLPF--S AISLCLSHLP MPLPSPRYIL VTPRVLRVGS PESIHIQAHS DSRQPLTRTL  58
NP_000055.   MGPTSGP--S LLLLLLTHLP LALGSPMYSI ITPNILRLES EETMVLEAHD AQGD-----V  53
AF154933     MGSTSGP--R LLLLLLTSLP LALGDPIYTI ITPNVLRLES EEMVVLEAHE GQGD-----I  53
K02782       MGPASGSQLL VLLLLLASSP LALGIPMYSI ITPNVLRLES EETIVLEAHD AQGD-----I  55

                     70         80         90        100        110        120
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   KVNLTVWDFP MRKTVLARSQ LILSPGNNFM DQAPVTVPES LMYLPKP-GQ QYVIIRATWA  117
NP_000055.   PVTVTVHDFP GKKLVLSSEK TVLTPATNHM GNVTFTIPAN REFKSEKGRN KFVTVQATFG  113
AF154933     RVSVTVHDFP AKRQVLSSET TTLNNANNYL STVNIKIPAS KEFKSEK-GH KFVTVQALFG  112
K02782       PVTVTVQDF- LKRQVLTSEK TVLTGASGHL RSVSIKIPAS KEFNSDKEGH KYVTVVANFG  114

                    130        140        150        160        170        180
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   PTSGSSFMEK MVLVALHAGY IFIQTEKTIY TPSPLVHYRV FTVNHKMDPV TRIFTLDIKN  177
NP_000055.   ----TQVVEK VVLVSLQSGY LFIQTDKTIY TPGSTVLYRI FTVNHKLLPV GRTVMVNIEN  169
AF154933     ----NVQVEK VVLVSLQSGY LFIQTDKTIY TPGSTVLYRI FTVDHKLLPV GQTIVVTIET  168
K02782       ----ETVVEK AVMVSFQSGY LFIQTDKTIY TPGSTVLYRI FTVDNNLLPV GKTVVILIET  170

                    190        200        210        220        230        240
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   PDGSPASRVL VHSQDQPGVL ALSWGPEKSL CLSLGTWTIE ASYQSTPKQK FEAAFDVKEY  237
NP_000055.   PEGIPVKQDS LSSQNQLGVL PLSWD--IPE LVNMGQWKIR AYYENSPQQV FSTEFEVKEY  227
AF154933     PEGIDIKRDS LSSHNQFGIL ALSWN--IPE LVNMGQWKIR AHYEDAPQQV FSAEFEVKEY  226
K02782       PDGIPVKRDI LSSNNQHGIL PLSWN--IPE LVNMGQWKIR AFYEHAPKQI FSAEFEVKEY  228

                    250        260        270        280        290        300
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   VLPSFEVQLV PNKTFFYLKD -EALGVDIQA RYIFNKPVDG HALVIFGVKL DSCRIPIQSS  296
NP_000055.   VLPSFEVIVE PTEKFYYIYN EKGLEVTITA RFLYGKKVEG TAFVIFGIQD GEQRISLPES  287
AF154933     VLPSFEVQVE PSEKFYYIDD PNGLTVNIIA RFLYGESVDG TAFVIFGVQD GDQRISLSQS  286
K02782       VLPSFEVRVE PTETFYYIDD PNGLEVSIIA KFLYGKNVDG TAFVIFGVQD GDKKISLAHS  288

                    310        320        330        340        350        360
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   LQRVEVTETG GEMVQAETSG VKIIQSPYNI KFTRTPQYFK PGMPFHFRVR VVQS--SPIQ  354
NP_000055.   LKRIPIEDGS GEVVLSRKVL LDGVQNLRAE DLVGKSLYVS ATVILHSGSD MVQAERSGIP  347
AF154933     LTRVPIIDGT GEATLSQGVL LNGVHYSSVN DLVGKSIYVS VTVILNSGSD MVEAERTGIP  346
K02782       LTRVVIEDGV GDAVLTRKVL MEGVRPSNAD ALVGKSLYVS VTVILHSGSD MVEAERSGIP  348

                    370        380        390        400        410        420
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   IIFQSHLSHQ ATAGFSFTLP Q-IPPQVFIS NPDGSPASRV LVHSQDQ--- KVYTSAEGLA  410
NP_000055.   IVTSPYQIHF TKTPKYFKPG MPFDLMVFVT NPDGSPAYRV PVAVQGEDTV QSLTQGDGVA  407
AF154933     IVTSPYQIHF TKTPKFFKPA MPFDLMVYVT NPDGSPARHI PVVTEDF-KV RSLTQEDGVA  405
K02782       IVTSPYQIHF TKTPKFFKPA MPFDLMVFVT NPDGSPASKV LVVTQGS-NA KALTQDDGVA  407

                    430        440        450        460        470        480
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   TLTINTDANL DKLPIEVKTE ESLQPE-EQA SAKMTAWPYL TQDGSGNFLH IEVKTLGTEV  469
NP_000055.   KLSINTHPSQ KPLSITVRTK KQELSEAEQA TRTMQALPYS TVGNSNNYLH LSVLRTELRP  467
AF154933     KLSINTPDNR NSLPITVRTE KDGIPAARQA SKTMHVLPYN TQGNSKNYLH LSLPRVELKP  465
K02782       KLSINTPNSR QPLTITVRTK KDTLPESRQA TKTMEAHPYS TMHNSNNYLH LSVSRMELKP  467

                    490        500        510        520        530        540
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote   GSSIQLSLNT RHQDPKTKDK ITHFTILVVR EGKARQLGRQ VAQVG----- ---------V  515
NP_000055.   GETLNVNFLL R-MDRAHEAK IRYYTYLIMN KGRLLKAGRQ VREPGQDLVV LPLSITTDFI  526
AF154933     GENLNVNFHL R-TDPGYQDK IRYFTYLIMN KGKLLKVGRQ PRESGQVVVV LPLTITTDFI  524
```

```
K02782        GDNLNVNFHL R-TDPGHEAK IRYYTYLVMN KGKLLKAGRQ VREPGQDLVV LSLPITPEFI  526

                     550        560        570        580        590        600
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    PSFRILAFYL LPRGASQDPE LVADSIWIDV NDRCIGLKVG LKNDRFFQSL EPNSQVELKV  575
NP_000055.    PSFRLVAYYT LIG-ASGQRE VVADSVWVDV KDSCVGSLVV KSGQSEDRQP VPGQQMTLKI  585
AF154933      PSFRLVAYYT LIA-ANGQRE VVADSVWVDV KDSCVGTLVV KGGGKQDKQH RPGQQMTLEI  583
K02782        PSFRLVAYYT LIG-ASGQRE VVADSVWVDV KDSCIGTLVV KGDPR-DNHL APGQQTTLRI  584

                     610        620        630        640        650        660
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    TGDAEATVGL VAVDKAVYVL NSKHKLTQKK VWNVVEEHDI GCTGGSGKDR FAVFKDAGLD  635
NP_000055.    EGDHGARVVL VAVDKGVFVL NKKNKLTQSK IWDVVEKADI GCTPGSGKDY AGVFSDAGLT  645
AF154933      QGERGARVGL VAVDKGVFVL NKKNKLTQRR IWDVVEKADI GCTPGSGKDF AGVFTDAGLA  643
K02782        EGNQGARVGL VAVDKGVFVL NKKNKLTQSK IWDVVEKADI GCTPGSGKNY AGVFMDAGLA  644

                     670        680        690        700        710        720
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    LKISTGMDSG HQQSHSCQEA EVGESLEPGR QRLRSAETAP LHSSVNKFKT ELEQKCCEAG  695
NP_000055.    FTSSSGQQTA QRAELQCPQP AA-------R RRRSVQLTEK RMDKVGKYP- KELRKCCEDG  697
AF154933      FKSSKGLQTP QRADLECPKP AA-------R KRRSVQLMEK RMDKLGQYS- KDVRRCCEHG  695
K02782        FKTSQGLQTE QRADLECTKP AA-------R RRRSVQLMER RMDKAGQYTD KGLRKCCEDG  697

                     730        740        750        760        770        780
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    LRESPVGLSC EERTWHVRHG PACVAAFLDC CSHLLPP--- ---------A DEEEDFDDLF  743
NP_000055.    MRENPMRFSC QRRTRFISLG EACKKVFLDC CNYITELRRQ HARASHLGLA RSNLDEDIIA  757
AF154933      MRDNPMKFSC QRRAQFIQHG DACVKAFLDC CEYIAKLRQQ HSRNKPLGLA RSDLDEEIIP  755
K02782        MRDIPMRYSC QRRARLITQG ENCIKAFIDC CNHITKLREQ HRRDHVLGLA RSELEEDIIP  757

                     790        800        810        820        830        840
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    LDDMPVRTLF PESWLW---- -N-----SIS HYPISVKVPD SITTWQFVVV SLKAGQGGLC  793
NP_000055.    EENIVSRSEF PESWLWNVED LKEPPKNGIS TKLMNIFLKD SITTWEILAV SMSDKKG-IC  816
AF154933      EEDIISRSQF PESWLWTIEE FKEPDKNGIS TKTMNVFLKD SITTWEILAV SLSDKKG-IC  814
K02782        EEDIISRSHF PQSWLWTIEE LKEPEKNGIS TKVMNIFLKD SITTWEILAV SLSDKKG-IC  816

                     850        860        870        880        890        900
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    VSDPFELTVM KSFFVDLKLP SSVIRNEQVQ IQAMLYNFRD RQ-AKVRVEF PHKETLCSAS  852
NP_000055.    VADPFEVTVM QDFFIDLRLP YSVVRNEQVE IRAVLYNYRQ NQELKVRVEL LHNPAFCSLA  876
AF154933      VADPYEVVVK QDFFIDLRLP YSVVRNEQVE IRAILYNYRE AEDLKVRVEL LYNPAFCSLA  874
K02782        VADPYEIRVM QDFFIDLRLP YSVVRNEQVE IRAVLFNYRE QQELKVRVEL LHNPAFCSMA  876

                     910        920        930        940        950        960
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    KPGAPSHQVV VVPPTSSKIV HFVLLPLETG KVDVEVKAVG YG--VQDHVK KTLLVEGCGY  910
NP_000055.    TTKRRHQQTV TIPPKSSLSV PYVIVPLKTG LQEVEVKAAV YHHFISDGVR KSLKVVPEGI  936
AF154933      TAKKRHQQTL TVPAKSSVPV PYIIVPLKTG LQEVEVKAAV YNHFISDGVK KTLKVVPEGM  934
K02782        TAKNRYFQTI KIPPKSSVAV PYVIVPLKIG QQEVEVKAAV FNHFISDGVK KTLKVVPEGM  936

                     970        980        990       1000       1010       1020
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    ---------- --S-----GQ TQTKLVPRQE FLNMVPDTEA EVFISVQGDI LGETIVGSLT  953
NP_000055.    RMNKTVAVRT LDPERLGREG VQKEDIPPAD LSDQVPDTES ETRILLQGTP VAQMTEDAVD  996
AF154933      RVNKTVVTRT LDPEHKGQQG VQREEIPPAD LSDQVPDTES ETKILLQGTP VAQMVEDAID  994
K02782        RINKTVAIHT LDPEKLGQGG VQKVDVPAAD LSDQVPDTDS ETRIILQGSP VVQMAEDAVD  996

                    1030       1040       1050       1060       1070       1080
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    PSEIQQLLRV PTGCPEQTLS SLTPVIILSR YLDTTGQWGK VGVEHRDQVM KNI--GYTQM  1011
NP_000055.    AERLKHLIVT PSGCGEQNMI GMTPTVIAVH YLDETEQWEK FGLEKRQGAL ELIKKGYTQQ  1056
AF154933      GDRLKHLIQT PSGCGEQNMI GMTPTVIAVH YLDSTEQWEK FGLEKRQEAL ELIKKGYTQQ  1054
K02782        GERLKHLIVT PAGCGEQNMI GMTPTVIAVH YLDQTEQWEK FGIEKRQEAL ELIKKGYTQQ  1056

                    1090       1100       1110       1120       1130       1140
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    LTHRSSDGTY HTSKGNPGST WLTSYVFRVF ALAYSMMTTQ VLSLSSLCDM ANWIIIDRQA  1071
NP_000055.    LAFRQPSSAF AAFVKRAPST WLTAYVVKVF SLAVNLIA-- -IDSQVLCGA VKWLILEKQK  1113
AF154933      LAFRQKNSAF AAFQDRLSST LLTAYVVKVF AMAANLIA-- -IDSQVLCGA VKWLILEKQK  1111
K02782        LAFKQPSSAY AAFNNRPPST WLTAYVVKVF SLAANLIA-- -IDSHVLCGA VKWLILEKQK  1113

                    1150       1160       1170       1180       1190       1200
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote    EDGHFLEKGP VVMTSMS--- ---EE-DVSL TALVLIALNE GKELCRQKVG PNLMASIEKA  1124
NP_000055.    PDGVFQEDAP VIHQEMIGGL PNNNEKDMAL TAFVLISLQE AKDICEEQVN -SLPGSITKA  1172
```

```
AF154933        PDGVFEENGP VIHQEMIGGF KNTEEKDVSL TAFVLIALQE AKDICEPQVN -SLLRSINKA  1170
K02782          PDGVFQEDGP VIHQEMIGGF RNAKEADVSL TAFVLIALQE ARDICEGQVN -SLPGSINKA  1172

                      1210       1220       1230       1240       1250       1260
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      GGLLELRRLR LQRSYAVAIA SYALA----- -----DKTHW PVDEQNLG-- ---SLYTIEA  1169
NP_000055.      GDFLEANYMN LQRSYTVAIA GYALAQMGRL KGPLLNKFLT TAKDKNRWED PGKQLYNVEA  1232
AF154933        RDFLADYYLE LKRPYTVAIA GYALALSDKL DEPFLNKLLS TAKERNRWEE PGQKLHNVEA  1230
K02782          GEYIEASYMN LQRPYTVAIA GYALALMNKL EEPYLGKFLN TAKDRNRWEE PDQQLYNVEA  1232

                      1270       1280       1290       1300       1310       1320
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      TAYGLMQKLE LGRYNETHAL AKWLLEKQEL GGGFRSTQPG RSSRLSHPQR WPQGSLXALE  1229
NP_000055.      TSYALLALLQ LKDFDFVPPV VRWLNEQRYY GGGYGST--- ---------- --QATFMVFQ  1277
AF154933        TSYALLALLV VKDFDSVPPI VRWLNEQRYY GGGYGST--- ---------- --QATFMVFQ  1275
K02782          TSYALLALLL LKDFDSVPPV VRWLNEQRYY GGGYGST--- ---------- --QATFMVFQ  1277

                      1330       1340       1350       1360       1370       1380
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      ALTRFREAVP FKGIQDLHVQ IRAPKTALNV NWYIDHSNAY QQRSAKFLAQ DDLEIKASGN  1289
NP_000055.      ALAQYQKDAP DHQELNLDVS LQLPSRSSKI THRIHWESAS LLRSEETKEN EGFTVTAEGK  1337
AF154933        ALAQYQKDVP DHKDLNLDVS IHLPSRSAPV RHRILWESAS LLRSEETKEN EGFTLIAEGK  1335
K02782          ALAQYQTDVP DHKDLNMDVS FHLPSRSSAT TFRLLWENGN LLRSEETKQN EAFSLTAKGK  1337

                      1390       1400       1410       1420       1430       1440
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      GRGTISILTM YHKSPESRED NCNLYHLNAT LHSALEENKK ---GGETFRL RMETRFQNNG  1346
NP_000055.      GQGTLSVVTM YHAKAKD-QL TCNKFDLKVT IKPAPETEKR PQDAKNTMIL EICTRYRGDQ  1396
AF154933        GQGTLSVVTM YHGKAKG-KT TCKKFDLKVS IHPAPEPVKK PQEAKSSMVL DICTRYLGNQ  1394
K02782          GRGTLSVVAV YHAKLKS-KV TCKKFDLRVS IRPAPETAKK PEEAKNTMFL EICTKYLGDV  1396

                      1450       1460       1470       1480       1490       1500
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      EATMTIMEVS LLTGFYPNQD DLKQLTSDVE RYAFQYKTKT STSDS-TVVL YLEKLSHEKN  1405
NP_000055.      DATMSILDIS MMTGFAPDTD DLKQLANGVD RYISKYELDK AFSDRNTLII YLDKVSHSED  1456
AF154933        DATMSILDIS MMTGFSPDTE DLKLLSTGVD RYISKYELNK ALSNKNTLII YLDKISHTLE  1454
K02782          DATMSILDIS MMTGFAPDTK DLELLASGVD RYISKYEMNK AFSNKNTLII YLEKISHTEE  1456

                      1510       1520       1530       1540       1550       1560
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      TVLGFRVHRM LQAEFLQAAL VTIYDYYEPS RRCSTFYNLP TEQSSLRKIC HKDICRCAEG  1465
NP_000055.      DCLAFKVHQY FNVELIQPGA VKVYAYYNLE ESCTRFYHPE KEDGKLNKLC RDELCRCAEE  1516
AF154933        DCISFKVHQY FNVGLIQPGS VKVYSYYNLD ESCTRFYHPE KEDGMLNKLC HKEMCRCAEE  1514
K02782          DCLTFKVHQY FNVGLIQPGS VKVYSYYNLE ESCTRFYHPE KDDGMLSKLC HSEMCRCAEE  1516

                      1570       1580       1590       1600       1610       1620
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      QCPSLQKPSG QLRQEELQTT ACEAGVDFVY KTKLESVEVS ASNPYVYYNT QLEDIIKSGT  1525
NP_000055.      NC-FIQKSDD KVTLEERLDK ACEPGVDYVY KTRLVKVQLS ND--FDEYIM AIEQTIKSGS  1573
AF154933        NC-FMHHDEE EVTLDDRLER ACEPGVDYVY KTRLLKKELS DD--FDDYIM VIEQIIKSGS  1571
K02782          NC-FMQQSQE KINLNVRLDK ACEPGVDYVY KTELTNIKLL DD--FDEYTM TIQQVIKSGS  1573

                      1630       1640       1650       1660       1670       1680
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL3 Prote      DPAKPLAMKK FVSHATCHDS LGLQEQESYL IMGQTSDLWR IKSDYSYVLG KETFLILWPA  1585
NP_000055.      DEVQVGQQRT FISPIKCREA LKLEEKKHYL MWGLSSDFWG EKPNLSYIIG KDTWVEHWPE  1633
AF154933        DEVQVGQERR FISHIKCREA LKLKEGGHYL VWGVSSDLWG EKPNISYIIG KDTWVELWPD  1631
K02782          DEVQAGQQRK FISHIKCRNA LKLQKGKKYL MWGLSSDLWG EKPNTSYIIG KDTWVEHWPE  1633

                      1690       1700       1710
                ....|....| ....|....| ....|....|
MOL3 Prote      DG---DASKK ELRDQLEEFL EYMRTHGCQS  1612
NP_000055.      EDECQDEENQ KQCQDLGAFT ESMVVFGCPN  1663
AF154933        GDVCQDEENQ KQCQDLANFS ENMVVFGCPN  1661
K02782          AEECQDQKYQ KQCEELGAFT ESMVVYGCPN  1663
```

MOL3 shows significant homologies to human complement C3 proteins, as described in, but not limited to, the references below.

It was found that transforming growth factor-beta1 acts as a potent inhibitor of complement C3 biosynthesis in human pancreatic cancer cell lines. Andoh et al. determined how transforming growth factor (TGF)-beta1 affects complement C3 secretion in the pancreatic cancer cell lines PANC-1 and BxPC-3. It is suggested that TGF-beta1 may act as a potent inhibitor of C3 secretion in pancreatic cancer cell lines under inflammatory conditions. This action of TGF-beta1 did not correlate with NF-kappaB activation, but associated with the translocation of Fos protein into the nucleus.

The cellular localization of complement C3 and C4 transcripts were analyzed in intestinal specimens from patients with Crohn's disease. It has been suggested that the increase in C3 and C4 levels in jejunal perfusates of patients with Crohn's disease results from local intestinal synthesis of complement. Laufer et al. suggest that there is local regulated production of complement in the intestine of patients with CD, and subsequent complement activation may contribute to the inflammatory process.

The generation of complement C3 and expression of cell membrane complement inhibitory proteins by human bronchial epithelium cell line. They found that the interrelationship between human airway epithelium and complement proteins may affect airway defence, airway function, and airway epithelial integrity. Local generation of complement C3 and expression of cell membrane CIP by human bronchial epithelium and its modulation by proinflammatory cytokines might be an additional regulatory mechanism of local airway defence and may affect airway function and epithelial integrity in health and disease.

Janssen et al, Am J Kidney Dis 2000 Jan;35(1):21-8 suggested the activation of the acute phase response and complement C3 in patients with IgA nephropathy. The authors have shown ystemic complement activation in patients with immunoglobulin A (IgA) nephropathy and reported that plasma levels of actC3 can indicate disease activity and renal outcome.

Therapeutic applications

The expression pattern, and protein similarity information forMOL3 may function as a human complement C3-like protein. Therefore, the nucleic acid and protein of the invention are useful in potential therapeutic applications implicated, for example but not limited to, cancer, lung diseases, including asthma, immundeficiencies, inflammation, Crohn's disease, neurological disorders, nephropathy, and other diseases and disorders.

The homology to antigenic secreted and membrane proteins suggests that antibodies directed against the novel genes may be useful in treatment and prevention of cancer, lung diseases, including asthma, immundeficiencies, inflammation, Crohn's disease, neurological disorders, nephropathy, and other diseases and disorders.

Potential therapeutic uses for the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in cancer, lung diseases, including asthma, immundeficiencies, inflammation, Crohn's disease, neurological disorders, nephropathy, and other diseases and disorders. For example, but not limited to, a cDNA encoding the human complement C3-like protein may be useful in gene therapy, and the human complement C3-like protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from, for example, but not limited to, cancer, lung diseases, including asthma, immundeficiencies, inflammation, Crohn's disease, neurological disorders, nephropathy, and other diseases and disorders. The novel nucleic acid encoding the human complement C3-like protein, and the human complement C3-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL4

MOL4a

The disclosed Wnt 8-like protein, MOL4a (also referred to herein as AC004826), is encoded by a nucleic acid, 1064 nucleotides long (SEQ ID NO:7). An open reading frame was identified beginning with an ATG initiation codon at nucleotides 4-6 and ending with a TGA codon at nucleotides 1057-1059. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4A, and the start and stop codons are in bold letters. The encoded protein having 351 amino acid residues is presented using the one-letter code in Table 4B (SEQ ID NO:8).

Table 4A. MOL4a Nucleotide Sequence (SEQ ID NO:7).
GCGATGGGGAACCTGTTTATGCTCTGGGCAGCTCTGGGCATATGCTGTGCTGCATTCAGTGCCTCTGCCTGGTCA
GTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACGACTAGTGTGGCCTTGGGTGCCCAGAGT
GGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCTGAAAATGCTCTTCAGCTCTCCACC
CACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTGCTGGAGTCATGTACATC
ATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAAACAATGGAAAAATAGGAGGC
CATGGCTGGATCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAAAGGATCTCCAAACTCTTTGTGGACAGT
TTGGAGAAGGGGAAGGATGCCAGAGCCCTGATGAATCTTCACAACAACAGGGCCGGCAGACTGGCAGTGAGAGCC
ACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAGCATACAGACATGCTGGCTGCAGCTGGCT
GAATTCCGGGAGATGGGAGACTACCTAAAGGCCAAGTATGACCAGGCGCTGAAAATTGAAATGGATAAGCGGCAG
CTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTGAGGCCTTCCTTCCTAGCGCAGAGGCGGAACTG
ATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATTCCAGCCTGGGCATCTATGGCACAGAGGGTCGTGAG
TGCCTACAGAACAGCCACAACACATCCAGGTGGGAGCGACGTAGCTGTGGGCGCCTGTGCACTGAGTGTGGGCTG
CAGGTGGAAGAGAGGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCAGTGGTGCTGTACGGTCAAGTGT
GACCAGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCCAGGCAGTGCCCAGTCCCTGGGTAAGGGC
AGTGCCTGATAATA

The disclosed nucleic acid MOL4a sequence has 881 of 1050 bases (83%) identical to a *Mus musculus* Wnt 8 mRNA (GENBANK-ID: MMWNT8DPT\|acc:Z68889) and 637 of 955 bases (66%) identical to a *Homo sapiens* Wnt 8 mRNA (GENBANK-ID: HSWNT8\|acc:Y11094).

The MOL4a polypeptide (SEQ ID NO:8) encoded by SEQ ID NO:7 is presented using the one-letter amino acid code in Table 4B. The Psort profile for MOL4a predicts that this sequence has a signal peptide and is likely to be localized outside the cell with a certainty of 0.7700. The most likely cleavage site for a MOL4a peptide is between amino acids 24 and 25 based on the SignalP result.

Table 4B. MOL4a protein sequence (SEQ ID NO:8)
MGNLFMLWAALGICCAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHN
RLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKIGGHGWIWGGCSDNVEFGERISKLFVDSLEK
GKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAG
NSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEER
KTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA

The full amino acid sequence of the disclosed MOL4a polypeptide has 282 of 349 amino acid residues (80%) identical to, and 306 of 349 residues (87%) positive with, the 354 amino acid residue WNT-8D protein from *Mus musculus* (ptnr:SPTREMBL-ACC: Q64527), ($E = 1.5x10^{-16}$)

MOL4b

The disclosed Wnt 8-like protein, MOL4b (also referred to herein as CG53138-05), is encoded by a nucleic acid, 1155 nucleotides long (SEQ ID NO:140). An open reading frame was identified beginning with an ATG initiation codon at nucleotides 41-43 and ending with a TGA codon at nucleotides 1148-1150. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4C, and the start and stop codons are in bold letters.

Table 4C. MOL4b Nucleotide Sequence (SEQ ID NO:140).
CGATGGGGAACCTGTTTATGCTCTGGGCAGCTCTGGGCAT**ATG**CTGTGCTGCATTCAGTGCCTCTGCCTGGTAAG TCCTTTCCCAACCCTCACTCCTTGCCAAGGAGGCCCCCATTGTCTCATCCCCATTCACCTCTGCCTCACTTTTTC TCTTTTTGGTAGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACGACTAGTGTGGC CTTGGGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCTGAAAATGC TCTTCAGCTCTCCACCCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTGC TGGAGTCATGTACATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAAACAA TGGAAAAACAGGAGGCCATGGCTGGATCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAAAGGATCTCCAA ACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCCGATGAATCTTCACAACAACAGGGCCGGCAG ACTGGCAGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAGCATACAGACATG CTGGCTGCAGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGCCAAGTATGACCAGGCGCTGAAAATTGA AATGGATAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTGAGGCCTTCCTTCCTAG CGCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATTCCAGCCTGGGCATCTATGG CACAGAGGGTCGTGAGTGCCTACAGAACAGCCACAACACATCCAGGTGGGAGCGACGTAGCTGTGGGCGCCTGTG CACTGAGTGTGGGCTGCAGGTGGAAGAGAGGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCAGTGGTG CTGTACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCCAGGCAGTGCCCA GTCCCTGGGTAAGGGCAGTGCC**TGA**TAATA

The disclosed nucleic acid MOL4b sequence has been localized to chromosome 5 and has 993 of 994 bases (99%) identical to a gb:GENBANK-ID:AB057725|acc:AB057725.1 mRNA from *Homo sapiens* (*Homo sapiens* mRNA for WNT8A, complete cds) (E= $1.7e^{-232}$).

The MOL4b 369 amino acid polypeptide (SEQ ID NO:141) encoded by SEQ ID NO:140 is presented using the one-letter amino acid code in Table 4D. The Psort profile for MOL4b predicts that this sequence has a signal peptide and is likely to be localized outside the cell with a certainty of 0.4132. In other embodiments, NOV4b could also be localized to the lysosome (lumen) with a certainty of 0.1900, to the endoplasmic reticulum (membrane) with a certainty of 0.1000, or to the endoplasmic reticulum (lumen) with a certainty of 0.1000. The most likely cleavage site for a MOL4b peptide is between amino acids 42and 43 (GRS-VN) based on the SignalP result.

Table 4D. MOL4b protein sequence (SEQ ID NO:141)
MLCCIQCLCLVSPFPTLTPCQGGPHCLIPIHLCLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQF AWERWNCPENALQLSTHNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD

NVEFGERISKLFVDSLEKGKDARAPMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKA KYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWE RRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA

The full amino acid sequence of the disclosed MOL4b polypeptide has 2330 of 337 amino acid residues (97%) identical to, and 330 of 337 amino acid residues (97%) similar to, the 351 amino acid residue ptnr:TREMBLNEW-ACC:BAB60960 protein from *Homo sapiens* (Human) (WNT8A) ($E = 2.0x10^{-185}$)

Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of MOL4b and MOL4c. The sequences are predicted to be expressed in the teratocarcinoma cell line NT2 because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AB057725|acc:AB057725.1) a closely related *Homo sapiens* mRNA for WNT8A, complete cds homolog.

MOL4c

The disclosed Wnt 8-like protein, MOL4c (also referred to herein as CG53138-06), is encoded by a nucleic acid, 1175 nucleotides long (SEQ ID NO:142). An open reading frame was identified beginning with an ATG initiation codon at nucleotides 41-43 and ending with a TAG codon at nucleotides 1160-1162. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4E, and the start and stop codons are in bold letters.

Table 4E. MOL4c Nucleotide Sequence (SEQ ID NO:142).
CGATGGGAACCTGTTTATGCTCTGGCAGCTCTGGGCATATGCTGTGCTGCATTCAGTGCCTCTGCCTGGTAAG TCCTTTCCCAACCCTCACTCCTTGCCAAGGAGGCCCCCATTGTCTCATCCCCATTCACCTCTGCCTCACTTTTTC TCTTTTTGGTAGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACGACTAGTGTGGC CTTGGGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCTGAAAATGC TCTTCAGCTCTCCACCCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTGC TGGAGTCATGTACATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAAACAA TGGAAAAACAGGAGGCCATGGCTGGATCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAAAGGATCTCCAA ACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCCGATGAATCTTCACAACAACAGGGCCGGCAG ACTGGCAGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAGCATACAGACATG CTGGCTGCAGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGCCAAGTATGACCAGGCGCTGAAAATTGA AATGGATAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTGAGGCCTTCCTTCCTAG CGCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATTCCAGCCTGGGCATCTATGG CACAGAGGGTCGTGAGTGCCTACAGAACAGCCACAACACATCCAGGTGGGAGCGACGTAGCTGTGGGCGCCTGTG CACTGAGTGTGGGCTGCAGGTGGAAGAGAGGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCAGTGGTG CTGTACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCCAGGCAGTGCCCA GTCCCTGGGGAGAGTTTGGTTTGGGGTCTATATCTAGAGGGACCTTCAAA

The MOL4c 373 amino acid polypeptide (SEQ ID NO:143) encoded by SEQ ID NO:142 is presented using the one-letter amino acid code in Table 4F.

Table 4F. MOL4c protein sequence (SEQ ID NO:143)
MLCCIQCLCLVSPFPTLTPCQGGPHCLIPIHLCLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQF
AWERWNCPENALQLSTHNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD
NVEFGERISKLFVDSLEKGKDARAPMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKA
KYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWE
RRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGRVWFGVYI

Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of MOL4b and MOL4c. The sequences are predicted to be expressed in the teratocarcinoma cell line NT2 because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AB057725|acc:AB057725.1) a closely related *Homo sapiens* mRNA for WNT8A, complete cds homolog.

MOL4d

The disclosed Wnt 8-like protein, MOL4d (also referred to herein as CG53138-04), is encoded by a nucleic acid, 1597 nucleotides long (SEQ ID NO:144). An open reading frame was identified beginning with an ATG initiation codon at nucleotides 41-43 and ending with a TAG codon at nucleotides 1166-1168. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4G, and the start and stop codons are in bold letters.

Table 4G. MOL4d Nucleotide Sequence (SEQ ID NO:144).
CAGAATTTTCTCACATAAATACTGAGGAAGACCCTGCCCTCTCCTCACTCCTCTGGACTTGGCCCTGAGCTGGAC
CTGGTCCACTGGGGTAGGCAGGGC**ATG**GGGAACCTGTTTATGCTCTGGGCAGCTCTGGGCATATGCTGTGCTGC
ATTCAGTGCCTCTGCCTGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACGACTAG
TGTGGCCTTGGGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCTGA
AAATGCTCTTCAGCTCTCCACCCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAG
CTCTGCTGGAGTCATGTACATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTC
AAACAATGGAAAAACAGGAGGCCATGGCTGGATCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAAAGGAT
CTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATGAATCTTCACAACAACAGGGC
CGGCAGACTGGCAGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAGCATACA
GACATGCTGGCTGCAGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGCCAAGTATGACCAGGCGCTGAA
AATTGAAATGGATAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTGAGGCCTTCCT
TCCTAGCGCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATTCCAGCCTGGGCAT
CTATGGCACAGAGGGTCGTGAGTGCCTACAGAACAGCCACAACACATCCAGGTGGGAGCGACGTAGCTGTGGGCG
CCTGTGCACTGAGTGTGGGCTGCAGGTGGAAGAGAGGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCA
GTGGTGCTGTACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCCAGGCAG
TGCCCAGTCCCTGGGGAGAGTTTGGTTTGGGGTCTATATC**TAG**AGGGACCTTCAAAGTATTTGTTCCTTTAAATT
TCAGACCATGTCCAACCCAGCTGTGCTGCTGGGAATCAGGAGAATAGAAGCAAAAAACGAAAGAGTTCTGTTCAG
ACTTCTGAAGAGCAGCCTGTGGCTACAAATCTATGCTGATAAATGAGATTGAGAACTCAACTGTATTTTGCCATA
AATGCTTCTAAGATATATCCAGCTGGGACTTCTATTACTCCCTTTGGAAACCTTAAGATCAAAAAGGGAATAAGA
AACCCTTCTTCTGTATCCCAATAATCCACCAGGATAAAGGAGAAACTAGAAATATGCAACTCCCTTGATTTCAGT
GTTTGGCAGGTAACAAAAAATTGAGACCCAGACACTGGTCAACAGGAAAACAATACAGACTCCCAGAATTAGAAA
GTGTTATTTTAATGCAACCTAG

The MOL4d 355 amino acid polypeptide (SEQ ID NO:145) encoded by SEQ ID NO:144 is presented using the one-letter amino acid code in Table 4H.

Table 4H. MOL4d protein sequence (SEQ ID NO:145)
MGNLFMLWAALGICCAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHN
RLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEK
GKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAG
NSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEER
KTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGRVWFGVYI

MOL4e

The disclosed Wnt 8-like protein, MOL4e (also referred to herein as 251445570), is encoded by a nucleic acid, 964 nucleotides long (SEQ ID NO:146). An open reading frame was identified beginning with an ACC initiation codon at nucleotides 2-4 and ending with a GGC codon at nucleotides 962-964. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4I, and the start and stop codons are in bold letters. Because the start and stop codons for MOL4e are not tradistional initiation and termination codons, MOL4e could be a partial reading frame that extends further in the 5' and/or 3' directions.

Table 4I. MOL4e Nucleotide Sequence (SEQ ID NO:146).
CACCGGATCCTCTGCCTGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACGACTAG
TGTGGCCTTGGGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCTGA
AAATGCTCTTCAGCTCTCCACCCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAG
CTCTGCTGGAGTCATGTACATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTC
AAACAATGGAAAAACAGGAGGCCATGGCTGGATCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAAAGGAT
CTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATGAATCTTCACAACAACAGGGC
CGGCAGACTGGCAGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAGCATACA
GACATGCTGGCTGCAGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGCCAAGTATGACCAGGCGCTGAA
AATTGAAATGGATAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTGAGGCCTTCCT
TCCTAGCGCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATTCCAGCCTGGGCAT
CTATGGCACAGAGGGTCGTGAGTGCCTACAGAACAGCCACAACACATCCAGGTGGGAGCGACGTAGCTGTGGGCG
CCTGTGCACTGAGTGTGGGCTGCAGGTGGAAGAGAGGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCA
GTGGTGCTGTACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGAGCAAGTATTACCTCGAGGGC

The MOL4e 321 amino acid polypeptide (SEQ ID NO:147) encoded by SEQ ID NO:146 is presented using the one-letter amino acid code in Table 4J.

Table 4J. MOL4e protein sequence (SEQ ID NO:147)
TGSSAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATRETSFIHAISS
AGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALMNLHNNRAGR
LAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSA
EAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCT
VKCDQCRHVVSKYYLEG

MOL4f

The disclosed Wnt 8-like protein, MOL4f (also referred to herein as 250059708), is encoded by a nucleic acid, 952 nucleotides long (SEQ ID NO:148). An open reading frame was identified beginning with an GGC initiation codon at nucleotides 2-4 and ending with a GGC codon at nucleotides 950-952. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table 4K, and the start and stop codons are in bold letters. Because the start and stop codons for MOL4f are not tradistional initiation and termination codons, MOL4f could be a partial reading frame that extends further in the 5' and/or 3' directions.

Table 4K. MOL4f Nucleotide Sequence (SEQ ID NO:148).
CACCGGATCCGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACGACTAGTGTGGCCTTGGG
TGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCTGAAAATGCTCTTCA
GCTCTCCACCCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTGCTGGAGT
CATGTACATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAAACAATGGAAA
AACAGGAGGCCATGGCTGGATCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAAAGGATCTCCAAACTCTT
TGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATGAATCTTCACAACAACAGGGCCGGCAGACTGGC
AGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAGCATACAGACATGCTGGCT
GCAGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGCCAAGTATGACCAGGCGCTGAAAATTGAAATGGA
TAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTGAGGCCTTCCTTCCTAGCGCAGA
GGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATTCCAGCCTGGGCATCTATGGCACAGA
GGGTCGTGAGTGCCTACAGAACAGCCACAACACATCCAGGTGGGAGCGACGTAGCTGTGGGCGCCTGTGCACTGA
GTGTGGGCTGCAGGTGGAAGAGAGGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCAGTGGTGCTGTAC
GGTCAAGTGTGACCAGTGTAGGCATGTGGTGAGCAAGTATTACCTCGAGGGC

The MOL4f 317 amino acid polypeptide (SEQ ID NO:149) encoded by SEQ ID NO:148 is presented using the one-letter amino acid code in Table 4L.

Table 4L. MOL4f protein sequence (SEQ ID NO:149)
TGSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATRETSFIHAISSAGVM
YIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVR
ATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAEL
IFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCD
QCRHVVSKYYLEG

MOL4g

The disclosed Wnt 8-like protein, MOL4g (also referred to herein as 246861879), is encoded by a nucleic acid, 726 nucleotides long (SEQ ID NO:150). An open reading frame was identified beginning with an CGCinitiation codon at nucleotides 1-3 and ending with a GCG codon at nucleotides 724-726. Putative untranslated regions upstream from the initiation codon and downstream from the termination codon are underlined in Table

4M, and the start and stop codons are in bold letters. Because the start and stop codons for MOL4g are not tradistional initiation and termination codons, MOL4g could be a partial reading frame that extends further in the 5' and/or 3' directions.

Table 4M. MOL4g Nucleotide Sequence (SEQ ID NO:150).
CGCGGATCCACCATGAAATATGTCTTCTATTTGGGTGTCCTCGCTGGGACATTTTTCTTTGCTGACTCATCTGTT CAGAAAGAAGACCCTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAA CCCAGCTGGGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGA GTCAGAGACGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCA CAGGATGACCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTCCCCTCGCC ACCACCAATGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGGAGCCAAGAAAACAGTGGCCGACAC CCTGACTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGCCAAAAAACAGAACAAGGAAAAAGC CACAGGAATTCCTTATGTGTGAAATTTGTGAAAGTATTCAGCCGAATTTTTGGGGAGGTGGCCGTTGCTACTGTC ATCTGCAAAGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGGAGGGGACGTCGGCATCTACACCAATGTT TACAAATATGTATCCTGGATTGAGAACACTGCTAAGGACAAGCTCGAGGCG

The MOL4g 242 amino acid polypeptide (SEQ ID NO:151) encoded by SEQ ID NO:150 is presented using the one-letter amino acid code in Table 4N.

Table 4N. MOL4g protein sequence (SEQ ID NO:151)
RGSTMKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRV RDGTEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPD LRQNLEAPVMSDRECQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIEVGHFMGGDVGIYTNVYKY VSWIENTAKDKLEA

BLASTP (Non-Redundant Composite database) analysis of the best hits for alignments with MOL4a are listed in Table 4C.

Table 4C. BLASTP results for MOL4a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi|11693046|gb|AAG38662.1|(AY009402)	WNT8d precursor [Homo sapiens]	355	335/348 (96%)	336/348 (96%)	0.0
gi|6678169|ref|NP_033316.1|	stimulated by retinoic acid gene 11 [Mus musculus]	354	271/349 (77%)	295/349 (83%)	1.0e-148
gi|104264|pir||S18771	developmental regulator Xwnt-8 - African clawed frog	387	246/335 (73%)	285/335 (84%)	1.0e-136
gi|1722844|sp|P51030|WN8C_CHICK	WNT-8C PROTEIN PRECURSOR (CWNT-8)	357	242/337 (71%)	283/337 (83%)	1.0e-134

This information is presented graphically in the multiple sequence alignment given in Table 4D (with MOL4 being shown on line 1) as a ClustalW analysis comparing MOL4 with related sequences.

Table 4D Information for the ClustalW proteins:

```
1)  MOL4 (SEQ ID NO:8)
2)  gi|11693046|gb|AAG38662.1| (AY009402) WNT8d precursor [Homo sapiens]
(SEQ ID NO:44)
3)  gi|6678169|ref|NP_033316.1| stimulated by retinoic acid gene 11 [Mus
musculus] (SEQ ID NO:45)
4)  gi|104264|pir||S18771 developmental regulator Xwnt-8 - African clawed
frog (SEQ ID NO:46)
5)  gi|1722844|sp|P51030|WN8C_CHICK WNT-8C PROTEIN PRECURSOR (CWNT-8) (SEQ
ID NO:47)
```

```
                     10         20         30         40         50         60
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL4 Prote   -MGNLFMLWA ALGICCAAFS ASAWSVNNFL ITGPKAYLTY TTSVALGAQS GIEECKFQFA  59
AY009402     -MGNLFMLWA ALGICCAAFS ASAWSVNNFL ITGPKAYLTY TTSVALGAQS GIEECKFQFA  59
NP_033316.   -MGHLLMLWV AAGMCYPALG ASAWSVNNFL ITGPKAYLTY TASVALGAQI GIEECKFQFA  59
S18771       MQNTTLFILA TLLIFCPFFT ASAWSVNNFL MTGPKAYLTY SASVAVGAQN GIEECKYQFA  60
P51030       MRGSTFLLLS IVGIYGAILN AAAWSVNNFL MTGPKAYLTY SSSVAAGAQS GMEECKFQFG  60

                     70         80         90        100        110        120
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL4 Prote   WERWNCPENA LQLSTHNRLR SATRETSFIH AISSAGVMYI ITKNCSMGDF ENCGCDGSNN  119
AY009402     WERWNCPENA LQLSTHNRLR SATRETSFIH AISSAGVMYI ITKNCSMGDF ENCGCDGSNN  119
NP_033316.   WERWNCPEHA FQFSTHNRLR AATRETSFIH AIRSAAIMYA VTKNCSMGDL ENCGCDESQN  119
S18771       WERWNCPEST LQLATHNGLR SATRETSFVH AISSAGVMYT LTRNCSMGDF DNCGCDDSRN  120
P51030       WERWNCPESA LQLSTHNRLR SATRETSFVH AISSAGVMYT LTRNCSLGDF ESCGCDDSRN  120

                    130        140        150        160        170        180
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL4 Prote   GKIGGHGWIW GGCSDNVEFG ERISKLFVDS LEKGKDARAL MNLHNNRAGR LAVRATMKRT  179
AY009402     GKTGGHGWIW GGCSDNVEFG ERISKLFVDS LEKGKDARAL MNLHNNRAGR LAVRATMKRT  179
NP_033316.   GKTGGHGWIW GGCSDNVEFG EKISRLFVDS LEKGKDARAL VNLHNNRAGR LAVRASTKRT  179
S18771       GRIGGRGWVW GGCSDNAEFG ERISKLFVDG LETGQDARAL MNLHNNEAGR LAVKETMKRT  180
P51030       GRVGGRGWVW GGCSDNVEFG ERISKLFVDA LETGHDTRAL INLHNNEVGR LAVKATMKRA  180

                    190        200        210        220        230        240
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL4 Prote   CKCHGISGSC SIQTCWLQLA EFREMGDYLK AKYDQALKIE MDKRQLRAGN SAEGHWVPAE  239
AY009402     CKCHGISGSC SIQTCWLQLA EFREMGDYLK AKYDQALKIE MDKRQLRAGN SAEGHWVPAE  239
NP_033316.   CKCHGISGSC SIQTCWLQLA DFRQMGNYLK AKYDRALKIE MDKRQLRAGN RAEGRWALTE  239
S18771       CKCHGISGSC SIQTCWLQLA EFRDIGNHLK IKHDQALKLE MDKRKMRSGN SADNRGAIAD  240
P51030       CKCHGVSGSC SIQTCWLQLA DFREIGNYLK MKYDQAHKLE MDKRRMRAGN SADSRGATAE  240

                    250        260        270        280        290        300
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL4 Prote   AFLPSAEAEL IFLEESPDYC TCNSSLGIYG TEGRECLQNS HNTSRWERRS CGRLCTECGL  299
AY009402     AFLPSAEAEL IFLEESPDYC TCNSSLGIYG TEGRECLQNS HNTSRWERRS CGRLCTECGL  299
NP_033316.   AFLPSTEAEL IFLEGSPDYC NRNASLSIQG TEGRECLQNA RSASRREQRS CGRLCTECGL  299
S18771       AFSSVAGSEL IFLEDSPDYC LKNISLGLQG TEGRECLQSG KNLSQWERRS CKRLCTDCGL  300
P51030       TFHHVHSTEL VFLEDSPDYC TRNASLGHHG TEGRECLQTG KNLSQWERRS CRRLSTECGL  300

                    310        320        330        340        350        360
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL4 Prote   QVEERKTEVI SSCNCKFQWC CTVKCDQCRH VVSKYYCARS P-----GSAQ SLGKGSA---  351
AY009402     QVEERKTEVI SSCNCKFQWC CTVKCDQCRH VVSKYYCARS P-----GSAQ SLGRVWFGVY  354
NP_033316.   QVEERRAEAV SSCDCNFQWC CTVKCGQCRR VVSRYYCTRP V-----GSAR PRGRGKDSAW  354
S18771       RVEEKKTEII SSCNCKFHWC CTVKCEQCKQ VVIKHFCARR ERDSNMLNTK RKNRGHQEMT  360
P51030       KVEERRTEVV SSCNCKFHWC CTVRCEQCRQ LVAKHFCARR D-AAVANHTK RRNKGHRR--  357

                    370        380
             ....|....| ....|....| ....|..
MOL4 Prote   ---------- ---------- ------- 351
AY009402     I--------- ---------- ------- 355
```

```
NP_033316.  ---------- ---------- ------- 354
S18771      AFQKMSPTST RASGFVCLQD FFLNLWT 387
P51030      ---------- ---------- ------- 357
```

WNT genes encode intercellular signaling glycoproteins that play important roles in key processes of embryonic development such as mesoderm induction, specification of the embryonic axis, and patterning of the central nervous system, spinal cord, and limbs. The name WNT denotes the relationship of this family to the *Drosophila* segment polarity gene 'wingless,' and to its vertebrate ortholog Int1, a mouse protooncogene; see WNT1. It was noted that multiple WNT genes are known to exist in several species that have been investigated ranging from *Drosophila* to man. They have been classified into various groups and subgroups on the basis of high sequence homology and common expression patterns. The vertebrate WNT8 subfamily includes genes from *Xenopus*, zebrafish, and chicken; The first mammalian WNT8 homolog, a human member of the Wnt8 family that they termed WNT8B was characterized on the basis of the very high sequence similarity (90-91% identity) of the inferred protein to those encoded by the *Xenopus* and zebrafish Wnt8b genes. The human cDNA encodes a 295-amino acid polypeptide that contains a C2H2 zinc finger-like motif. A predominant 1.9-kb mRNA was detected in a variety of adult and fetal tissues. They used PCR typing of a human monochromosomal hybrid cell panel to map the gene to chromosome 10, and fluorescence *in situ* hybridization for localization at 10q24.

The full-length cDNA sequence and genomic organization of the human WNT8B gene was presented and reported studies of expression of the gene in human and mouse embryos. The WNT8B gene contains six exons separated by small introns, with the exception of intron 1. The predicted protein has 351 amino acids. The gene is expressed predominantly as a transcript of approximately 2.1 kb. The human and mouse expression patterns appeared to be identical and were restricted to the developing brain, with the great majority of expression being found in the developing forebrain. In the latter case, expression was confined to the germinative neuroepithelium of three sharply delimited regions: the dorsomedial wall of the telencephalic ventricles (which includes the developing hippocampus), a discrete region of the dorsal thalamus, and the mammillary and retromammillary regions of the posterior hypothalamus. Expression in the developing hippocampus may suggest a role for WNT8B in patterning of this region, and subchromosomal localization of the human gene to 10q24 may suggest it as a candidate gene for partial epilepsy (EPT; OMIM-600512) in families in which the disease has been linked to markers in this region.

WNT1 is a member of a family of cysteine-rich, glycosylated signaling proteins that mediate diverse developmental processes such as the control of cell proliferation, adhesion, cell polarity, and the establishment of cell fates. Wnt1 was identified as an oncogene activated by the insertion of mouse mammary tumor virus in virus-induced mammary adenocarcinomas. Although Wnt1 is not expressed in the normal mammary gland, expression of Wnt1 in transgenic mice causes mammary tumors. To identify downstream genes in the WNT signaling pathway that are relevant to the transformed cell phenotype, A PCR-based cDNA subtraction strategy was used, suppression subtractive hybridization. It was reported that the identification of two genes, WISP1 and WISP2, that are upregulated in the mouse mammary epithelial cell line transformed by Wnt1, but not by Wnt4. Together with a third related gene, WISP3, these proteins define a subfamily of the connective tissue growth factor family. Two distinct systems demonstrated WISP induction to be associated with the expression of WNT1. WISP1 genomic DNA was amplified in colon cancer cell lines and in human colon tumors and its RNA overexpressed in 84% of the tumors examined compared with patient-matched normal mucosa. WISP3 also was overexpressed in 63% of colon tumors analyzed. In contrast, WISP2 showed reduced RNA expression in 79% of the tumors. These results suggested that WISP genes may be downstream of WNT1 signaling and that aberrant levels of WISP expression in colon cancer may play a role in colon tumorigenesis.

It was found that the WISP1 cDNA encodes a 367-amino acid protein. Mouse and human WISP1 proteins are 84% identical; both have hydrophobic N-terminal signal sequences, 38 conserved cysteine residues, and 4 potential N-linked glycosylation sites. Alignment of the three human WISP proteins showed that WISP1 and WISP3 are most similar (42%), whereas WISP2 had 37% identity with WISP1 and 32% identity with WISP3.

Uses of the Compositions of the Invention

The above defined information for this invention suggests that MOL4 may function as a member of the "Wnt 8 family". Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in neurodegenerative disorders, epilepsy, cancers including but not limited to brain tumor, colon cancer and breast cancer, developmental disorders, neural tube defects, and/or other pathologies and disorders. For example, a cDNA encoding the Wnt 8-like protein may be useful in gene therapy, and the Wnt 8-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from neurodegenerative disorders, epilepsy, cancers including but not limited to brain tumor, colon cancer and breast cancer, developmental disorders, and neural tube defects,. The novel nucleic acid encoding Wnt 8-like protein, and the Wnt 8-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL5

The disclosed novel Beta Thymosin-like MOL5 nucleic acid of 215 nucleotides (also referred to as AC025535) is shown in Table 5A. An ORF begins with an ATG initiation codon at nucleotides 4-7 and ends with a TGA codon at nucleotides 211-213. A putative untranslated region upstream from the initiation codon and downstream from the termination codon is underlined in Table 5A, and the start and stop codons are in bold letters.

Table 5A. MOL5 Nucleotide Sequence (SEQ ID NO:9)
AGTATGGTCTCAGCCCAGCGTTTCACGAGTCTTCAAGCCTTCAGGCTTTCTTTAATCAAGATGAGTGATAACCCA AACTTGTCAGAAGTGAAGTTTGACAGGTCAAAATTGAAGAAAACTAACACTGGAGAAAAAAATAGGCTTTCTTCC AAGGAAACTATCCAGCAGGAGAAATACGGTGTTCAAACATCATATAATGGGGGCTGGGCATGATG

The MOL protein encoded by SEQ ID NO:9 has 69 amino acid residues and is presented using the one-letter code in Table 5B. The Psort profile for MOL5 predicts that this sequence has a signal peptide and is likely to be localized at the mitochondrial intermembrane space with a certainty of 0.8800. Using the SIGNALP analysis, the protein of the invention does not appear to contain a predictable signal peptide.

Table 5B. Encoded MOL5 protein sequence (SEQ ID NO:10)
MVSAQRFTSLQAFRLSLIKMSDNPNLSEVKFDRSKLKKTNTGEKNRLSSKETIQQEKYGVQTSYNGGWA

The disclosed nucleic acid sequence for MOL5 has167 of 191 bases (87%) identical to a *Homo sapiens* Beta Thymosin mRNA (GENBANK-ID: D82345|acc:D82345) (E= 5.1e^{-26}).

The full MOL5 amino acid sequence has 37 of 45 amino acid residues (82%) identical to, and 38 of 45 residues (84%) positive with, the 45 amino acid residue Thymosin beta protein from *Homo sapiens* (ptnr: PIR-ID:JC5274) (E= 1.2e^{-11}).

MOL5 also has homology to other proteins as shown in BLAST alignment results in Table 5C.

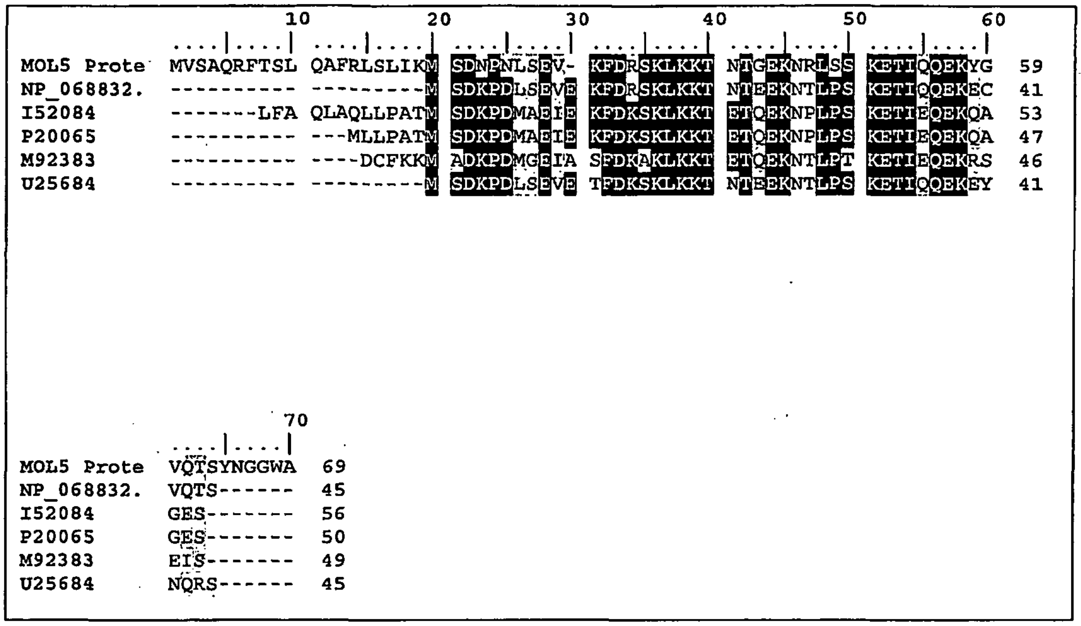
Table 5C. BLAST results for MOL5

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
ref|NP_068832.1|	thymosin, beta, identified in neuroblastoma cells [Homo sapiens]	45	37/45 (82%)	38/45 (84%)	5e-06
pir||I52084	thymosin beta-4 precursor - rat (fragment)	56	27/39 (69%)	33/39 (84%)	2e-04
sp|P20065|TYB4_MOUSE	THYMOSIN BETA-4	50	27/39 (69%)	33/39 (84%)	3e-04
gb|AAA36746.1| (M92383)	thymosin beta-10 [Homo sapiens]	49	24/40 (60%)	32/40 (80%)	0.002
gb|AAB37101.1| (U25684)	thymosin beta-like protein [Rattus norvegicus]	45	31/39 (79%)	34/39 (86%)	0.002

This information is presented graphically in the multiple sequence alignment given in Table 5D (with MOL5 being shown on line 1) as a ClustalW analysis comparing MOL5 with related protein sequences.

Table 5D Information for the ClustalW proteins:

1) MOL5 (SEQ ID NO:10)
2) ref|NP_068832.1| thymosin, beta, identified in neuroblastoma cells [Homo sapiens] (SEQ ID NO:48)
3) pir||I52084 thymosin beta-4 precursor - rat (fragment) (SEQ ID NO:49)
4) sp|P20065|TYB4_MOUSE THYMOSIN BETA-4 (SEQ ID NO:50)
5) gb|AAA36746.1| (M92383) thymosin beta-10 [Homo sapiens] (SEQ ID NO:51)
6) gb|AAB37101.1| (U25684) thymosin beta-like protein [Rattus norvegicus] (SEQ ID NO:52)



```
                     10         20         30         40         50         60
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL5 Prote   MVSAQRFTSL QAFRLSLIKM SDNPNLSEV- KFDRSKLKKT NTGEKNRLSS KETIQQEKYG  59
NP_068832.   ---------- ---------M SDKPDLSEVE KFDRSKLKKT NTEEKNTLPS KETIQQEKEC  41
I52084       -------LFA QLAQLLPATM SDKPDMAEIE KFDKSKLKKT ETQEKNPLPS KETIEQEKQA  53
P20065       ---------- ---MLLPATM SDKPDMAEIE KFDKSKLKKT ETQEKNPLPS KETIEQEKQA  47
M92383       ---------- ----DCFKKM ADKPDMGEIA SFDKAKLKKT ETQEKNTLPT KETIEQEKRS  46
U25684       ---------- ---------M SDKPDLSEVE TFDKSKLKKT NTEEKNTLPS KETIQQEKEY  41

                     70
             ....|....|
MOL5 Prote   VQTSYNGGWA  69
NP_068832.   VQTS------  45
I52084       GES-------  56
P20065       GES-------  50
M92383       EIS-------  49
U25684       NQRS------  45
```

Thymosin-beta-4 induces the expression of terminal deoxynucleotidyl transferase activity *in vivo* and *in vitro*, inhibits the migration of macrophages, and stimulates the secretion of hypothalamic luteinizing hormone-releasing hormone. It was noted that the protein was originally isolated from a partially purified extract of calf thymus, thymosin fraction 5, which induced differentiation of T cells and was partially effective in some immuno-compromised animals. Further studies demonstrated that the molecule is ubiquitous; it had been found in all tissues and cell lines analyzed. It is found in highest concentrations in spleen, thymus, lung, and peritoneal macrophages. It was stated that thymosin-beta-4 is an actin monomer sequestering protein that may have a critical role in modulating the dynamics of actin polymerization and depolymerization in nonmuscle cells. Its regulatory role is consistent with the many examples of transcriptional regulation of T-beta-4 and of tissue-specific expression. Lymphocytes have a unique T-beta-4 transcript relative to the ubiquitous transcript found in many other tissues and cells. It was stated that rat thymosin-beta-4 is synthesized as a 44-amino acid propeptide which is processed into a 43-amino acid peptide by removal of the first methionyl residue. The molecule does not have a signal peptide. Human thymosin-beta-4 has a high degree of homology to rat thymosin-beta-4; the coding regions differ by only 9 nucleotides, and these are all silent base changes.

By differential screening of a cDNA library prepared from leukocytes of an acute lymphocytic leukemia patient, a cDNA encoding thymosin-beta-4 was isolated. Using Northern blot analysis, the expression of the 830-nucleotide thymosin-beta-4 mRNA in various primary myeloid and lymphoid malignant cell lines and in hemopoietic cell lines was studied. It was stated that the pattern of thymosin-beta-4 gene expression suggests that it may be involved in an early phase of the host defense mechanism.

A cDNA clone for the human interferon-inducible gene 6-26 was isolated and showed that its sequence was identical to that for the human thymosin-beta-4 gene. By use of a panel of human rodent somatic cell hybrids, it was shown that the 6-26 cDNA recognized seven genes, members of a multigene family, present on chromosomes 1, 2, 4, 9, 11, 20, and X. These genes are symbolized TMSL1, TMSL2, etc., respectively. Li et al. (1996) established that in the mouse there is a single Tmsb4 gene and that the lymphoid-specific transcript is generated by extending the ubiquitous exon 1 with an alternate downstream splice site. By interspecific backcross mapping, they located the mouse gene, which they symbolized Ptmb4, to the distal region of the mouse X chromosome, linked to Btk and Gja6. Thus, the human gene could be predicted to reside on the X chromosome in the general region of Xq21.3-q22, where BTK is located. By analysis of somatic cell hybrids, the thymosin-beta-4, or TB4X, gene were mapped to the X chromosome. They noted that a homologous gene, TB4Y, is present on the Y chromosome.

It was stated that prostate carcinoma is the most prevalent form of cancer in males and the second leading cause of cancer death among older males. The use of the serum prostate-specific antigen test permits early detection of human prostate cancer; however, early detection has not been accompanied by an improvement in determining which tumors may progress to the metastatic stage. The process of tumor metastasis is a multistage event involving local invasion and destruction of extracellular matrix; intravasation into blood vessels, lymphatics or other channels of transport; survival in the circulation; extravasation out of the vessels into the secondary site; and growth in the new location. Common to many components of the metastatic process is the requirement for tumor cell motility. A well-characterized series of cell lines that showed varying metastatic potential was developed from the Dunning rat prostate carcinoma. A direct correlation between cell motility and metastatic potential in the Dunning cell lines was shown. In studies comparing gene expression in poorly and highly motile metastatic cell lines derived from Dunning rat prostate carcinoma using differential mRNA display, Bao et al. (1996) found a novel member of the thymosin-beta family of actin-binding molecules. The molecule, named thymosin-beta-15 by them, was found to deregulate motility in prostate cells directly. In addition, it was expressed in advanced human prostate cancer specimens, but not in normal human prostate or benign prostatic hyperplasia, suggesting its potential use as a new marker for prostate carcinoma progression. Bao et al. (1996) found that thymosin-beta-15 levels correlated positively with the Gleason tumor grade. Coffey (1996) pointed out that the upregulation of thymosin-beta-15 as a positive motility factor and the down regulation of the motility suppressor KAI1 (OMIM- 600623) provide the 'yin and yang' for metastasis; he speculated that these pathways may provide a new target for therapy.

Angiogenesis is an essential step in the repair process that occurs after injury. In a study, the angiogenic thymic peptide thymosin beta4 (Tbeta4) enhanced wound healing in a rat full thickness wound model was examined. Addition of Tbeta4 topically or intraperitoneally increased reepithelialization by 42% over saline controls at 4 d and by as much as 61% at 7 d post-wounding. Treated wounds also contracted at least 11% more than controls by day 7. Increased collagen deposition and angiogenesis were observed in the treated wounds. We also found that Tbeta4 stimulated keratinocyte migration in the Boyden chamber assay. After 4-5 h, migration was stimulated 2-3-fold over migration with medium alone when as little as 10 pg of Tbeta4 was added to the assay. These results suggest that Tbeta4 is a potent wound healing factor with multiple activities that may be useful in the clinic.

Uses of the Compositions of the Invention

The above defined information for this invention suggests thatMOL5 may function as a member of a "Beta Thymosin family". Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in cancer including but not limited to prostate cancer, immunological and autoimmune disorders (*i.e.*, hyperthyroidism), angiogenesis and wound healing, modulation of apoptosis, neurodegenerative and neuropsychiatric disorders, age-related disorders, and other pathological disorders involving spleen, thymus, lung, and peritoneal macrophages and/or other pathologies and disorders. For example, a cDNA encoding the Beta Thymosin-like protein may be useful in gene therapy, and the Beta Thymosin-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from cancer including but not limited to prostate cancer, immunological and autoimmune disorders (*i.e.*, hyperthyroidism), angiogenesis and wound healing, modulation of apoptosis, neurodegenerative and neuropsychiatric disorders, age-related disorders, and other pathological disorders involving spleen, thymus, lung, and peritoneal macrophages. The novel nucleic acid encoding Beta Thymosin-like protein, and the Beta Thymosin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL6

MOL6a

The disclosed novel Trypsin-like MOL6a nucleic acid of 730 nucleotides (also referred to as GM_87760758_A) is shown in Table 6A. An open reading begins with an ATG initiation codon at nucleotides 8-10 and ends with a TGA codon at nucleotides 713-715. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 6A, and the start and stop codons are in bold letters.

Table 6A. MOL6a Nucleotide Sequence (SEQ ID NO:11)
GATCACCATGAAATATGTCTTCTATTTGGGTGTCCTCGCTGGGACATTTTTCTTTGCTGACTCATCTGTTCAGAA AGAAGACCCTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAACCCAG

CTGGGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGAGTCAG
AGACGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCACAGGA
TGACCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTCCCCTCGCCACCAC
CAATGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGGAGCCAAGAAAACAGTGGCCGACACCCTGA
CTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGCCAAAAAACAGAACAAGGAAAAAGCCACAG
GAATTCCTTATGTGTGAAATTTGTGAAAGTATTCAGCCGAATTTTTGGGGAGGTGGCCGTTGCTACTGTCATCTG
CAAAGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGGAGGGGACGTCGGCATCTACACCAATGTTTACAA
ATATGTATCCTGGATTGAGAACACTGCTAAGGACAAGTGAGACCCTACTTCTCCC

The disclosed nucleic acid sequence has 354 of 581 bases (60%) identical to a *Mus musculus* prepro-Trypsininogen mRNA (GENBANK-ID: MMTRYAR|acc:X04574) (E value = 9.9e-^{24}).

The MOL6a protein encoded by SEQ ID NO:11 has 235 amino acid residues, and is presented using the one-letter code in Table 6B (SEQ ID NO:12). The Psort profile for MOL6a predicts that this sequence has a signal peptide and is likely to be localized on the outside with a certainty of 0.3700. The most likely cleavage site for a peptide is between amino acids 19 and 20, ADS-SV based on the SignalP result.

Table 6B. Encoded MOL6a protein sequence (SEQ ID NO:12).
MKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGT
EQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPDLRQN
LEAPVMSDRECQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIEVGHFMGGDVGIYTNVYKYVSWI
ENTAKDK

The full amino acid sequence of MOL6a was found to have 79 of 208 amino acid residues (37%) identical to, and 118 of 208 residues (56%) positive with, the 248 amino acid residue TRYPSINOGEN I-P1 PRECURSOR (EC 3.4.21.4) protein from *Gallus gallus* (ptnr: SWISSNEW--ACC: Q90627) (E value = 1.1e-^{33}).

MOL6b

The disclosed novel Trypsin-like MOL6b nucleic acid of 720 nucleotides (also referred to as CG54548-03) is shown in Table 6C. An open reading begins with an ATG initiation codon at nucleotides 5-7 and ends with a TGA codon at nucleotides 710-712. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 6C, and the start and stop codons are in bold letters.

Table 6C. MOL6b Nucleotide Sequence (SEQ ID NO:152)
TACCATGAAATATGTCTTCTATTTGGGTGTCCTCGCTGGGACATTTTTCTTTGCTGACTCATCTGTTCAGAAAGA
AGACCCTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAACCCAGCTG
GGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGAGTCAGAGA
CGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCACAGGATGA

CCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTCCCCTCGCCACCACCAA
TGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGGAGCCAAGAAAACAGTGGCCGACACCCTGACTT
GCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGCCAAAAAACAGAACAAGGAAAAAGCCACAGGAA
TTCCTTATGTGTGAAATTTGTGAAAGTATTCAGCCGAATTTTTGGGGAGGTGGCCGTTGCTACTGTCATCTGCAA
AGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGGAGGGGACGTCGGCATCTACACCAATGTTTACAAATA
TGTATCCTGGATTGAGAACACTGCTAAGGACAAGTGAGACCGTAA

The MOL6b protein encoded by SEQ ID NO:152 has 235 amino acid residues, and is presented using the one-letter code in Table 6D (SEQ ID NO:153).

Table 6D. Encoded MOL6b protein sequence (SEQ ID NO:153).
MKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGT
EQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPDLRQN
LEAPVMSDRECQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIEVGHFMGGDVGIYTNVYKYVSWI
ENTAKDK

MOL6c

The disclosed novel Trypsin-like MOL6c nucleic acid of 516 nucleotides (also referred to as 246861979) is shown in Table 6E. An open reading begins with an CGC initiation codon at nucleotides 1-3 and ends with a GCGcodon at nucleotides 514-516. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 6E, and the start and stop codons are in bold letters. Because the start and stop codons of MOL6c are not traditioonal initiation and termination codons, MOL6c could be a partial reading frame extending further in the 5' and/or 3' directions.

Table 6E. MOL6c Nucleotide Sequence (SEQ ID NO:154)
CGCGGATCCACCATGAAATATGTCTTCTATTTGGGTGTCCTCGCTGGGACATTTTTCTTTGCTGACTCATCTGTT
CAGAAAGAAGACCCTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAA
CCCAGCTGGGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGA
GTCAGAGACGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCA
CAGGATGACCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTCCCCTCGCC
ACCACCAATGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGGAGCCAAGAAAACAGTGGCCGACAC
CCTGACTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGCCAAAAACTCGAGGCG

The MOL6c protein encoded by SEQ ID NO:154 has 172 amino acid residues, and is presented using the one-letter code in Table 6F (SEQ ID NO:155).

Table 6F. Encoded MOL6c protein sequence (SEQ ID NO:155).
RGSTMKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRV
RDGTEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPD
LRQNLEAPVMSDRECQKLEA

MOL6d

The disclosed novel Trypsin-like MOL6d nucleic acid of 600 nucleotides (also referred to as 246862070) is shown in Table 6G. An open reading begins with an CGC initiation codon at nucleotides 1-3 and ends with a GCG codon at nucleotides 598-600. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 6G, and the start and stop codons are in bold letters. Because the start and stop codons of MOL6d are not traditioonal initiation and termination codons, MOL6d could be a partial reading frame extending further in the 5' and/or 3' directions.

Table 6G. MOL6d Nucleotide Sequence (SEQ ID NO:156)
CGCGGATCCGGCGTCCTCATCAAACCCAGCTGGGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTG ATGCTGGGAAATTTCAAGAGCAGAGTCAGAGACGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTAC TGGAACTACAGTCATAGCGCCCCACAGGATGACCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCC AAAGTCCAGCCCCTTCCCCTCGCCACCACCAATGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGG AGCCAAGAAAACAGTGGCCGACACCCTGACTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGC CAAAAAACAGAACAAGGAAAAAGCCACAGGAATTCCTTATGTGTGAAATTTGTGAAAGTATTCAGCCGAATTTTT GGGGAGGTGGCCGTTGCTACTGTCATCTGCAAAGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGAGGG GACGTCGGCATCTACACCAATGTTTACAAATATGTATCCTGGATTGAGAACACTGCTAAGGACAAGCTCGAG**GCG**

The MOL6d protein encoded by SEQ ID NO:156 has 200 amino acid residues, and is presented using the one-letter code in Table 6H (SEQ ID NO:157).

Table 6H. Encoded MOL6d protein sequence (SEQ ID NO:157).
RGSGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGTEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPK VQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRECQKTEQGKSHRNSLCVKFVKVFSRIFGE VAVATVICKDKLQGIEVGHFMGGDVGIYTNVYKYVSWIENTAKDKLEA

MOL6a also has high homology to the proteins shown in the BLAST data in Table 6I.

SNP analysis of MOL6a is described in Example 2.

Table 6I. BLAST results for MOL6a

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi|2499862|sp|Q90627|TRY1_CHICK	TRYPSIN I-P1 PRECURSOR	248	79/208 (37%)	118/208 (55%)	2e-31
gi|2118087|pir||S55067	trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken	248	78/208 (37%)	117/208 (55%)	5e-31
gi|6678439|ref|NP_033456.1|	trypsin 2 [Mus musculus]	246	77/215 (35%)	115/215 (52%)	8e-29

gi|1633123|pdb|1SLW|B	Chain B, Rat Anionic N143h, E151h Trypsin Complexed To A86h Ecotin	223	74/212 (34%)	116/212 (53%)	1e-28

MOL6e

In the present invention, the target sequence identified previously, MOL6a, Accession Number GM_87760758_A, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such suitable sequences were then employed as the forward and reverse primers in a PCR amplification based on library containing a wide range of cDNA species. The resulting amplicon was gel purified, cloned and sequenced to high redundancy to provide the sequence reported below, which is designated MOL6e, Accession Number GM_87760758_A_da

The disclosed novel Trypsin-like MOL6e nucleic acid of 730 nucleotides (also referred to as GM_87760758_A_da) is shown in Table 6J. An open reading frame begins with an ATG initiation codon at nucleotides 8-10 and ends with a TGA codon at nucleotides 713-715. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 6J, and the start and stop codons are in bold letters.

Table 6J. MOL6e Nucleotide Sequence (SEQ ID NO:13)
GATCACCATGAAATATGTCTTCTATTTGGGTGTCCTCGCTGGGACATTTTTCTTTGCTGACTCATCTGTCCAGAA
AGAAGACCCTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAACCCAG
CTGGGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGAGTCAG
AGACGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCACAGGA
TGACCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTCCCCTCGCCACCAC
CAATGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGGAGCCAAGAAAACAGTGGCCGACACCCTGA
CTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGCCAAAAAACAGAACAAGGAAAAAGCCACAG
GAATTCCTTATGTGTGAAATTTGTGAAAGTATTCAGCCGAATTTTTGGGGAGGTGGCCGTTGCTACTGTCATCTG
CAAAGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGAGGGGACGTCGGCATCTACACCAATGTTTACAA
ATATGTATCCTGGATTGAGAACACTGCTAAGGACAAGTGAGACCCTACTTCTCCC

The MOL6e protein encoded by SEQ ID NO:13 has 235 amino acid residues, and is presented using the one-letter code in Table 6K (SEQ ID NO:14). The Psort profile for MOL6a predicts that this sequence has a signal peptide and is likely to be localized on the outside with a certainty of 0.3700. The most likely cleavage site for a peptide is between amino acids 19 and 20 based on the SignalP result.

Table 6K. Encoded MOL6e protein sequence (SEQ ID NO:14).
MKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGT EQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPDLRQN LEAPVMSDRECQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIEVGHFMGGDVGIYTNVYKYVSWI ENTAKDK

The full amino acid sequence of MOL6e was found to have homology with several proteins including those disclosed in the BLASTP data in Table 6L.

Table 6L. BLAST results for MOL6e

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
ACC:Q90627	TRYPSIN I-P1 PRECURSOR (EC 3.4.21.4) - Gallus gallus (Chicken)	248	79/208 (37%)	118/208 (56%)	3.8e-34
PIR-ID:S55067	trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken	248	78/208 (37%)	117/208 (55%)	7.9e-34
ACC:Q90628	TRYPSIN I-P38 PRECURSOR (EC 3.4.21.4) - Gallus gallus (Chicken)	248	78/208 (37%)	117/208 (56%)	1.0e-33
ACC:P07477	TRYPSIN I PRECURSOR (EC 3.4.21.4) (CATIONIC TRYPSINOGEN) - Homo sapiens (Human)	247	76/212 (35%)	112/212 (52%)	1.3e-31

MOL6e also has high homology to the proteins shown in the BLASTX alignment data in Table 6M.

Table 6M. BLASTX results for MOL6e

```
                                                                Smallest
                                                                Sum
                                                Reading  High   Prob
Sequences producing High-scoring Segment Pairs:   Frame  Score  P(N)      N

ptnr:SWISSPROT-ACC:Q90627 TRYPSIN I-P1 PRECURSOR (EC 3.+2   372  2.3e-33   1
ptnr:PIR-ID:S55067 trypsin (EC 3.4.21.4) I precursor, .+2   369  4.7e-33   1
ptnr:SWISSPROT-ACC:Q90628 TRYPSIN I-P38 PRECURSOR (EC .+2   368  6.0e-33   1
ptnr:SWISSPROT-ACC:P07146 TRYPSIN II, ANIONIC PRECURSO.+2   350  4.9e-31   1
ptnr:SWISSPROT-ACC:P07477 TRYPSIN I PRECURSOR (EC 3.4..+2   348  7.9e-31   1
ptnr:SPTREMBL-ACC:Q9R0T7 PANCREATIC TRYPSIN - Mus musc.+2   348  7.9e-31   1
ptnr:SWISSPROT-ACC:P15951 TRYPSIN III PRECURSOR (EC 3..+2   347  1.0e-30   1
```

MOL6f

The disclosed novel Trypsin-like MOL6f nucleic acid of 390 nucleotides (also referred to as 256801454) is shown in Table 6BBA. An open reading begins with an CGC initiation codon at nucleotides 1-3 and ends with a GCG codon at nucleotides 388-390. Because the start and stop codons of MOL6f are not traditioonal initiation and termination codons, MOL6f could be a partial reading frame extending further in the 5' and/or 3' directions.

Table 6BBA. MOL6f Nucleotide Sequence (SEQ ID NO:176)
CGCGGATCCGGCGTCCTCATCAAACCCAGCTGGGTGCTGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTG ATGCTGGGAAATTTCAAGAGCAGAGTCAGAGACGGTACTGAACAGACAATTAACCCCATTCAGATCGTCCGCTAC TGGAACTACAGTCATAGCGCCCCACAGGATGACCTCATGCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCC AAAGTCCAGCCCCTTCCCCTCGCCACCACCAATGTCAGGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGG AGCCAAGAAAACAGTGGCCGACACCCTGACTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGC CAAAAACTCGAGGCG

The MOL6f protein encoded by SEQ ID NO:156 has 130 amino acid residues, and is presented using the one-letter code in Table 6BBB (SEQ ID NO:157).

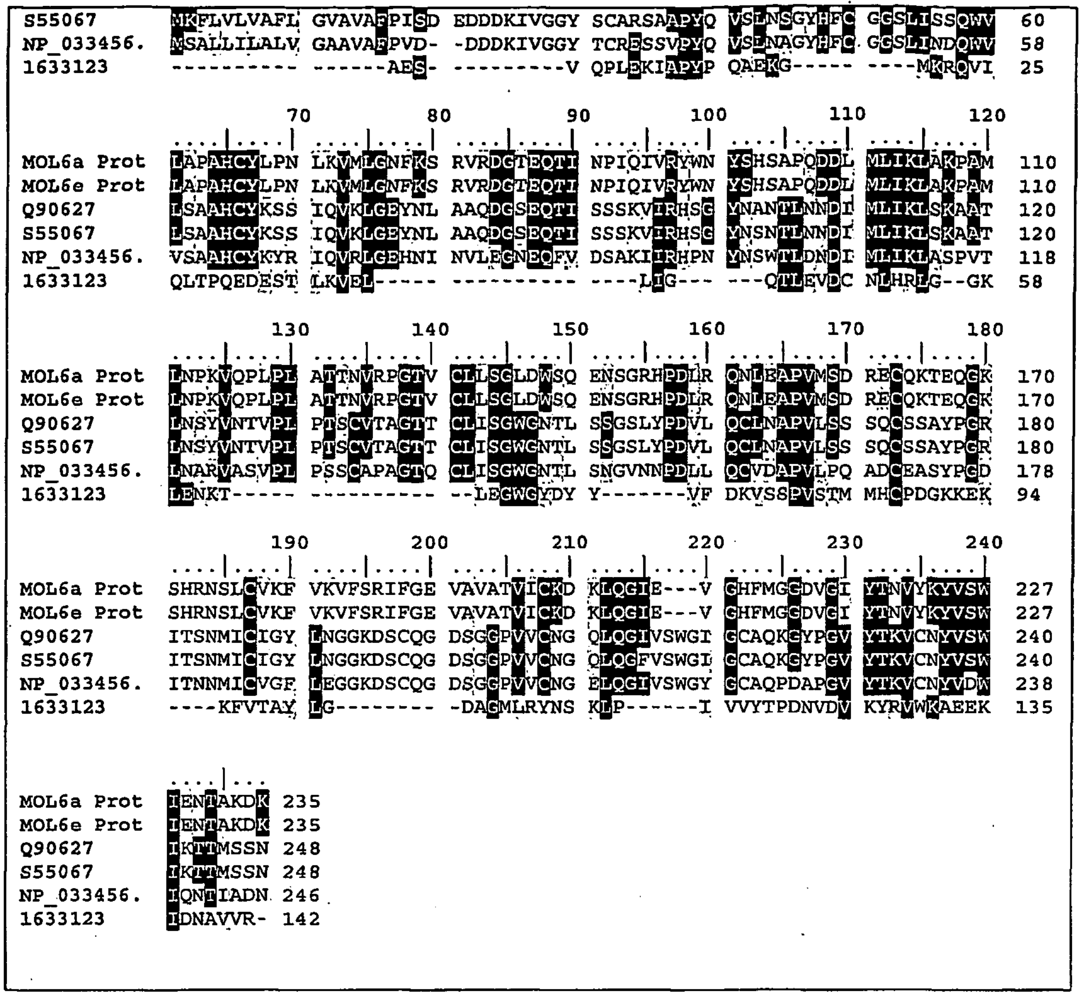
Table 6BBB. Encoded MOL6f protein sequence (SEQ ID NO:177).
RGSGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGTEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPK VQPLPLATTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRECQKLEA

This information is presented graphically in the multiple sequence alignment given in Table 6N (with MOL6a being shown on line 1 and MOL6e being shown on line 2) as a ClustalW analysis comparing MOL6 with related protein sequences.

Table 6N Information for the ClustalW proteins:

```
1) MOL6a (SEQ ID NO:12)
2) MOL6e (SEQ ID NO:14)
3) gi|2499862|sp|Q90627|TRY1_CHICK TRYPSIN I-P1 PRECURSOR (SEQ ID NO:53)
4) gi|2118087|pir||S55067 trypsin (EC 3.4.21.4) I precursor, pancreatic -
chicken (SEQ ID NO:54)
5) gi|6678439|ref|NP_033456.1| trypsin 2 [Mus musculus] (SEQ ID NO:55)
6) gi|1633123|pdb|1SLW|B Chain B, Rat Anionic N143h, E151h Trypsin
Complexed To A86h Ecotin (SEQ ID NO:56)
```

```
                      10         20         30         40         50         60
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL6a Prot    MKYVFYLGVL AGTFFFADS- ---------S VQKEDPAPYL VYLKSHFNPC VGVLIKPSWV  50
MOL6e Prot    MKYVFYLGVL AGTFFFADS- ---------S VQKEDPAPYL VYLKSHFNPC VGVLIKPSWV  50
Q90627        MKFLVLVAFV GVTVAFPISD EDDDKIVGGY SCARSAAPYQ VSLNSGYHFC GGSLISSQWV  60
```



```
S55067         MKFLVLVAFL GVAVAFPISD EDDDKIVGGY SCARSAAPYQ VSLNSGYHFC GGSLISSQWV  60
NP_033456.     MSALLILALV GAAVAFPVD- -DDDKIVGGY TCRESSVPYQ VSLNAGYHFC GGSLINDQWV  58
1633123        ---------- ------AES- ---------V QPLEKIAPYP QAEKG----- ----MKRQVI  25

                       70         80         90        100        110        120
               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL6a Prot     LAPAHCYLPN LKVMLGNFKS RVRDGTEQTI NPIQIVRYWN YSHSAPQDDL MLIKLAKPAM  110
MOL6e Prot     LAPAHCYLPN LKVMLGNFKS RVRDGTEQTI NPIQIVRYWN YSHSAPQDDL MLIKLAKPAM  110
Q90627         LSAAHCYKSS IQVKLGEYNL AAQDGSEQTI SSSKVIRHSG YNANTLNNDI MLIKLSKAAT  120
S55067         LSAAHCYKSS IQVKLGEYNL AAQDGSEQTI SSSKVIRHSG YNSNTLNNDI MLIKLSKAAT  120
NP_033456.     VSAAHCYKYR IQVRLGEHNI NVLEGNEQFV DSAKIIRHPN YNSWTLDNDI MLIKLASPVT  118
1633123        QLTPQEDEST LKVEL----- ---------- ----LIG--- ---QTLEVDC NLHRLG--GK  58

                      130        140        150        160        170        180
               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL6a Prot     LNPKVQPLPL ATTNVRPGTV CLLSGLDWSQ ENSGRHPDLR QNLEAPVMSD RECQKTEQGK  170
MOL6e Prot     LNPKVQPLPL ATTNVRPGTV CLLSGLDWSQ ENSGRHPDLR QNLEAPVMSD RECQKTEQGK  170
Q90627         LNSYVNTVPL PTSCVTAGTT CLISGWGNTL SSGSLYPDVL QCLNAPVLSS SQCSSAYPGR  180
S55067         LNSYVNTVPL PTSCVTAGTT CLISGWGNTL SSGSLYPDVL QCLNAPVLSS SQCSSAYPGR  180
NP_033456.     LNARVASVPL PSSCAPAGTQ CLISGWGNTL SNGVNNPDLL QCVDAPVLPQ ADCEASYPGD  178
1633123        LENKT----- ---------- --LEGWGYDY Y-------VF DKVSSPVSTM MHCPDGKKEK  94

                      190        200        210        220        230        240
               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL6a Prot     SHRNSLCVKF VKVFSRIFGE VAVATVICKD KLQGIE---V GHFMGGDVGI YTNVYKYVSW  227
MOL6e Prot     SHRNSLCVKF VKVFSRIFGE VAVATVICKD KLQGIE---V GHFMGGDVGI YTNVYKYVSW  227
Q90627         ITSNMICIGY LNGGKDSCQG DSGGPVVCNG QLQGIVSWGI GCAQKGYPGV YTKVCNYVSW  240
S55067         ITSNMICIGY LNGGKDSCQG DSGGPVVCNG QLQGFVSWGI GCAQKGYPGV YTKVCNYVSW  240
NP_033456.     ITNNMICVGF LEGGKDSCQG DSGGPVVCNG ELQGIVSWGY GCAQPDAPGV YTKVCNYVDW  238
1633123        ----KFVTAY LG-------- -DAGMLRYNS KLP------I VVYTPDNVDV KYRVWKAEEK  135


               ....|...
MOL6a Prot     IENTAKDK 235
MOL6e Prot     IENTAKDK 235
Q90627         IKTTMSSN 248
S55067         IKTTMSSN 248
NP_033456.     IQNTIADN 246
1633123        IDNAVVR- 142
```

MOL6e also contained several single polynucleotide polymorphisms described in Table 6O.

Table 6O. SNP for MOL6e		
Position	Nucleotide Change	Number of Occurrences
70	C>A	2
70	C>G	6
261	T>C	2
406	A>C	2
573	G>T	2
585	C>T	2
737	A>G	4

Trypsin (EC 3.4.21.4), like elastase, is a member of the pancreatic family of serine proteases. The gene encoding trypsin-1 (TRY1) is also referred to as serine protease-1

(PRSS1). MacDonald et al. (1982) reported nucleotide sequences of cDNAs representing 2 pancreatic rat trypsinogens. Using a rat cDNA probe, Honey et al. (1984, 1984) found that a 3.8-kb DNA fragment containing human trypsin-1 gene sequences cosegregated with chromosome 7, and assigned the gene further to 7q22-7qter by study of hybrids with a deletion of this segment. The trypsin gene is on mouse chromosome 6 (Honey et al., 1984). Carboxypeptidase A and trypsin are a syntenic pair conserved in mouse and man. Emi et al. (1986) isolated cDNA clones for two major human trypsinogen isozymes from a pancreatic cDNA library. The deduced amino acid sequences had 89% homology and the same number of amino acids (247), including a 15-amino acid signal peptide and an 8-amino acid activation peptide. Southern blot analysis of human genomic DNA with the cloned cDNA as a probe showed that the human trypsinogen genes constitute a family of more than ten, some of which may be pseudogenes or may be expressed in other stages of development.

Rowen et al. (1996) found that there are eight trypsinogen genes embedded in the beta T cell receptor locus or cluster of genes (TCRB; OMIM- 186930), which maps to 7q35. In the 685-kb DNA segment that they sequenced they found five tandemly arrayed 10-kb locus-specific repeats (homology units) at the 3-prime end of the locus. These repeats exhibited 90 to 91% overall nucleotide similarity, and embedded within each is a trypsinogen gene. Alignment of pancreatic trypsinogen cDNAs with the germline sequences showed that these trypsinogen genes contain five exons that span approximately 3.6 kb. Further analyses revealed 2 trypsinogen pseudogenes and one relic trypsinogen gene at the 5-prime end of the sequence, all in inverted transcriptional orientation. They denoted eight trypsinogen genes T1 through T8 from 5-prime to 3-prime. Rowen et al. (1996) found that only two of three pancreatically expressed trypsinogen cDNAs correspond to trypsinogen genes in the TCRB locus; T4 was denoted trypsinogen 1 and T8 was denoted trypsinogen 2 (OMIM- 601564). The third pancreatic cDNA, identified independently as trypsinogen 3 (Tani et al., 1990) and 4 (Wiegand et al., 1993), is distinct from the third apparently functional trypsinogen gene (T6) in the TCRB locus but related to the other pancreatic trypsinogens. Rowen et al. (1996) stated that the T6 gene is deleted in a common insertion-deletion polymorphism; if it is functional, its function is apparently not essential. Some of the trypsinogen genes are expressed in nonpancreatic tissues where their function is unknown. Rowen et al. (1996) noted that the intercalation of the trypsinogen genes in the TCRB locus is conserved in mouse and chicken, suggesting shared functional or regulatory constraints, as has been postulated for genes in the major histocompatibility complex (such as class I, II, and III genes) that share similar long-term organizational relationships.

Rowen et al. (1996) mapped the gene corresponding to the third pancreatic trypsinogen cDNA by fluorescence *in situ* hybridization. They used a cosmid clone containing 3 trypsinogen genes. Strong hybridization to chromosome 7 and weaker hybridization to chromosome 9 were observed. They isolated and partially sequenced 4 cosmid clones from the chromosome 9 region. They found that the region represents a duplication and translocation of a DNA segment from the 3-prime end of the TCRB locus that includes at least seven V(beta) elements and a functional trypsinogen gene denoted T9. The assignment of the PRSS1 gene to 7q35 is established by the demonstration of its sequence within the sequence of the 'locus' (OMIM- 186930) for the T-cell receptor beta-chain (Rowen et al., 1996). It is further supported by the linkage between microsatellite markers in the 7q35 region and hereditary pancreatitis (OMIM- 167800) and the demonstration of mutations in the PRSS1 gene in hereditary pancreatitis.

Whitcomb et al. (1996) stated that the high degree of DNA sequence homology (more than 91%) present among this cluster of five trypsinogen genes identified by Rowen et al. (1996) demanded that highly specific sequence analysis strategies be developed for mutational screening in families with hereditary pancreatitis. This was necessary to ensure that each sequencing run contained only the two alleles corresponding to a single gene, thereby permitting detection of heterozygotes in this autosomal dominant disorder, and not a dozen or more alleles from multiple related trypsinogen-like genes, which would make detection of heterozygotes nearly impossible. In a family with hereditary pancreatitis, Whitcomb et al. (1996) found that affected individuals had a single G-to-A transition mutation in the third exon of cationic trypsinogen (276000.0001). This mutation was predicted to result in an arg105-to-his substitution in the trypsin gene (residue number 117 in the more common chymotrypsin number system). Subsequently, the same mutation was found in a total of five different hereditary pancreatitis kindreds (four from the U.S. and one from Italy) containing a total of 20 affected individuals and six obligate carriers. The mutation was found in none of the obligate unaffected members (individuals who married into the family). Subsequent haplotyping revealed that all four of the American families displayed the same high risk haplotype over a 4-cM region encompassing seven STR markers, confirming the likelihood that these kindreds shared a common ancestor, although no link could be found through eight generations. A fifth family from Italy displayed a unique haplotype indicating that the same mutation had occurred on at least 2 occasions. The G-to-A mutation at codon 117 created a novel enzyme recognition site for AflIII which provided a facile means to screen for the mutation. As with the obligate unaffected members of the pancreatitis kindreds, none of 140 controls possessed the G-to-A mutation as assayed by the lack of AflIII digestion of the amplified exonic DNA.

Failure to thrive, nutritional edema, and hypoproteinemia with normal sweat electrolytes were features of 2 affected male infants reported by Townes (1965) and Townes et al. (1967). A protein hydrolysate diet was beneficial. A male sib of the first patient reported by Townes (1965) had died, apparently of the same condition. Morris and Fisher (1967) reported an affected female who also had imperforate anus. The clinical picture in enterokinase deficiency (OMIM- 226200) is closely similar; however, the defect is not in the synthesis of trypsinogen but in the synthesis of the enterokinase which activates proteolytic enzymes produced by the pancreas. Oral pancreatin represents a therapeutically successful form of enzyme replacement (Townes, 1972).

Since hereditary pancreatitis has been mapped rather precisely to 7q35 and since a defect in the trypsinogen gene has been identified in hereditary pancreatitis, the assignment of the trypsinogen gene can be refined from 7q32-qter to 7q35.

Ferec et al. (1999) studied 14 families with hereditary pancreatitis and found mutations in the PRSS1 gene in 8 families. In 4 of these families, the mutation (R117H; 276000.0001) had been described by Whitcomb et al. (1996). Three novel mutations were described in 4 other families.

Sahin-Toth et al. (1999) studied the roles of the R117H and N21I (276000.0002) mutations in hereditary pancreatitis. They stated that the R117H mutation is believed to cause pancreatitis by eliminating an essential autolytic cleavage site in trypsin, thereby rendering the protease resistant to inactivation through autolysis. Sahin-Toth et al. (1999) demonstrated that the R117H mutation also significantly inhibited autocatalytic trypsinogen breakdown under Ca(2+)-free conditions and stabilized the zymogen form of rat trypsin. Taken together with findings demonstrating that the N21I mutation stabilized rat trypsinogen against autoactivation and consequent autocatalytic degradation, the observations suggested a unifying molecular pathomechanism for hereditary pancreatitis in which zymogen stabilization plays a central role.

Uses of the Compositions of the Invention

The above defined information for this invention suggests that this Trypsin-like protein may function as a member of a “Trypsin family”. Therefore, the novel nucleic acids and proteins identified here may be useful in potential therapeutic applications implicated in (but not limited to) various pathologies and disorders as indicated below. The potential therapeutic applications for this invention include, but are not limited to: protein therapeutic, small molecule drug target, antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), diagnostic and/or prognostic marker, gene therapy (gene delivery/gene ablation), research tools, tissue regeneration *in vivo* and *in vitro* of all tissues and cell types composing (but not limited to) those defined here.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in failure to thrive, nutritional edema, and hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, cancer and/or related pathologies and disorders and/or other pathologies and disorders. For example, a cDNA encoding the Trypsin-like protein may be useful in gene therapy, and the Trypsin-like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from failure to thrive, nutritional edema, and hypoproteinemia, trypsinogen deficiency disease, chronic and heriditary pancreatitis, enterkinase defieciency, cancer. The novel nucleic acid encoding Trypsin-like protein, and the Trypsin-like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL7

A novel nucleic acid encoding a Kallikrein-like-protein MOL7 was identified by TblastN using CuraGen Corporation's sequence file for MOL7 probes or homologs, and run against the Genomic Daily Files made available by GenBank. The nucleic acid was further predicted by the program GenScan™, including selection of exons. These were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. The disclosed novel MOL7 nucleic acid of 1811 nucleotides (also referred to as 30675745.0.499) is shown in Table 7A. An open reading frame begins with an ATG initiation codon at nucleotides 368-370 and ends with a TAG codon at nucleotides 1553-1555. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 7A, and the start and stop codons are in bold letters.

Table 7A. MOL7 Nucleotide Sequence (SEQ ID NO:15)
ACAAATCCTTCTGTTGAACTCTACTGTGTCAGGCCAGCCTGAGTTCATTTCTCCTTGAGCAGGAACAGTT
CATGGACGAACTCTGAGGACCATTCTGAGGACAAGAGGCATCCAGTGTCATGAGTGGAACATGCAGCATT
TTATGGCTACAGAGTTAAGGCAAGGGTTGAATTCCACGAGTCAAAAAGCAGCCCTTTTCAGAGACCCAAC
TCTCTGGGGTGCTCAGGGGCTTGGGCTGGATTGAGAAGAAAACTGACAAGAGTAAGCTGCCCTCTCTTCT
CTGGCCATCTCACAAACCACAGTGCGGGCCAACTGGTCCTGCCTCTTTACCACACAGAACCAAGCACTAG
GGATAAGACAGCTGCCC**ATG**GTGTCCGCGGCGGGTCTCTCTGGGGATGGCAAGATGCGAGGGGTGCTCCT
GGTGCTGCTCGGCCTTCTCTATTCTTCCACCAGTTGTGGCGTCCAGAAAGCTTCCGTTTTCTACGGTCCT
GACCCCAAGGAGGGCTTGGTCAGCAGCATGGAGTTCCCGTGGGTGGTGTCGCTGCAGGACTCCCAGTACA
CACACCTGGCTTTCGGCTGCATCCTGAGCGAGTTCTGGGTCCTCAGCATCGCATCCGCCATTCAGAACAG
GAAGGACATTGTCGTTATAGTGGGTATAAGTAACATGGATCCTAGCAAGATTGCTCACACAGAGTATCCA
GTCAATACCATCATCATCCATGAGGACTTTGATAACAACTCCATGAGCAACAACATAGCCCTCCTGAAGA
CAGACACAGCGATGCATTTTGGCAACCTGGTCCAGTCCATCTGCTTCCTCGGCAGAATGCTGCATACACC
ACCAGTCTTGCAGAACTGCTGGGTGTCAGGATGGAATCCCACATCTGCAACAGGAAATCACATGACGATG
AGTGTCCTGAGGAAAATCTTCGTGAAAGATCTTGACATGTGTCCCCTATACAAACTCCAGAAGACAGAAT
GCGGCAGCCACACGAAAGAGGAAACCAAGACTGCCTGCTTGGGGGACCCAGGAAGCCCAATGATGTGCCA
GCTACAGCAGTTCGATCTGTGGGTTCTGAGAGGAATCCTGAACTTCGGTGGTGAGACGTGCCCTGGCCTG
TTTCTGTACACCAAGGTGGAAGACTACAGCAAATGGATCACATCCAAGGCTGAGAGGGCCGGCCCTCCCC
TGTCCTCACTCCACCACTGGGAAAAGTTGATTTCTTTCTCCCACCATGGACCAAATGCCGCCATGACACA
GAAGACATATTCTGATTCTGAACTGGGCCATGTTGGATCATACTTGCAGGGACAAAGAAGGACCATCACG
CATTCACGACTAGGAAACAGCTCTAGAGATAGTCTAGATGTTAGGGAGAAGGATGTAAAGGAATCAGGCA
GGTCTCCTGAGGCGTCTGTACAACCCTTATACTATGACTATTACGGTGGGAGGTGGGGAAGGTAGGAT
TTTTGCAGGTCAGAACAGGTTGTATCAGCCCGAAGAAATCATCTTGGTTTCCTTCGTGCTTGTTTTCTTT
TGCAGCAGTATC**TAG**TCCAGGAGCTACCCCACCAAACTGAAGAGTAAACTGAGAATGCTGAGTGCCAGGC
ATTCACCATGCTGTTTTGATGTCTGTTTTTGATAGTTGCACACTGGGGCTGCCACGGATAAGCCCATGGC
ATACACTGGGCTGGCTCTCCCTCCTCTATCCCTCTCCCAGGTGTGGGAAGGTCACTTTCACTATGCTTGT
GAACTAAATGCTGGCTAACAAGTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

The MOL7 protein encoded by SEQ ID NO:15 has 395 amino acid residues, and is presented using the one-letter code in Table 7B (SEQ ID NO:16). The SignalP, Psort and/or Hydropathy profile for MOL7 predict that MOL7 has a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0. 9190. The SignalP shows a signal sequence is coded for in the first 44 amino acids with the most likely cleavage site being between amino acids 30 and 31. This is typical of this type of membrane protein. The molecular weight of MOL7 is 43815.7 Daltons.

Table 7B. Encoded MOL7 protein sequence (SEQ ID NO:16).
MVSAAGLSGDGKMRGVLLVLLGLLYSSTSCGVQKASVFYGPDPKEGLVSSMEFPWVVSLQDSQYTHLAFGCILSE FWVLSIASAIQNRKDIVVIVGISNMDPSKIAHTEYPVNTIIIHEDFDNNSMSNNIALLKTDTAMHFGNLVQSICF LGRMLHTPPVLQNCWVSGWNPTSATGNHMTMSVLRKIFVKDLDMCPLYKLQKTECGSHTKEETKTACLGDPGSPM MCQLQQFDLWVLRGILNFGGETCPGLFLYTKVEDYSKWITSKAERAGPPLSSLHHWEKLISFSHHGPNAAMTQKT YSDSELGHVGSYLQGQRRTITHSRLGNSSRDSLDVREKDVKESGRSPEASVQPLYYDYYGGEVGEGRIFAGQNRL YQPEEIILVSFVLVFFCSSI

MOL7 was found to have 290 of 290 amino acid residues (100 %) identical to the 290 amino acid residue hypothetical 32.6 kD protein from *Homo sapiens* (human) (ACC:CAB70765). This protein has similarity to kallikrein.

MOL7 shows significant homologies to human hypothetical 32.6 kD protein (a protein with similiarities to Kallikrein), as described in, but not limited to, the references below.

Kallikreins are a subgroup of serine proteases and these proteolytic enzymes have diverse physiological functions in many tissues. Growing evidence suggests that many kallikreins are implicated in carcinogenesis. The human kallikrein gene family is localized on chromosome 19q13.3-q13.4 and currently includes three members: KLK1 or pancreatic/renal kallikrein, KLK2 or human glandular kallikrein and KLK3 or prostate-specific antigen (PSA). The latter two genes are almost prostate-specific and they are used for diagnosis and monitoring of prostate cancer and more recently, in breast cancer applications (Yousef *et al.*, Anticancer Res 1999 Jul-Aug;19(4B):2843-52). These new genes, like the already known kallikreins, may have utility for diagnosis, monitoring and therapeutics of various cancers including those of the breast, prostate and testis.

Monsees *et al.*, Immunopharmacology 1999 Dec;45(1-3):107-14, found that elements of the kallikrein-kinin system are present in rat seminiferous epithelium. Peptide hormones are involved in the paracrine regulation of several physiological processes. The paracrine peptide system may play a role in the regulation of Sertoli cell function or in the Sertoli cell-germ cell crosstalk, and therefore, be involved in mammalian reproduction, especially spermatogenesis.

Chen *et al.*, J Biol Chem 1996 Nov 1;271(44):27590-4, found that the kallikrein-kinin system participates in blood pressure regulation. One of the kallikrein-kinin system components, kallikrein-binding protein, binds to tissue kallikrein and inhibits its activity *in vitro*.

The glandular kallikreins are a distinct group of serine proteases with a molecular weight of 25,000-40,000 and an ability to release vasoactive peptides from kininogen *in vitro*, although the kininogenase activity of different kallikreins is highly variable. The true physiologic role of specific kallikreins is often unrelated to the kininogenase activity. In the mouse a major site of kallikrein synthesis is the male submaxillary gland. Glandular kallikreins are also synthesized in the pancreas and kidney. The several kallikreins found in this tissue include epidermal growth factor binding protein (EGF-BP) and the gamma subunit of nerve growth factor (NGFG; 162040) which are responsible for the processing of EGF (131530) and NGF (162030), respectively. Although EGF-BP and NGFG exhibit strict substrate specificity, they share extensive amino acid sequence homology and immunologic crossreactivity. Mason *et al.* (1983) concluded that the glandular kallikrein gene family comprises 25-30 highly homologous genes that encode specific proteases involved in the processing of biologically active peptides. All are closely linked on mouse chromosome 7 (assignment by Chinese hamster-mouse hybrid cell studies). Several human kallikrein genes have been isolated.

Schedlich *et al.* (1987) described a human glandular preprokallikrein gene, hGK-1, isolated from a human genomic library. The 5.2-kb gene encodes a prepropeptide of 261 amino acids. The mature protein is 237 amino acids long and has 66% homology with the sequence predicted for the human kallikrein synthesized in pancreas, kidney, and salivary gland (KLK1; 147910). Seventy-three percent homology with human prostate-specific antigen (APS; 176820) was observed. Expression of the glandular kallikrein gene, like that of the APS gene, seems to be restricted to the prostate. Riegman *et al.* (1989) found that the glandular kallikrein gene and that for prostate-specific antigen are aligned in a head-to-tail orientation and are separated by about 12 kb. Southern blot analysis of DNA from a panel of human-hamster hybrid cells showed that the genes are situated on chromosome 19. Since the KLK1 gene is also on chromosome 19, these 3 genes probably represent a cluster. From in situ hybridization studies, Qin *et al.* (1991) concluded that the glandular kallikrein gene and probably other kallikrein genes are located in q13.3 and q13.4 bands of chromosome 19 and are probably near the border of these two bands.

Therapeutic applications

The expression pattern, and protein similarity information for MOL7 suggest that it may function as human Kallikrein-like protein. Therefore, the nucleic acid and protein of the invention are useful in potential therapeutic applications implicated, for example but not limited to, various cancers including those of the testis, prostate, and breast; mammalian reproduction, especially spermatogenesis; blood pressure regulation; and other diseases and disorders. The homology to antigenic secreted and membrane proteins suggests that antibodies directed against the novel genes may be useful in treatment and prevention of various cancers including those of the testis, prostate, and breast; mammalian reproduction, especially spermatogenesis; blood pressure regulation; and other diseases and disorders.

Potential therapeutic uses for the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various cancers including those of the testis, prostate, and breast; mammalian reproduction, especially spermatogenesis; blood pressure regulation;and other diseases and disorders. For example, but not limited to, a cDNA encoding the novel human plasma membrane protein may be useful in gene therapy, and the novel human plasma membrane protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from, for example, but not limited to, various cancers including those of the testis, prostate, and breast; mammalian reproduction, especially spermatogenesis; blood pressure regulation; and other diseases and disorders. The novel nucleic acid encoding the novel human plasma membrane protein, and the novel human plasma membrane protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

MOL8

MOL8a

A novel human Acetyl LDL Receptor-like nucleic acid was identified by TblastN using CuraGen Corporation's sequence file for MOL probes or homologs and run against the Genomic Daily Files made available by GenBank. The nucleic acid was further predicted by the program GenScan™, including selection of exons. These were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. The disclosed novel MOL8a nucleic acid of 980 nucleotides (also referred to as 11800699-0-16) is shown in Table 8B. An open reading frame begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA codon at nucleotides 2803-2805. A putative untranslated region downstream from the termination codon are underlined in Table 8A, and the start and stop codons are in bold letters.

Table 8A. MOL8a Nucleotide Sequence (SEQ ID NO:17)
ATGGAGGGCGCAGGGCCCCGGGGGGCCGGGCCGGCGCGGCGCCGGGGAGCCGGGGGGCCGCCGTCACCGCTGCTGC
CGTCGCTGCTGCTGCTGCTGCTGCTCTGGATGCTGCCGGACACCGTGGCGCCTCAGGAACTGAACCCTCGCGGCCG
CAACGTGTGCCGTGCTCCCGGCTCCCAGGTGCCCACGTGCTGCGCTGGCTGGAGGCAGCAAGGGGACGAGTGTGGG
ATTGCGGTGTGCGAAGGCAACTCCACGTGCTCAGAGAACGAGGTGTGCGTGAGGCCTGGCGAGTGCCGCTGCCGCC
ACGGCTACTTCGGTGCCAACTGCGACACCAGTGAGCGTGGGGTCGGGCCGGTATTGGTCGGTGGGGCGGAATCCTG
GAGAGATGGGGCGGGGTCCAAGGTGGGGCGGGGTCGGATCCGCCTTCGGGGCGGGTCCCCAGAGGTGGCGGCTGGA
GTGCGGGACGCGGGCAGGTTCCGGCTGGCTGGGGGCACCTACTCAAGCACCGGGGCCTTCCACCCCCTCCGCTCCT
CCCCTGCAGAGTGCCCGCGCCAGTTCTGGGGCCCCGACTGCAAGGAGCTGTGTAGCTGCCACCCACACGGGCAGTG
CGAGGACGTGACAGGCCAGTGTACTTGTCACGCGCGGCGCTGGGGCGCGCGCTGCGAGCATGCGTGCCAGTGCCAG
CACGGCACGTGCCACCCCCGGAGCGGCGCGTGCCGCTGTGAGTCCGGCTGGTGGGGCGCGCAGTGCGCCAGCGCGT
GCTACTGCAGCGCCACGTCGCGCTGCGACCCACAGACCGGCGCCTGCCTGTGCCACGCAGGCTGGTGGGGCCGCAG
CTGCAACAACCAGTGCGCCTGCAACTCGTCTCCCTGCGAGCAGCAGAGCGGCCGCTGTCAGTGCCGCGAGCGTACG
TTCGGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCCGCGGCCGCTGCCACCCTGTGGACGGCACGTGTGCCTGCG
AGCCGGGCTACCGCGGCAAGTACTGTCGCGAGCCGTGCCCCGCCGGCTTCTACGGCTTGGGCTGTCGCCGCCGGTG
TGGCCAGTGCAAGGGCCAGCAGCCGTGCACGGTGGCCGAGGGCCGCTGCTTGACGTGCGAGCCCGGCTGGAACGGA
ACCAAGTGCGACCAGCCTTGCGCCACCGGTTTCTATGGCGAGGGCTGCAGCCACCGCTGTCCGCCATGCCGCGACG
GGCATGCCTGTAACCATGTCACCGGCAAGTGTACGCGCTGCAACGCGGGCTGGATCGGCGACCGGTGCGAGACCAA
GTGTAGCAATGGCACTTACGGCGAGGACTGCGCCTTCGTGTGCGCCGACTGCGGCAGCGGACACTGCGACTTCCAG
TCGGGGCGCTGCCTGTGCAGCCCTGGCGTCCACGGGCCCCACTGTAACGTGACGTGCCCGCCCGGACTCCACGGCG
CGGACTGTGCTCAGGCCTGCAGCTGCCACGAGGACACGTGCGACCCGGTCACTGGTGCCTGCCACCTAGAAACCAA
CCAGCGCAAGGGCGTGATGGGCGCGGGCGCGCTGCTCGTCCTGCTCGTCTGCCTGCTGCTCTCGCTGCTCGGCTGC

TGCTGCGCTTGCCGCGGCAAGGACCCTACGCGCCGGGAGCTTTCGCTTGGGAGGAAGAAGGCGCCGCACCGACTAT GCGGGCGCTTCAGTCGCATCAGCATGAAGCTGCCCCGGATCCCGCTCCGGAGGCAGAAACTACCCAAAGTCGTAGT GGCCCACCACGACCTGGATAACACACTCAACTGCAGCTTCCTGGAGCCACCCTCAGGGCTGGAGCAGCCCTCACCA TCCTGGTCCTCTCGGGCCTCCTTCTCCTCGTTTGACACCACTGATGAAGGCCCTGTGTACTGTGTACCCCATGAGG AGGCACCAGCGGAGAGCCGGGACCCCGAAGTCCCCACTGTCCCTGCCGAGGCGCCGGCGCCGTCCCCTGTGCCCTT GACCACGCCAGCCTCCGCCGAGGAGGCGATACCCCTCCCCGCGTCCTCCGACAGCGAGCGGTCGGCGTCCAGCGTG GAGGGGCCCGGAGGGGCTCTGTACGCGCGCGTGGCCCGACGCGAGGCCCGGCCGGCCCGGGCCCGGGGCGAGATTG GGGGCCTGTCGCTGTCGCCATCGCCCGAGCGCAGGAAACCGCCGCCACCTGACCCCGCCACCAAGCCTAAGGTGTC CTGGATCCACGGCAAGCACAGCGCCGCTGCAGCTGGCCGTGCGCCCTCACCACCGCCGCCAGGCTCCGAGGCCGCG CCCAGCCCCAGCAAGAGGAAACGGACGCCCAGCGACAAATCGGCGCATACGGTCGAACACGGCAGCCCCCGGACCC GCGACCCAACGCCGCGCCCCCCGGGGCTGCCCGAGGAGGCGACAGCCCTCGCTGCGCCCTCGCCGCCCAGGGCCCG AGCGCGCGCCGCGCCCCGGCCTCTTGGAGCCCACGGACGCCGGCGGTCCCCCGCGAAGCGCGCCGAGGCTGCCTCC ATGTTGGCCGCTGACGTGCGCGGCAAGACTCGCAGCCTGGGCCGCGCCGAGGTGGCCCTGGGCGCGCAGGGCCCCA GGGAAAAGCCGGCGCCCCCACAGAAAGCCAAGCGCTCCGTGCCGCCAGCCTCGCCCGCCCGCGCGCCCCCAGCGAC CGAAACCCCGGGGCCTGAGAAGGCGGCGACCGACTTGCCCGCGCCTGAGACCCCCCGGAAGAAGACCCCCATCCAG AAGCCGCCGCGCAAGAAGAGCCGGAGGCGGCGGGCGAGCTGGGCAGGGCGGGCGCACCCACCCTGTAG

The MOL8a protein encoded by SEQ ID NO:16 has 324 amino acid residues, and is presented using the one-letter code in Table 8B (SEQ ID NO:18). The SignalP, Psort and/or Hydropathy profile for MOL8a predict that MOL8a has a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.6000. The SignalP shows a signal sequence with a cleavage site between amino acids 43 and 44. This is typical of this type of membrane protein. Therefore it is likely that this novel human plasma membrane protein is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 8B. Encoded MOL8a protein sequence (SEQ ID NO:18).
MEGAGPRGAGPARRRGAGGPPSPLLPSLLLLLLLWMLPDTVAPQELNPRGRNVCRAPGSQVPTCCAGWRQQGDECG IAVCEGNSTCSENEVCVRPGECRCRHGYFGANCDTSERGVGPVLVGGAESWRDGAGSKVGRGRIRLRGGSPEVAAG VRDAGRFRLAGGTYSSTGAFHPLRSSPAECPRQFWGPDCKELCSCHPHGQCEDVTGQCTCHARRWGARCEHACQCQ HGTCHPRSGACRCESGWWGAQCASACYCSATSRCDPQTGACLCHAGWWGRSCNNQCACNSSPCEQQSGRCQCRERT FGARCDRYCQCFRGRCHPVDGTCACEPGYRGKYCREPCPAGFYGLGCRRRCGQCKGQQPCTVAEGRCLTCEPGWNG TKCDQPCATGFYGEGCSHRCPPCRDGHACNHVTGKCTRCNAGWIGDRCETKCSNGTYGEDCAFVCADCGSGHCDFQ SGRCLCSPGVHGPHCNVTCPPGLHGADCAQACSCHEDTCDPVTGACHLETNQRKGVMGAGALLVLLVCLLLSLLGC CCACRGKDPTRRELSLGRKKAPHRLCGRFSRISMKLPRIPLRRQKLPKVVVAHHDLDNTLNCSFLEPPSGLEQPSP SWSSRASFSSFDTTDEGPVYCVPHEEAPAESRDPEVPTVPAEAPAPSPVPLTTPASAEEAIPLPASSDSERSASSV EGPGGALYARVARREARPARARGEIGGLSLSPSPERRKPPPPDPATKPKVSWIHGKHSAAAAGRAPSPPPPGSEAA PSPSKRKRTPSDKSAHTVEHGSPRTRDPTPRPPGLPEEATALAAPSPPRARARAAPRPLGAHGRRRSPAKRAEAAS MLAADVRGKTRSLGRAEVALGAQGPREKPAPPQKAKRSVPPASPARAPPATETPGPEKAATDLPAPETPRKKTPIQ KPPRKKSREAAGELGRAGAPTL

The full amino acid sequence of the protein of the invention was found to have 576/729 (79%) identical and 596/729 (81%) similarity to a murine nurse cell receptor amino acid sequence (PatP Accession No. Y85616). The full amino acid sequence of the protein of the invention was also found to have 296 of 741 amino acid residues (39 %) identical and 383 of 741 amino acid residues (51 %) homolog to the 830 amino acid residue acetyl LDL receptor precursor from *Homo sapiens* (human) (ACC:O43701).

MOL8a is expressed in the following tissues: fetal thymus, mammary gland, fetal thymus, pool of ten tissues (adrenal, mammary, prostate, testis, uterus, bone marrow*, melanoma*, pituitary*, thyroid*, spleen) (*from mRNA rather than from total RNA).

MOL8b

A novel nucleic acid was identified by laboratory cloning of cDNA fragments, by *in silico* prediction of the sequence. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, were cloned. In silico prediction was based on sequences available in Curagen's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof. These were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. The disclosed novel MOL8b nucleic acid of 2598 nucleotides (also referred to as CG50889-02) is shown in Table 8C. An open reading frame begins with an ATG initiation codon at nucleotides 1-3 and ends with a TAG codon at nucleotides 2596-2598. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 8D, and the start and stop codons are in bold letters.

Table 8D. MOL8b Nucleotide Sequence (SEQ ID NO:19)
ATGGAGGGCGCAGGGCCCCGGGGGGCCGGGCCGGCGCGGCGCCGGGGAGCCGGGGGGCCGCCGTCACCGCTGCTGC
CGTCGCTGCTGCTGCTGCTGCTGCTCTGGATGCTGCCGGACACCGTGGCGCCTCAGGAACTGAACCCTCGCGGCCG
CAACGTGTGCCGTGCTCCCGGCTCCCAGGTGCCCACGTGCTGCGCTGGCTGGAGGCAGCAAGGGGACGAGTGTGGG
ATTGCGGTGTGCGAAGGCAACTCCACGTGCTCAGAGAACGAGGTGTGCGTGAGGCCTGGCGAGTGCCGCTGCCGCC
ACGGCTACTTCGGTGCCAACTGCGACACCAAGTGCCCGCGCCAGTTCTGGGGCCCCGACTGCAAGGAGCTGTGTAG
CTGCCACCCACACGGGCAGTGCGAGGACGTGACAGGCCAGTGTACTTGTCACGCGCGGCGCTGGGGCGCGCGCTGC
GAGCATGCGTGCCAGTGCCAGCACGGCACGTGCCACCCGCGGAGCGGCGCGTGCCGCTGTGAGCCCGGCTGGTGGG
GCGCGCAGTGCGCCAGCGCGTGCTACTGCAGCGCCACGTCGCGCTGCGACCCACAGACCGGCGCCTGCCTGTGCCA
CGCAGGCTGGTGGGGCCGCAGCTGCAACAACCAGTGCGCCTGCAACTCGTCTCCCTGCGAGCAGCAGAGCGGCCGC
TGTCAGTGCCGCGAGCGTACGTTCGGCGCGCGCTGCGATCGCTACTGCCAGTGCTTCCGCGGCCGCTGCCACCCTG
TGGACGGCACGTGTGCCTGCGAGCCGGGCTACCGCGGCAAGTACTGTCGCGAGCCGTGCCCCGCCGGCTTCTACGG
CTTGGGCTGTCGCCGCCGGTGTGGCCAGTGCAAGGGCCAGCAGCCGTGCACGGTGGCCGAGGGCCGCTGCTTGACG
TGCGAGCCCGGCTGGAACGGAACCAAGTGCGACCAGCCTTGCGCCACCGGTTTCTATGGCGAGGGCTGCAGCCACC
GCTGTCCGCCATGCCGCGACGGGCATGCCTGTAACCATGTCACCGGCAAGTGTACGCGCTGCAACGCGGGCTGGAT
CGGCGACCGGTGCGAGACCAAGTGTAGCAATGGCACTTACGGCGAGGACTGCGCCTTCGTGTGCGCCGACTGCGGC
AGCGGACACTGCGACTTCCAGTCGGGGCGCTGCCTGTGCAGCCCTGGCGTCCACGGGCCCCACTGTAACGTGACGT
GCCCGCCCGGACTCCACGGCGCGGACTGTGCTCAGGCCTGCAGCTGCCACGAGGACACGTGCGACCCGGTCACTGG
TGCCTGCCACCTAGAAACCAACCAGCGCAAGGGCGTGATGGGCGCGGGCGCGCTGCTCGTCCTGCTCGTCTGCCTG
CTGCTCTCGCTGCTCGGCTGCTGCTGCGCTTGCCGCGGCAAGGACCCTACGCGCCGGGAGCTTTCGCTTGGAGGA
AGAAGGCGCCGCACCGACTATGCGGGCGCTTCAGTCGCATCAGCATGAAGCTGCCCCGGATCCCGCTCCGGAGGCA
GAAACTACCCAAAGTCGTAGTGGCCCACCACGACCTGGATAACACACTCAACTGCAGCTTCCTGGAGCCACCCTCA
GGGCTGGAGCAGCCCTCACCATCCTGGTCCTCTCGGGCCTCCTTCTCCTCGTTTGACACCACTGATGAAGGCCCTG
TGTACTGTGTACCCCATGAGGAGGCACCAGCGGAGAGCCGGGACCCCGAAGTCCCCACTGTCCCTGCCGAGGCGCC
GGCGCCGTCCCCTGTGCCCTTGACCACGCCAGCCTCCGCCGAGGAGGCGATACCCCTCCCCGCGTCCTCCGACAGC
GAGCGGTCGGCGTCCAGCGTGGAGGGGCCCGGAGGGGCTCTGTACGCGCGCGTGGCCCGACGCGAGGCCCGGCCGG
CCCGGGCCCGGGGCGAGATTGGGGGCCTGTCGCTGTCGCCATCGCCCGAGCGCAGGAAACCGCCGCCACCTGACCC

CGCCACCAAGCCTAAGGTGTCCTGGATCCACGGCAAGCACAGCGCCGCTGCAGCTGGCCGTGCGCCCTCACCACCG
CCGCCAGGCTCCGAGGCCGCGCCCAGCCCCAGCAAGAGGAAACGGACGCCCAGCGACAAATCGGCGCATACGGTCG
AACACGGCAGCCCCCGGACCCGCGACCCAACGCCGCGCCCCCCGGGGCTGCCCGAGGAGGCGACAGCCCTCGCTGC
GCCCTCGCCGCCCAGGGCCCGAGCGCGCGCCGCGCCCCGGCCTCTTGGAGCCCACGGACGCCGGCGGTCCCCCGCG
AAGCGCGCCGAGGCTGCCTCCATGTTGGCCGCTGACGTGCGCGGCAAGACTCGCAGCCTGGGCCGCGCCGAGGTGG
CCCTGGGCGCGCAGGGCCCCAGGGAAAAGCCGGCGCCCCCACAGAAAGCCAAGCGCTCCGTGCCGCCAGCCTCGCC
CGCCCGCGCGCCCCCAGCGACCGAAACCCCGGGGCCTGAGAAGGCGGCGACCGACTTGCCCGCGCCTGAGACCCCC
CGGAAGAAGACCCCCATCCAGAAGCCGCCGCGCAAGAAGAGCCGGGAGGCGGCGGGCGAGCTGGGCAGGGCGGGCG
CACCCACCCTGTAG

The disclosed nucleic acid sequence has 1311 of 2041 bases (64%) identical to a gb:GENBANK-ID:D86864|acc:D86864.1 mRNA from Homo sapiens (Homo sapiens mRNA for acetyl LDL receptor, complete cds) (E value = 3.2e-^{98}).

The MOL8b protein encoded by SEQ ID NO:17 has 865 amino acid residues, and is presented using the one-letter code in Table 8E (SEQ ID NO:20). The SignalP, Psort and/or Hydropathy profile for MOL8a predict that MOL8a has a signal peptide and is likely to be localized at the plasma membrane with a certainty of 0.6000. The SignalP shows a signal sequence with a cleavage site between amino acids 43 and 44. This is typical of this type of membrane protein. Therefore it is likely that this novel human plasma membrane protein is available at the appropriate sub-cellular localization and hence accessible for the therapeutic uses described in this application.

Table 8E. Encoded MOL8b protein sequence (SEQ ID NO:20).
MEGAGPRGAGPARRRGAGGPPSPLLPSLLLLLLLWMLPDTVAPQELNPRGRNVCRAPGSQVPTCCAGWRQQGDECG
IAVCEGNSTCSENEVCVRPGECRCRHGYFGANCDTKCPRQFWGPDCKELCSCHPHGQCEDVTGQCTCHARRWGARC
EHACQCQHGTCHPRSGACRCEPGWWGAQCASACYCSATSRCDPQTGACLCHAGWWGRSCNNQCACNSSPCEQQSGR
CQCRERTFGARCDRYCQCFRGRCHPVDGTCACEPGYRGKYCREPCPAGFYGLGCRRRCGQCKGQQPCTVAEGRCLT
CEPGWNGTKCDQPCATGFYGEGCSHRCPPCRDGHACNHVTGKCTRCNAGWIGDRCETKCSNGTYGEDCAFVCADCG
SGHCDFQSGRCLCSPGVHGPHCNVTCPPGLHGADCAQACSCHEDTCDPVTGACHLETNQRKGVMGAGALLVLLVCL
LLSLLGCCCACRGKDPTRRELSLGRKKAPHRLCGRFSRISMKLPRIPLRRQKLPKVVVAHHDLDNTLNCSFLEPPS
GLEQPSPSWSSRASFSSFDTTDEGPVYCVPHEEAPAESRDPEVPTVPAEAPAPSPVPLTTPASAEEAIPLPASSDS
ERSASSVEGPGGALYARVARREARPARARGEIGGLSLSPSPERRKPPPPDPATKPKVSWIHGKHSAAAAGRAPSPP
PPGSEAAPSPSKRKRTPSDKSAHTVEHGSPRTRDPTPRPPGLPEEATALAAPSPPRARARAAPRPLGAHGRRRSPA
KRAEAASMLAADVRGKTRSLGRAEVALGAQGPREKPAPPQKAKRSVPPASPARAPPATETPGPEKAATDLPAPETP
RKKTPIQKPPRKKSREAAGELGRAGAPTL

The full amino acid sequence of the protein of the invention was found to have 340 of 823 amino acid residues (41%) identical to, and 443 of 823 amino acid residues (53%) similar to, the 830 amino acid residue ptnr:SPTREMBL-ACC:O43701 protein from Homo sapiens (Human) (ACETYL LDL RECEPTOR PRECURSOR) (E value = 9.0e-^{164}).

Homology between MOL8a, 8b and the human acetyl LDL receptor are presented graphically in the multiple sequence alignment given in Table 8F (with MOL8a being shown on line 1, and MOL8b being shown on line 2) as a ClustalW analysis comparing MOL8 with related protein sequences.

Table 8F. Information for the ClustalW proteins:

1) MOL8a (SEQ ID NO:18)
2) MOL8b (SEQ ID NO:20)
3) gi|4507203|ref|NP_003684.1| acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells [Homo sapiens] (SEQ ID NO:57)

```
                    10         20         30         40         50         60
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  MEGAGPRGAG PARRRGAGGP PSPLLPSLLL LLLLWMLPDT VAPQELNPRG RNVCRAPG-S   59
MOL8b Prot  MEGAGPRGAG PARRRGAGGP PSPLLPSLLL LLLLWMLPDT VAPQELNPRG RNVCRAPG-S   59
NP_003684   ---------- ----MGLG-- ------LLLP LLLLWTR--G TQGSELDPKG QHVCVASSPS   36

                    70         80         90        100        110        120
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  QVPTCCAGWR QQGDECGIAV CEGNSTCSEN EVCVRPGECR CRHGYFGANC DTSERGVGPV  119
MOL8b Prot  QVPTCCAGWR QQGDECGIAV CEGNSTCSEN EVCVRPGECR CRHGYFGANC ----------  109
NP_003684   AELQCCAGWR QKDQECTIPI CEGPDACQKD EVCVKPGLCR CKPGFFGAHC SS--------   88

                   130        140        150        160        170        180
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  LVGGAESWRD GAGSKVGRGR IRLRGGSPEV AAGVRDAGRF RLAGGTYSST GAFHPLRSSP  179
MOL8b Prot  ---------- ---------- ---------- -----D---- ---------T ----------  111
NP_003684   ---------- ---------- ---------- ---------- ---------- ----------   88

                   190        200        210        220        230        240
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  AECPRQFWGP DCKELCSCHP HGQCEDVTGQ CTCHARRWGA RCEHACQC-Q HGTCHPRSGA  238
MOL8b Prot  -KCPRQFWGP DCKELCSCHP HGQCEDVTGQ CTCHARRWGA RCEHACQC-Q HGTCHPRSGA  169
NP_003684   -RCPGQYWGP DCRESCPCHP HGQCEPATGA CQCQADRWGA RCEFPCACGP HGRCDPATGV  147

                   250        260        270        280        290        300
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  CRCESGWWGA QCASACYCS- ATSRCDPQTG ACLCHAGWWG RSCNNQCACN SSPCEQQSGR  297
MOL8b Prot  CRCEPGWWGA QCASACYCS- ATSRCDPQTG ACLCHAGWWG RSCNNQCACN SSPCEQQSGR  228
NP_003684   CHCEPGWWSS TCRRPCQCNT AAARCEQATG ACVCKPGWWG RRCSFRCNCH GSPCEQDSGR  207

                   310        320        330        340        350        360
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  CQCRERTFGA RCDRYCQCFR GRCHPVDGTC ACEPGYRGKY CREPCPAGFY GLGCRRRCGQ  357
MOL8b Prot  CQCRERTFGA RCDRYCQCFR GRCHPVDGTC ACEPGYRGKY CREPCPAGFY GLGCRRRCGQ  288
NP_003684   CACRPGWWGP ECQQQCECVR GRCSAASGEC TCPPGFRGAR CELPCPAGSH GVQCAHSCGR  267

                   370        380        390        400        410        420
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  CKGQQPCTVA EGRCLTCEPG WNGTKCDQPC ATGFYGEGCS HRCPPCRDGH ACNHVTGKCT  417
MOL8b Prot  CKGQQPCTVA EGRCLTCEPG WNGTKCDQPC ATGFYGEGCS HRCPPCRDGH ACNHVTGKCT  348
NP_003684   CKHNEPCSPD TGSCESCEPG WNGTQCQQPC LPGTFGESCE QQCPHCRHGE ACEPDTGHCQ  327

                   430        440        450        460        470        480
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  RCNAGWIGDR CETKCSNGTY GEDCAFVCAD CGSGHCDFQS GRCLCSPGVH GPHCNVTCPP  477
MOL8b Prot  RCNAGWIGDR CETKCSNGTY GEDCAFVCAD CGSGHCDFQS GRCLCSPGVH GPHCNVTCPP  408
NP_003684   RCDPGWLGPR CEDPCPTGTF GEDCGSTCPT CVQGSCDTVT GDCVCSAGYW GPSCNASCPA  387

                   490        500        510        520        530        540
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  GLHGADCAQA CSCHEDTCDP VTGACHLETN QRKGVMGAGA LLVLLVCLL- LSLLGCCCAC  536
MOL8b Prot  GLHGADCAQA CSCHEDTCDP VTGACHLETN QRKGVMGAGA LLVLLVCLL- LSLLGCCCAC  467
NP_003684   GFHGNNCSVP CECPEGLCHP VSGSCQPGSG SRDTALIVGS LVPLLLLFLG LACCACCCWA  447

                   550        560        570        580        590        600
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  RGKDPTRREL SLGR--KKAP HRLCGRFSRI SMKLPRIPLR RQKLPKVVVA HHDLDNTLNC  594
MOL8b Prot  RGKDPTRREL SLGR--KKAP HRLCGRFSRI SMKLPRIPLR RQKLPKVVVA HHDLDNTLNC  525
NP_003684   PRSDLKDRPA RDGATVSRMK LQVWGTLTSL GSTLPCRSLS SHKLPWVTVS HHDPEVPFNH  507

                   610        620        630        640        650        660
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot  SFLEPPSGLE QPSPSWSSRA SFSS---FDT TDEGPVYCVP HEEAPAESRD PEVPTVPAEA  651
MOL8b Prot  SFLEPPSGLE QPSPSWSSRA SFSS---FDT TDEGPVYCVP HEEAPAESRD PEVPTVPAEA  582
NP_003684   SFIEPPS--- ---AGWATDD SFSSDPESGE ADEVPAYCVP PQEG------ -MVPVAQAGS  554

                   670        680        690        700        710        720
```

```
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot    PAPSPVPLTT PASAEEAIPL PASSDSERSA SSVEGPGGAL YARVARREAR PARARGEIGG  711
MOL8b Prot    PAPSPVPLTT PASAEEAIPL PASSDSERSA SSVEGPGGAL YARVARREAR PARARGEIGG  642
NP_003684     SEASLAAGAF PPPEDASTPF AIPRTS--SL ARAKRPS-VS FAEGTKFAPQ SRRSSGE---  608

                     730        740        750        760        770        780
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot    LSLSPSPERR KPPPPDPATK PKVSWIHGKH SAAAAGRAPS PPPPGSEAAP SP---SKRKR  768
MOL8b Prot    LSLSPSPERR KPPPPDPATK PKVSWIHGKH SAAAAGRAPS PPPPGSEAAP SP---SKRKR  699
NP_003684     LS---SPLRK --P--KRLSR GAQSGPEGRE AEESTGPDEA EAPESFPAAA SPGDSATGHR  661

                     790        800        810        820        830        840
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot    TPSDKSAHTV EHGSPRTRDP TPRPPGLPEE ATALAAPSPP RARARAAPRP LGAHGRRRSP  828
MOL8b Prot    TPSDKSAHTV EHGSPRTRDP TPRPPGLPEE ATALAAPSPP RARARAAPRP LGAHGRRRSP  759
NP_003684     RPPLGSRTVA EHVEAIEGSV QESSGPVTTI YMLAGKPRGS EGPVRSVFRH FGSFQKGQAE  721

                     850        860        870        880        890        900
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL8a Prot    AKRAEAASML AADVRGKTR- --SLGRAEVA LGAQGPREKP APPQKAKRSV PPASPARAP-  884
MOL8b Prot    AKRAEAASML AADVRGKTR- --SLGRAEVA LGAQGPREKP APPQKAKRSV PPASPARAP-  815
NP_003684     AKVKRAIPKP PRQALNRKKG SPGLASGSVG QSPNSAPKAG LPGATGPMAV RPEEAVRGLG  781

                     910        920        930        940        950
              ....|....| ....|....| ....|....| ....|....| ....|....| .
MOL8a Prot    PATETPG-PE KAATDLPAPE TPRKKTPIQK PPRKKSREAA GELGRAGAPT L 934
MOL8b Prot    PATETPG-PE KAATDLPAPE TPRKKTPIQK PPRKKSREAA GELGRAGAPT L 865
NP_003684     AGTESSRRAQ EPVSGCGSPE QDPQKQAEEE RQEEPEYENV VPISRPPEP- - 830
```

Chromosomal information:

MOL8 maps to chromosome 22q11. This assignment was made using mapping information associated with genomic clones, public genes and ESTs sharing sequence identity with the disclosed sequence and CuraGen Corporation's Electronic Northern bioinformatic tool.

Tissue expression

MOL8 is expressed in at least the following tissues: kidney, senescent fibroblasts, lymphocyte, B cell, and germ cell tumors. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of CuraGen Acc. No. CG50889-02.

MOL8 shows significant homologies to human LDL Receptor-like protein, as described in, but not limited to, the references below. Hypercholesterolemia is an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL). Mutations in the LDL receptor (LDLR) gene on chromosome 19 cause this disorder. Familial hypercholesterolemia is characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL) and is, hence, one of the conditions producing the hyperlipoproteinemia II phenotype (see OMIM 144400). Heterozygotes develop tendinous xanthomas, corneal arcus, and coronary artery disease; the last usually becomes evident in the fourth or fifth decade. Homozygotes develop these features at a accelerated rate in addition to planar xanthomas, which may be evident at birth in the web between the first two digits.

Hepatitis C virus (HCV), the principal viral cause of chronic hepatitis, is not readily replicated in cell culture systems, making it difficult to ascertain information on cell receptors for the virus. However, several observations from studies on the role of HCV in mixed cryoglobulinemia provided some insight into HCV entry into cells. Evidence indicated that HCV and other viruses enter cells through the mediation of LDL receptors: by the demonstration that endocytosis of these viruses correlates with LDL receptor activity, by complete inhibition of detectable endocytosis by anti-LDL receptor antibody, by inhibition with anti-apolipoprotein E and anti-apolipoprotein B antibodies, by chemical methods abrogating lipoprotein/LDL receptor interactions, and by inhibition with the endocytosis inhibitor phenylarsine oxide. Agnello et al. (1999) provided confirmatory evidence by the lack of detectable LDL receptor on cells known to be resistant to infection by one of these viruses, bovine viral diarrheal virus (BVDV). Endocytosis via the LDL receptor was shown to be mediated by complexing of the virus to very low density lipoprotein (VLDL) or LDL, but not high density lipoprotein (HDL). Studies using LDL receptor-deficient cells or a cytolytic BVDV system indicated that the LDL receptor may be the main but not exclusive means of cell entry of these viruses.

Therapeutic uses of the composition

The expression pattern, and protein similarity information for MOL8 that it may function as human LDL Receptor-like protein. Therefore, the nucleic acid and protein of the invention are useful in potential therapeutic applications implicated, for example but not limited to, metabolic disorders, e.g. Hypercholesterolemia, viral diseases, and other diseases and disorders. The homology to antigenic secreted and membrane proteins suggests that antibodies directed against the novel genes may be useful in treatment and prevention of metabolic disorders, e.g. Hypercholesterolemia, viral diseases, and other diseases and disorders.

Potential therapeutic uses for the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various cancers including those metabolic disorders, e.g. Hypercholesterolemia, viral diseases, and other diseases and disorders. For example, but not limited to, a cDNA encoding the novel human plasma membrane protein may be useful in gene therapy, and the novel human plasma membrane protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from, for example, but not limited to, various cancers including those of the metabolic disorders, e.g. Hypercholesterolemia, viral diseases, and other diseases and disorders. The novel nucleic acid encoding the novel human plasma membrane protein, and the novel human plasma membrane protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL8 substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. For example the disclosed MOL8 protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL8 epitope is from about amino acids 1 to 10. In another embodiment, a MOL8 epitope is from about amino acids 50 to 200. In further embodiment, a MOL8 epitope contains amino acids 210-400, 475-600, or 625-850. These novel proteins can also be used to develop assay system for functional analysis.

MOL9

MOL9a

A novel nucleic acid encoding a neurolysin -like protein was identified by TblastN using CuraGen Corporation's sequence file for MOL9 probe or homolog, run against the Genomic Daily Files made available by GenBank. The nucleic acid was further predicted by the program GenScan™, including selection of exons. These were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. The disclosed novel MOL9a nucleic acid of 2355 nucleotides (also referred to as 19506719_B_EXT) is shown in Table 9A. An open reading frame begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA codon at nucleotides 1915-1917. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 9A, and the start and stop codons are in bold letters.

The nucleic acid sequence has 1307 of 1428 bases (91%) identical to a pig neurolysin mRNA (GENBANK-ID: AB000170) (Expect = 0.0).

Table 9A. MOL9a Nucleotide Sequence (SEQ ID NO:21)
ATGTTGACTTTGGACCAACAGAAATCCCTAATTCTTATTCTTTTTCTGATTCTTTTTAGAGTTGGTGGTTC
CAGGATTTTACTCAGAATGACGTTAGGAAGAGAAGTGATGTCTCCTCTTCAGGCAATGTCTTCCTATACTG
TGGCTGGCAGAAATGTTTTAAGATGGGATCTTTCACCAGAGCAAATTAAAACAAGAACTGAGGAGCTCATT
GTGCAGACCAAACAGGTGTACGATGCTGTTGGAATGCTCGGTATTGAGGAAGTAACTTACGAGAACTGTCT
GCAGGCACTGGCAGTGGAAAGGACCATGCTAGACTTTCCCCAGCATGTATCCTCTGACAAAGAAGTACGAG
CAGCAAGTACAGAAGCAGACAAAAGACTTTCTCGTTTTGATATTGAGATGAGCATGAGAGGAGATATATTT
GAGAGAATTGTTCATTTACAGCAGGAAACCTGTGATCTGGGGAAGATAAAACCTGAGGCCAGACGATACTT
GGAAAAGTCAATTAAAATGGGGAAAAGAAATGGGCTCCATCTTCCTGAACAAGTACAGAATGAAATCAAAT
CAATGAAGAAAAGAATGAGTGAGCTATGTATTGATTTTAACAAAAACCTCAATGAGGATGATACCTTCCTT
GTATTTTCCAAGGCTGAACTTGGTGCTCTTCCTGATGATTTCATTGACAGTTTAGAAAAGACAGATGATGA
CAAGTATAAAATTACCTTAAAATATCCACACTATTTCCCTGTCATGAAGAAATGTTGTATCCCTGAAACCA
GAAGAAGGATGGAAATGGCTTTTAATACAAGGTGCAAAGAGGAAAACACCATAATTTTGCAGCAGCTACTC
CCACTGCGAACCAAGGTGGCCAAACTACTCGGTTATAGCACACATGCTGACTTCGTCCTTGAAATGAACAC
TGCAAAGAGCACAAGCCGCGTAACAGCCTTTCTAGATGATTTAAGCCAGAAGTTAAAACCCTTGGGTGAAG
CAGAACGAGAGTTTATTTTGAATTTGAAGAAAAAGGAATGCAAAGACAGGGGTTTTGAATATGATGGGAAA
ATCAATGCCTGGGATCTATATTACTACATGACTCAGACAGAGGAACTCAAGTATTCCATAGACCAAGAGTT
CCTCAAGGAATACTTCCCAATTGAGGTGGTCACTGAAGGCTTGCTGAACACCTACCAGGAGTTGTTGGGAC
TTTCATTTGAACAAATGACAGATGCTCATGTTTGGAACAAGAGTGTTACACTTTATACTGTGAAGGATAAA
GCTACAGGAGAAGTATTGGGACAGTTCTATTTGGACCTCTATCCAAGGCCTAGGGAAGGAAAATACAATCA
TGCGGCCTGCTTCGGTCTCCAGCCTGGCTGCCTTCTGCCTGATGGAAGCCGGATGATGGCAGTGGCTGCCC
TCGTGGTGAACTTCTCACAGCCAGTGGCAGGTCGTCCCTCTCTCCTGAGACACGACGAGGTGAGGACTTAC
TTTCATGAGTTTGGTCACGTGATGCATCAGATTTGTGCACAGACTGATTTTGCACGATTTAGCGGAACAAA
TGTGGAAACTGACTTTGTAGAGGTGCCATCGCAAATGCTTGAAAATTGGGTGTGGACGTCGATTCCCTCC
GAAGATTGTCAAAACATTATAAAGATGGAAGCCCTATTGCAGACGATCTGCTTGAAAAACTTGTTGCTTCT
AGGCTGGTCAACACAGGTATGGGTTATGTTATTAGTAATATATATTTTCTAGATATGTTTTCATTTCAGTG
CATCCAAGTTGGAATGAAATACAGAAACCTAATCCTGAAACCTGGGGGATCTCTGGACGGCATGGACATGC
TCCACAATTTCTTGAAACGTGAGCCAAACCAAAAAGCGTTCCTAATGAGTAGAGGCCTGCATGCTCCG**TGA**
ACTGGGGATCTTTGGTAGCCGTCCATGTCTGGAGGACAAGTCGACATCACCATGTGTTACTGGCCTGGAAA
CTGAAGGGAGTTTTGCAAGTGAAAATTTAGATTTCTATTGACATCCTTTTGTTTTCTAATTTTAAAAATTA
TAAAGATGTAAATGGAATTATAAATACTGTGACCTAAGAAAAGACCCACTAGAAAGTAATTGTACTATAAA
ATTTCATAAAACTGGATTTGATTTCTTTTTATGAAAGTTTCATATGAATGTAACTTGATTTTTTACTATTA
TAATCTAGATAATATGATATAAGAGGGCTAAGAATTTTTAAATTGAATCATATATATGATATAATTTGATC
CTTCTTGTATCTTGAAGTTTTGTACTTGGGATTTCTGGACTGATAAATGAATCATCACATTCTTCTGGTAA
ATATTTTCTTGG

The MOL9a protein encoded by SEQ ID NO:21 and has 638 amino acid residues, and is presented using the one-letter code in Table 9B (SEQ ID NO:22). The SignalP, Psort and or Hydropathy profile indicate that this sequence has a signal peptide between positions 23 and 24 and is likely to be localized at endoplasmic reticulum and plasma membrane (Certainty = 0.8200).

Table 9B. Encoded MOL9a protein sequence (SEQ ID NO:22)
MLTLDQQKSLILILFLILFRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTRTEELI VQTKQVYDAVGMLGIEEVTYENCLQALAVERTMLDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIF ERIVHLQQETCDLGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFL VFSKAELGALPDDFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLL PLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGK INAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDK ATGEVLGQFYLDLYPRPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTY FHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVAS RLVNTGMGYVISNIYFLDMFSFQCIQVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP

The full amino acid sequence of the protein of the invention was found to have 483/564 (85%) identity and 508/564 (90%) similarity to a rabbit endopeptidase (PatP Accession No. R26114), and have 571 of 632 amino acid residues (90%) identical to, and 592 of 632 residues (93.6%) similar to, the 704 amino acid residue neurolysin protein from pig (ptnr:SPTREMBL-ACC: Q02038) (E value = 1.1e-^{302}).

MOL9a also has homology to the proteins shown in the BLAST alignments in Table 9C.

Table 9C. BLASTX results for MOL9a

Sequences producing High-scoring Segment Pairs:	High Score	Smallest Sum Prob P(N)	N
ptnr:SWISSNEW-ACC:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24....	2685	1.1e-302	2
ptnr:SWISSPROT-ACC:P42675 NEUROLYSIN PRECURSOR (EC 3.4.24...	2697	2.2e-302	2
ptnr:SPTREMBL-ACC:P79433 ENDOPEPTIDASE 24.16 (EC 3.4.-.-)...	2677	7.6e-302	2
ptnr:SWISSPROT-ACC:P42676 NEUROLYSIN PRECURSOR (EC 3.4.24...	2601	4.7e-291	2
ptnr:SWISSPROT-ACC:P47788 THIMET OLIGOPEPTIDASE (EC 3.4.2...	1792	8.4e-197	2

Chromosomal information

MOL9a maps to the Unigene entry Hs. 22151 which maps to chromosome 5 between markers D5S427-D5S647 (69.6-74.7 cM).

Tissue expression

MOL9a is expressed in at least the following tissues: fetal lung, testis, B-cell, aorta, brain, colon, foreskin, germ cell, heart, kidney, pancreas, stomach, uterus, whole embryo and cancer cell lines MDA-MB-231 and MCF-7.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL9a substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. For example the disclosed MOL9a protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL9a epitope is from about amino acids 50 to 75. In another embodiment, a MOL9a epitope is from about amino acids 100 to 150. In further embodiments, MOL9a epitopes are found in amino acids 175-200, 225-300, 325-375, 425-450, 500-550, and 600-625. These novel proteins can also be used to develop assay system for functional analysis.

MOL9b

The cloned open reading frame, codes for a 687 amino acid long protein with an overall 95% amino acid identity, to the mature form of the pig neurolysin precursor (SWISSPROT-ACC:Q02038).Oligonucleotide primers were designed to PCR amplify a DNA segment, representing an ORF, coding for the mature form of 19506719_B EXT.The forward primer includes an, in frame, BamHI restriction site. The reverse primer contains an, in frame, XhoI restriction site. The sequences of the PCR primers are the following:

19506719_B-EXT Mat-Forw:
GGATCCTCCAGGATTTTACTCAGAATGACGTTAGG (SEQ ID NO:58)
19506719_B-EXT FL-Rev:
CTCGAGCGGAGCATGCAGGCCTCTACTCATTAGGAACG (SEQ ID NO:59)

PCR reactions were set up using a total of 5ng cDNA, consisting equal amounts of cDNA derived from human fetal brain, testis, skeletal muscle and mammary, template, 1 microM of each of the 19506719_B-EXT Mat-Forw and 19506719_B-EXT FL-Rev primers, 5 micromoles dNTP (Clontech Laboratories, Palo Alto CA) and 1 microliter of 50xAdvantage-HF 2 polymerase (Clontech Laboratories, Palo Alto CA) in 50 microliter volume. The following reaction conditions were used:

a) 96°C 3 minutes
  b) 96°C 30 seconds denaturation
  c) 60°C 30 seconds annealing
d) 72°C 3 minute extension.
Repeat steps b-d 35 times
e) 72oC 10 minutes seconds final extension

A single, 2.1 kb large, PCR product, was isolated from agarose gel and ligated to pCR2.1 vector (Invitrogen, Carlsbad, CA). The cloned insert was sequenced, using vector specific, M13 Forward(-40) and M13 Reverse primers as well as the gene specific primers:

GGACCATGCTAGACTTTCC, 19506719_B-EXT S1; (SEQ ID NO:60)
GGAAAGTCTAGCATGGTCC, 19506719_B-EXT S2; (SEQ ID NO:61)
GGCTGAACTTGGTGCTCTTCC, 19506719_B-EXT S3; (SEQ ID NO:62)
GGAAGAGCACCAAGTTCAGCC, 19506719_B-EXT S4; (SEQ ID NO:63)
GGCTTGCTGAACACCTACC, 19506719_B-EXT S7; (SEQ ID NO:64)
GGTAGGTGTTCAGCAAGCC, 19506719_B-EXT S8; (SEQ ID NO:65)
GCACAGACTGATTTTGCACG, 19506719_B-EXT S9; (SEQ ID NO:66) and
CGTGCAAAATCAGTCTGTGC, 19506719_B-EXT S10 (SEQ ID NO:67).

The disclosed novel MOL9b nucleic acid of 2061 nucleotides (also referred to as MOL9b) is shown in Table 9D. It is thought that MOL9b is an internal fragment of an open reading frame. Therefore its 5' and 3' termini may be extended.

Table 9D. MOL9b Nucleotide Sequence (SEQ ID NO:23)
TCCAGGATTTTACTCAGAATGACGTTAGGAAGAGAAGTGATGTCTCCTCTTCAGGCAATGTCTTCCTATAC TGTGGCTGGCAGAAATGTTTTAAGATGGGATCTTTCACCAGAGCAAATTAAAACAAGAACTGAGGAGCTCA TTGTGCAGACCAAACAGGTGTACGATGCTGTTGGAATGCTCGGTATTGAGGAAGTAACTTACGAGAACTGT CTGCAGGCACTGGCAGATGTAGAAGTAAAGTATATAGTGGAAAGGACCATGCTAGACTTTCCCCAGCATGT ATCCTCTGACAAAGAAGTACGAGCAGCAAGTACAGAAGCAGACAAAAGACTTTCTCGTTTTGATATTGAGA TGAGCATGAGAGGAGATATATTTGAGAGAATTGTTCATTTACAGGAAACCTGTGATCTGGGGAAGATAAAA CCTGAGGCCAGACGATACTTGGAAAAGTCAATTAAAATGGGGAAAAGAAATGGGCTCCATCTTCCTGAACA AGTACAGAATGAAATCAAATCAATGAAGAAAAGAATGAGTGAGCTATGTATTGATTTTAACAAAAACCTCA ATGAGGATGATACCTTCCTTGTATTTTCCAAGGCTGAACTTGGTGCTCTTCCTGATGATTTCATTGACAGT TTAGAAAAGACAGATGATGACAAGTATAAAATTACCTTAAAATATCCACACTATTTCCCTGTCATGAAGAA ATGTTGTATCCCTGAAACCAGAAGAAGGATGGAAATGGCTTTTAATACAAGGTGCAAAGAGGAAAACACCA TAATTTTGCAGCAGCTACTCCCACTGCGAACCAAGGTGGCCAAACTACTCGGTTATAGCACACATGCTGAC TTCGTCCTTGAAATGAACACTGCAAAGAGCACAAGCCGCGTAACAGCCTTTCTAGATGATTTAAGCCAGAA GTTAAAACCCTTGGGTGAAGCAGAACGAGAGTTTATTTTGAATTTGAAGAAAAAGGAATGCAAAGACAGGG GTTTTGAATATGATGGGAAAATCAATGCCTGGGATCTATATTACTACATGACTCAGACAGAGGAACTCAAG TATTCCATAGACCAAGAGTTCCTCAAGGAATACTTCCCAATTGAGGTGGTCACTGAAGGCTTGCTGAACAC CTACCAGGAGTTGTTGGGACTTTCATTTGAACAAATGACAGATGCTCATGTTTGGAACAAGAGTGTTACAC TTTATACTGTGAAGGATAAAGCTACAGGAGAAGTATTGGGACAGTTCTATTTGGACCTCTATCCAAGGGAA GGAAAATACAATCATGCGGCCTGCTTCGGTCTCCAGCCTGGCTGCCTTCTGCCTGATGGAAGCCGGATGAT GGCAGTGGCTGCCCTCGTGGTGAACTTCTCACAGCCAGTGGCAGGTCGTCCCTCTCTCCTGAGACACGACG AGGTGAGGACTTACTTTCATGAGTTTGGTCACGTGATGCATCAGATTTGTGCACAGACTGATTTTGCACGA TTTAGCGGAACAAATGTGGAAACTGACTTTGTAGAGGTGCCATCGCAAATGCTTGAAAATTGGGTGTGGGA CGTCGATTCCCTCCGAAGATTGTCAAAACATTATAAAGATGGAAGCCCTATTGCAGACGATCTGCTTGAAA AACTTGTTGCTTCTAGGCTGGTCAACACAGGTCTTCTGACCCTGCGCCAGATTGTTTTGAGCAAAGTTGAT CAGTCTCTTCATACCAACACATCGCTGGATGCTGCAAGTGAATATGCCAAATACTGCTCAGAAATATTAGG AGTTGCAGCTACTCCAGGCACAAATATGCCAGCTACCTTTGGACATTTGGCAGGGGGATACGATGGCCAAT ATTATGGATATCTTTGGAGTGAAGTATTTTCCATGGATATGTTTTACAGCTGTTTTAAAAAAGAAGGATA ATGAATCCGGAGGTTGGAATGAAATACAGAAACCTAATCCTGAAACCTGGGGATCTCTGGACGGCATGGA CATGCTCCACAATTTCTTGAAACGTGAGCCAAACCAAAAAGCGTTCCTAATGAGTAGAGGCCTGCATGCTC CG

The MOL9b protein encoded by SEQ ID NO:21 has 687 amino acid residues, and is presented using the one-letter code in Table 9E (SEQ ID NO:24).

Table 9E. Encoded MOL9b protein sequence (SEQ ID NO:24)
SRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTRTEELIVQTKQVYDAVGMLGIEEVTYENC LQALADVEVKYIVERTMLDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIK PEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDS LEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHAD FVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWDLYYYMTQTEELK YSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDKATGEVLGQFYLDLYPRE GKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFAR FSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVD QSLHTNTSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGI MNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP

MOL9c

In the present invention, the target sequence identified previously, Accession Number 19506719_B_EXT, was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated Accession Number CG56222-01

The disclosed novel MOL9c nucleic acid of 2167 nucleotides (also referred to as CG56222-01) is shown in Table 9F An open reading frame begins with an ATG initiation codon at nucleotides 16-18 and ends with a TGA codon at nucleotides 2128-2130. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 9F, and the start and stop codons are in bold letters.

In a search of sequence databases, it was found, for example, that the nucleic acid sequence has 2000 of 2167 bases (92%) identical to a gb:GENBANK-ID:AB000170|acc:AB000170.1 mRNA from Sus scrofa (Porcine mRNA for endopeptidase 24.16, complete cds) (Expect = 0.0).

Table 9F. MOL9c Nucleotide Sequence (SEQ ID NO:25)
CCTCTCAGCGCTCCC**ATG**ATCGCCCGGTGCCTTTTGGCTGTGCGAAGCCTCCGCAGAGTTGGTGGTTCCAG
GATTTTACTCAGAATGACGTTAGGAAGAGAAGTGATGTCTCCTCTTCAGGCAATGTCTTCCTATACTGTGG
CTGGCAGAAATGTTTTAAGATGGGATCTTTCACCAGAGCAAATTAAAACAAGAACTGAGGAGCTCATTGTG
CAGACCAAACAGGTGTACGATGCTGTTGGAATGCTCGGTATTGAGGAAGTAACTTACGAGAACTGTCTGCA
GGCACTGGCAGATGTAGAAGTAAAGTATATAGTGGAAAGGACCATGCTAGACTTTCCCCAGCATGTATCCT
CTGACAAAGAAGTACGAGCAGCAAGTACAGAAGCAGACAAAAGACTTTCTCGTTTTGATATTGAGATGAGC
ATGAGAGGAGATATATTTGAGAGAATTGTTCATTTACAGGAAACCTGTGATCTGGGGAAGATAAAACCTGA
GGCCAGACGATACTTGGAAAAGTCAATTAAAATGGGGAAAAGAAATGGGCTCCATCTTCCTGAACAAGTAC
AGAATGAAATCAAATCAATGAAGAAAAGAATGAGTGAGCTATGTATTGATTTTAACAAAAACCTCAATGAG
GATGATACCTTCCTTGTATTTTCCAAGGCTGAACTTGGTGCTCTTCCTGATGATTTCATTGACAGTTTAGA
AAAGACAGATGATGACAAGTATAAAATTACCTTAAAATATCCACACTATTTCCCTGTCATGAAGAAATGTT
GTATCCCTGAAACCAGAAGAAGGATGGAAATGGCTTTTAATACAAGGTGCAAAGAGGAAAACACCATAATT
TTGCAGCAGCTACTCCCACTGCGAACCAAGGTGGCCAAACTACTCGGTTATAGCACACATGCTGACTTCGT
CCTTGAAATGAACACTGCAAAGAGCACAAGCCGCGTAACAGCCTTTCTAGATGATTTAAGCCAGAAGTTAA
AACCCTTGGGTGAAGCAGAACGAGAGTTTATTTTGAATTTGAAGAAAAAGGAATGCAAAGACAGGGGTTTT
GAATATGATGGGAAAATCAATGCCTGGGATCTATATTACTACATGACTCAGACAGAGGAACTCAAGTATTC
CATAGACCAAGAGTTCCTCAAGGAATACTTCCCAATTGAGGTGGTCACTGAAGGCTTGCTGAACACCTACC
AGGAGTTGTTGGGACTTTCATTTGAACAAATGACAGATGCTCATGTTTGGAACAAGAGTGTTACACTTTAT
ACTGTGAAGGATAAAGCTACAGGAGAAGTATTGGGACAGTTCTATTTGGACCTCTATCCAAGGGAAGGAAA
ATACAATCATGCGGCCTGCTTCGGTCTCCAGCCTGGCTGCCTTCTGCCTGATGGAAGCCGGATGATGGCAG
TGGCTGCCCTCGTGGTGAACTTCTCACAGCCAGTGGCAGGTCGTCCCTCTCTCCTGAGACACGACGAGGTG
AGGACTTACTTTCATGAGTTTGGTCACGTGATGCATCAGATTTGTGCACAGACTGATTTTGCACGATTTAG
CGGAACAAATGTGGAAACTGACTTTGTAGAGGTGCCATCGCAAATGCTTGAAAATTGGGTGTGGGACGTCG
ATTCCCTCCGAAGATTGTCAAAACATTATAAAGATGGAAGCCCTATTGCAGACGATCTGCTTGAAAAACTT
GTTGCTTCTAGGCTGGTCAACACAGGTCTTCTGACCCTGCGCCAGATTGTTTTGAGCAAAGTTGATCAGTC
TCTTCATACCAACACATCGCTGGATGCTGCAAGTGAATATGCCAAATACTGCTCAGAAATATTAGGAGTTG
CAGCTACTCCAGGCACAAATATGCCAGCTACCTTTGGACATTTGGCAGGGGGATACGATGGCCAATATTAT
GGATATCTTTGGAGTGAAGTATTTTCCATGGATATGTTTTACAGCTGTTTTAAAAAAGAAGGGATAATGAA
TCCGGAGGTTGGAATGAAATACAGAAACCTAATCCTGAAACCTGGGGGATCTCTGGACGGCATGGACATGC
TCCACAATTTCTTGAAACGTGAGCCAAACCAAAAAGCGTTCCTAATGAGTAGAGGCCTGCATGCTCCG**TGA**
ACTGGGGATCTTTGGTAGCCGTCCATGTCTGGAGGAC

The MOL9c protein encoded by SEQ ID NO:25 has 703 amino acid residues, and is presented using the one-letter code in Table 9G (SEQ ID NO:26). The SignalP, Psort and/or Hydropathy profile for MOL9c predict that MOL9c has a signal peptide and is likely to be localized at the cytoplasm with a certainty of 0.9200. The SignalP predicts a cleavage site at the sequence between amino acids 17 and 18.

Table 9G. Encoded MOL9c protein sequence (SEQ ID NO:26)
MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTRTEELIVQTKQV YDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRAASTEADKRLSRFDIEMSMRGDI FERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHLPEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFL VFSKAELGALPDDFIDSLEKTDDDKYKITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLL PLRTKVAKLLGYSTHADFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGK INAWDLYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTLYTVKDK ATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPVAGRPSLLRHDEVRTYFH EFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRRLSKHYKDGSPIADDLLEKLVASRL VNTGLLTLRQIVLSKVDQSLHTNTSLDAASEYAKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWS EVFSMDMFYSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP

The full amino acid sequence of MOL9c was found to have 657 of 704 amino acid residues (93%) identical to, and 687 of 704 amino acid residues (97%) similar to, the 704 amino acid residue ptnr:SWISSPROT-ACC:P42675 protein from Oryctolagus cuniculus (Rabbit) (NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (E value = 0.0)

MOL9c is expressed in at least the following tissues: Artery, Brain, Bronchus, Cartilage, Cervix, Colon, Coronary Artery, Dermis, Epidermis, Foreskin, Heart, Kidney, Liver, Ovary, Pancreas, Pituitary Gland, Placenta, Prostate, Salivary Glands, Synovium/Synovial membrane, Thalamus, Umbilical Vein, Uterus. This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

Possible SNPs found for MOL9c are listed in Table 9H.

Table 9H: SNPs

Consensus Position	Depth	Base Change
399	99	A > G
858	51	C > A
863	50	T > A
1242	48	T > C
1810	141	G > A

1824	143	T > C
1892	144	T > C

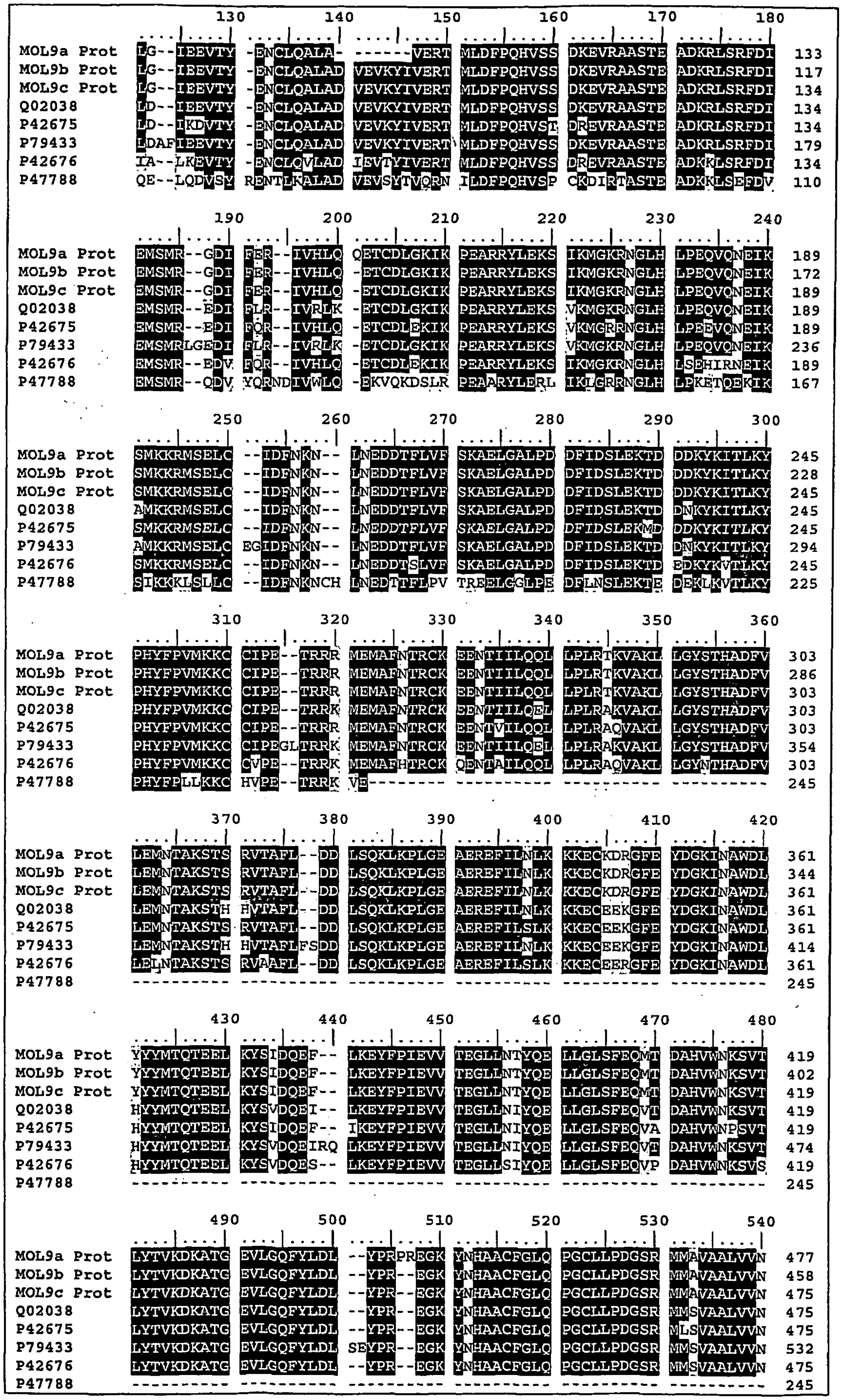
These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL9c substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. For example the disclosed MOL9c protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL9c epitope is from about amino acids 25 to 75. In another embodiment, a MOL9c epitope is from about amino acids 100 to 200. In further embodiments, MOL9a epitopes are found in amino acids 250-400, 450-550, and 650-700. These novel proteins can also be used to develop assay system for functional analysis.

Homology between the MOL9 isoforms and other homologous proteins is presented graphically in the multiple sequence alignment given in Table 9I (with MOL9a being shown on line 1, MOL9b on line 2, and MOL9c on line 3) as a ClustalW analysis comparing MOL9 with related protein sequences.

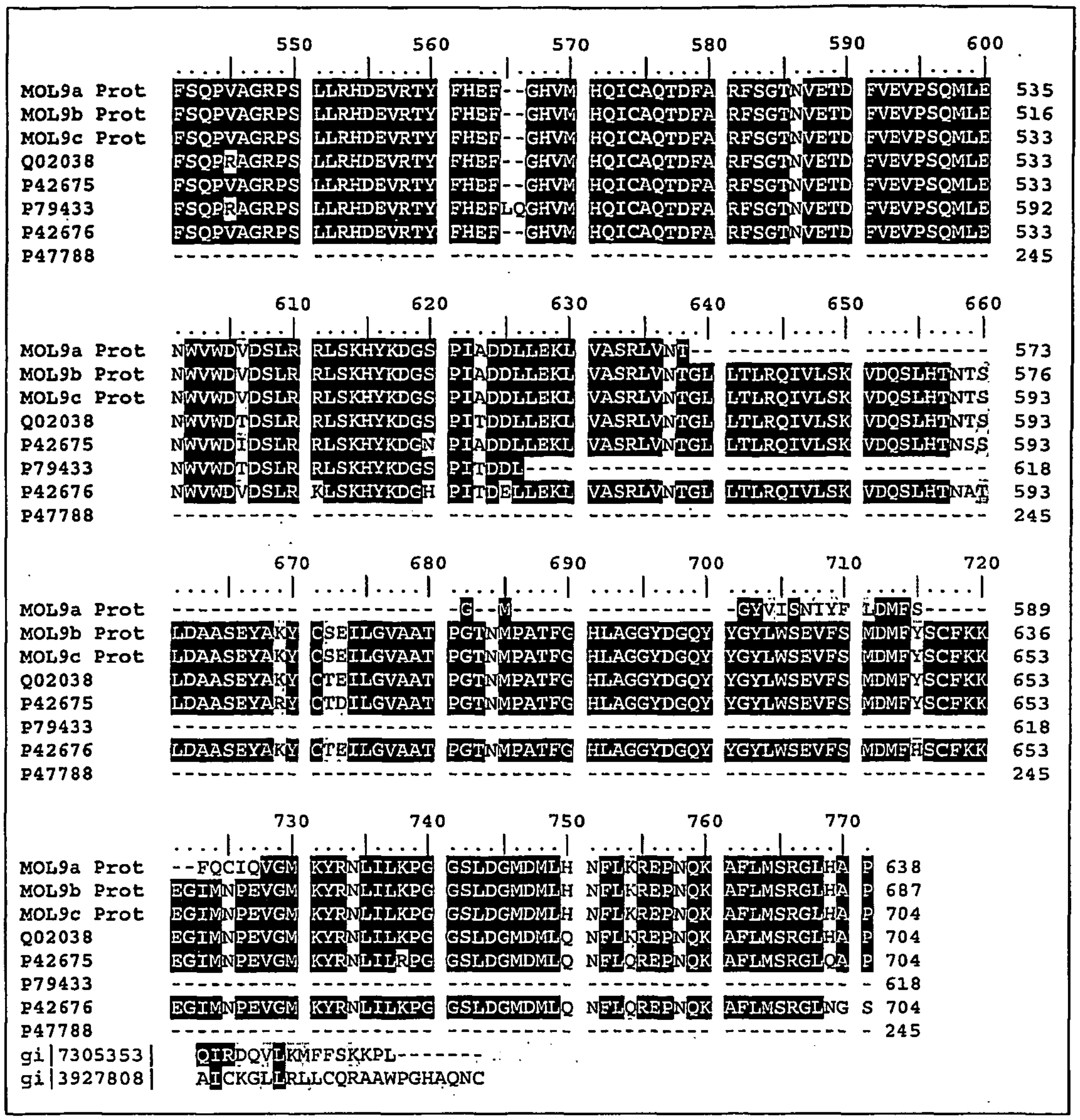
Table 9I. Information for the ClustalW proteins:

```
1)  MOL9a (SEQ ID NO:22)
2)  MOL9b (SEQ ID NO:24)
3)  MOL9c (SEQ ID NO:26)
4)  SWISSNEW-ACC:Q02038 NEUROLYSIN PRECURSOR (SEQ ID NO:68)
3)  SWISSPROT-ACC:P42675 NEUROLYSIN PRECURSOR (SEQ ID NO:69)
5)  SPTREMBL-ACC:P79433 ENDOPEPTIDASE 24.16 (SEQ ID NO:70)
6)  SWISSPROT-ACC:P42676 NEUROLYSIN PRECURSOR (SEQ ID NO:71)
7)  ACC:P47788 THIMET OLIGOPEPTIDASE (SEQ ID NO:72)
```

```
                    10         20         30         40         50         60
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot  ---------- ---------- ---------- -----MLTLD QQKSLILILF LILFRVGGSR  25
MOL9b Prot  ---------- ---------- ---------- ---------- ---------- --------SR  2
MOL9c Prot  ---------- ---------- ---------- ---------- -MIARCLLAV RSLRRVGGSR  19
Q02038      ---------- ---------- ---------- ---------- -MIVRCLSAA RRLHRVGGSG  19
P42675      ---------- ---------- ---------- ---------- -MIARCFSAV RGLHRVGGSR  19
P79433      MVYPEGHLAR ELGATFSSSA PLGGHPFPFV WDCLSCKQGD WSQARPKTNA ERRSGVGGSG  60
P42676      ---------- ---------- ---------- ---------- -MITLCLSTL RGLHRAGGSR  19
P47788      ---------- ---------- ---------- ---------- ---------- KPPAACAGDA  10

                    70         80         90        100        110        120
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot  --ILLRMTLG REVMSPLQAM SSYTVAGRNV LRWDLSPEQI KTRTEELIVQ TKQVYDAVGM  83
MOL9b Prot  --ILLRMTLG REVMSPLQAM SSYTVAGRNV LRWDLSPEQI KTRTEELIVQ TKQVYDAVGM  60
MOL9c Prot  --ILLRMTLG REVMSPLQAM SSYTVAGRNV LRWDLSPEQI KTRTEELIVQ TKQVYDAVGM  77
Q02038      --ILLRMTLG REAMSPLQAM SSYTVDGRNV LRWDLSPEQI KRRTEELIAQ TKQVYDDIGM  77
P42675      --ILFKMTLG REVMSPLQAV SSYTAAGRNV LRWDLSPEQI KTRTEELIAQ TKQVYDSVGM  77
P79433      NLILLRMTLG REAMSPLQAM SSYTVDGRNV LRWDLSPEQI KRRTEELIAQ TKQVYDDIGM  120
P42676      --LQLTMTLG KELASPLQAM SSYTAAGRNV LRWDLSPEQI KTRTEQLIAQ TKQVYDTVGT  77
P47788      ---------- LDVAAPCSAV ----N----Y LRWDLSAQQI GELTTELIEQ TKRVYDRVGT  52
```



```
                      130        140        150        160        170        180
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   LG--IEEVTY -ENCLQALA- ------VERT MLDFPQHVSS DKEVRAASTE ADKRLSRFDI   133
MOL9b Prot   LG--IEEVTY -ENCLQALAD VEVKYIVERT MLDFPQHVSS DKEVRAASTE ADKRLSRFDI   117
MOL9c Prot   LG--IEEVTY -ENCLQALAD VEVKYIVERT MLDFPQHVSS DKEVRAASTE ADKRLSRFDI   134
Q02038       LD--IEEVTY -ENCLQALAD VEVKYIVERT MLDFPQHVSS DKEVRAASTE ADKRLSRFDI   134
P42675       LD--IKDVTY -ENCLQALAD VEVKYIVERT MLDFPQHVST DREVRAASTE ADKRLSRFDI   134
P79433       LDAFIEEVTY -ENCLQALAD VEVKYIVERT MLDFPQHVSS DKEVRAASTE ADKRLSRFDI   179
P42676       IA--LKEVTY -ENCLQVLAD IEVTYIVERT MLDFPQHVSS DREVRAASTE ADKKLSRFDI   134
P47788       QE--LQDVSY RENTLKALAD VEVSYTVQRN ILDFPQHVSP CKDIRTASTE ADKKLSEFDV   110

                      190        200        210        220        230        240
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   EMSMR--GDI FER--IVHLQ QETCDLGKIK PEARRYLEKS IKMGKRNGLH LPEQVQNEIK   189
MOL9b Prot   EMSMR--GDI FER--IVHLQ -ETCDLGKIK PEARRYLEKS IKMGKRNGLH LPEQVQNEIK   172
MOL9c Prot   EMSMR--GDI FER--IVHLQ -ETCDLGKIK PEARRYLEKS IKMGKRNGLH LPEQVQNEIK   189
Q02038       EMSMR--EDI FLR--IVRLK -ETCDLGKIK PEARRYLEKS VKMGKRNGLH LPEQVQNEIK   189
P42675       EMSMR--EDI FQR--IVHLQ -ETCDLEKIK PEARRYLEKS VKMGRRNGLH LPEEVQNEIK   189
P79433       EMSMRLGEDI FLR--IVRLK -ETCDLGKIK PEARRYLEKS VKMGKRNGLH LPEQVQNEIK   236
P42676       EMSMR--EDV FQR--IVHLQ -ETCDLEKIK PEARRYLEKS IKMGKRNGLH LSEHIRNEIK   189
P47788       EMSMR--QDV YQRNDIVWLQ -EKVQKDSLR PEAARYLERL IKLGRRNGLH LPKETQEKIK   167

                      250        260        270        280        290        300
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   SMKKRMSELC --IDFNKN-- LNEDDTFLVF SKAELGALPD DFIDSLEKTD DDKYKITLKY   245
MOL9b Prot   SMKKRMSELC --IDFNKN-- LNEDDTFLVF SKAELGALPD DFIDSLEKTD DDKYKITLKY   228
MOL9c Prot   SMKKRMSELC --IDFNKN-- LNEDDTFLVF SKAELGALPD DFIDSLEKTD DDKYKITLKY   245
Q02038       AMKKRMSELC --IDFNKN-- LNEDDTFLVF SKAELGALPD DFIDSLEKTD DNKYKITLKY   245
P42675       SMKKRMSELC --IDFNKN-- LNEDDTFLVF SKAELGALPD DFIDSLEKMD DDKYKITLKY   245
P79433       AMKKRMSELC EGIDFNKN-- LNEDDTFLVF SKAELGALPD DFIDSLEKTD DNKYKITLKY   294
P42676       SMKKRMSELC --IDFNKN-- LNEDDTSLVF SKAELGALPD DFIDSLEKTD EDKYKVTLKY   245
P47788       SIKKKLSLLC --IDFNKNCH LNEDTTFLPV TREELGGLPE DFLNSLEKTE DEKLKVTLKY   225

                      310        320        330        340        350        360
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   PHYFPVMKKC CIPE--TRRR MEMAFNTRCK EENTIILQQL LPLRTKVAKL LGYSTHADFV   303
MOL9b Prot   PHYFPVMKKC CIPE--TRRR MEMAFNTRCK EENTIILQQL LPLRTKVAKL LGYSTHADFV   286
MOL9c Prot   PHYFPVMKKC CIPE--TRRR MEMAFNTRCK EENTIILQQL LPLRTKVAKL LGYSTHADFV   303
Q02038       PHYFPVMKKC CIPE--TRRK MEMAFNTRCK EENTIILQEL LPLRAKVAKL LGYSTHADFV   303
P42675       PHYFPVMKKC CIPE--TRRR MEMAFNTRCK EENTVILQQL LPLRAQVAKL LGYSTHADFV   303
P79433       PHYFPVMKKC CIPEGLTRRK MEMAFNTRCK EENTIILQEL LPLRAKVAKL LGYSTHADFV   354
P42676       PHYFPVMKKC CVPE--TRRK MEMAFHTRCK QENTAILQQL LPLRAQVAKL LGYNTHADFV   303
P47788       PHYFPLLKKC HVPE--TRRK VE-------- ---------- ---------- ----------   245

                      370        380        390        400        410        420
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   LEMNTAKSTS RVTAFL--DD LSQKLKPLGE AEREFILNLK KKECKDRGFE YDGKINAWDL   361
MOL9b Prot   LEMNTAKSTS RVTAFL--DD LSQKLKPLGE AEREFILNLK KKECKDRGFE YDGKINAWDL   344
MOL9c Prot   LEMNTAKSTS RVTAFL--DD LSQKLKPLGE AEREFILNLK KKECKDRGFE YDGKINAWDL   361
Q02038       LEMNTAKSTH HVTAFL--DD LSQKLKPLGE AEREFILNLK KKECEEKGFE YDGKINAWDL   361
P42675       LEMNTAKSTS RVTAFL--DD LSQKLKPLGE AEREFILSLK KKECEEKGFE YDGKINAWDL   361
P79433       LEMNTAKSTH HVTAFLFSDD LSQKLKPLGE AEREFILNLK KKECEEKGFE YDGKINAWDL   414
P42676       LELNTAKSTS RVAAFL--DD LSQKLKPLGE AEREFILSLK KKECEERGFE YDGKINAWDL   361
P47788       ---------- ---------- ---------- ---------- ---------- ----------   245

                      430        440        450        460        470        480
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   YYYMTQTEEL KYSIDQEF-- LKEYFPIEVV TEGLLNTYQE LLGLSFEQMT DAHVWNKSVT   419
MOL9b Prot   YYYMTQTEEL KYSIDQEF-- LKEYFPIEVV TEGLLNTYQE LLGLSFEQMT DAHVWNKSVT   402
MOL9c Prot   YYYMTQTEEL KYSIDQEF-- LKEYFPIEVV TEGLLNTYQE LLGLSFEQMT DAHVWNKSVT   419
Q02038       HYYMTQTEEL KYSVDQEI-- LKEYFPIEVV TEGLLNIYQE LLGLSFEQVT DAHVWNKSVT   419
P42675       HYYMTQTEEL KYSIDQEF-- IKEYFPIEVV TEGLLNIYQE LLGLSFEQVA DAHVWNPSVT   419
P79433       HYYMTQTEEL KYSVDQEIRQ LKEYFPIEVV TEGLLNIYQE LLGLSFEQVT DAHVWNKSVT   474
P42676       HYYMTQTEEL KYSVDQES-- LKEYFPIEVV TEGLLSIYQE LLGLSFEQVP DAHVWNKSVS   419
P47788       ---------- ---------- ---------- ---------- ---------- ----------   245

                      490        500        510        520        530        540
             ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot   LYTVKDKATG EVLGQFYLDL --YPRPREGK YNHAACFGLQ PGCLLPDGSR MMAVAALVVN   477
MOL9b Prot   LYTVKDKATG EVLGQFYLDL --YPR--EGK YNHAACFGLQ PGCLLPDGSR MMAVAALVVN   458
MOL9c Prot   LYTVKDKATG EVLGQFYLDL --YPR--EGK YNHAACFGLQ PGCLLPDGSR MMAVAALVVN   475
Q02038       LYTVKDKATG EVLGQFYLDL --YPR--EGK YNHAACFGLQ PGCLLPDGSR MMSVAALVVN   475
P42675       LYTVKDKATG EVLGQFYLDL --YPR--EGK YNHAACFGLQ PGCLLPDGSR MLSVAALVVN   475
P79433       LYTVKDKATG EVLGQFYLDL SEYPR--EGK YNHAACFGLQ PGCLLPDGSR MMSVAALVVN   532
P42676       LYTVKDKATG EVLGQFYLDL --YPR--EGK YNHAACFGLQ PGCLLPDGSR MMSVAALVVN   475
P47788       ---------- ---------- ---------- ---------- ---------- ----------   245
```



```
                     550        560        570        580        590        600
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot    FSQPVAGRPS LLRHDEVRTY FHEF--GHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 535
MOL9b Prot    FSQPVAGRPS LLRHDEVRTY FHEF--GHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 516
MOL9c Prot    FSQPVAGRPS LLRHDEVRTY FHEF--GHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 533
Q02038        FSQPRAGRPS LLRHDEVRTY FHEF--GHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 533
P42675        FSQPVAGRPS LLRHDEVRTY FHEF--GHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 533
P79433        FSQPRAGRPS LLRHDEVRTY FHEFLQGHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 592
P42676        FSQPVAGRPS LLRHDEVRTY FHEF--GHVM HQICAQTDFA RFSGTNVETD FVEVPSQMLE 533
P47788        ---------- ---------- ---------- ---------- ---------- ---------- 245

                     610        620        630        640        650        660
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot    NWVWDVDSLR RLSKHYKDGS PIADDLLEKL VASRLVNT-- ---------- ---------- 573
MOL9b Prot    NWVWDVDSLR RLSKHYKDGS PIADDLLEKL VASRLVNTGL LTLRQIVLSK VDQSLHTNTS 576
MOL9c Prot    NWVWDVDSLR RLSKHYKDGS PIADDLLEKL VASRLVNTGL LTLRQIVLSK VDQSLHTNTS 593
Q02038        NWVWDTDSLR RLSKHYKDGS PITDDLLEKL VASRLVNTGL LTLRQIVLSK VDQSLHTNTS 593
P42675        NWVWDIDSLR RLSKHYKDGN PIADDLLEKL VASRLVNTGL LTLRQIVLSK VDQSLHTNSS 593
P79433        NWVWDTDSLR RLSKHYKDGS PITDDL---- ---------- ---------- ---------- 618
P42676        NWVWDVDSLR KLSKHYKDGH PITDELLEKL VASRLVNTGL LTLRQIVLSK VDQSLHTNAT 593
P47788        ---------- ---------- ---------- ---------- ---------- ---------- 245

                     670        680        690        700        710        720
              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL9a Prot    ---------- ---------- -G--M----- ---------- -GYVISNIYF LDMFS----- 589
MOL9b Prot    LDAASEYAKY CSEILGVAAT PGTNMPATFG HLAGGYDGQY YGYLWSEVFS MDMFYSCFKK 636
MOL9c Prot    LDAASEYAKY CSEILGVAAT PGTNMPATFG HLAGGYDGQY YGYLWSEVFS MDMFYSCFKK 653
Q02038        LDAASEYAKY CTEILGVAAT PGTNMPATFG HLAGGYDGQY YGYLWSEVFS MDMFYSCFKK 653
P42675        LDAASEYARY CTDILGVAAT PGTNMPATFG HLAGGYDGQY YGYLWSEVFS MDMFYSCFKK 653
P79433        ---------- ---------- ---------- ---------- ---------- ---------- 618
P42676        LDAASEYAKY CTEILGVAAT PGTNMPATFG HLAGGYDGQY YGYLWSEVFS MDMFHSCFKK 653
P47788        ---------- ---------- ---------- ---------- ---------- ---------- 245

                     730        740        750        760        770
              ....|....| ....|....| ....|....| ....|....| ....|....| .
MOL9a Prot    --FQCIQVGM KYRNLILKPG GSLDGMDMLH NFLKREPNQK AFLMSRGLHA P 638
MOL9b Prot    EGIMNPEVGM KYRNLILKPG GSLDGMDMLH NFLKREPNQK AFLMSRGLHA P 687
MOL9c Prot    EGIMNPEVGM KYRNLILKPG GSLDGMDMLH NFLKREPNQK AFLMSRGLHA P 704
Q02038        EGIMNPEVGM KYRNLILKPG GSLDGMDMLQ NFLKREPNQK AFLMSRGLHA P 704
P42675        EGIMNPEVGM KYRNLILRPG GSLDGMDMLQ NFLQREPNQK AFLMSRGLQA P 704
P79433        ---------- ---------- ---------- ---------- ---------- - 618
P42676        EGIMNPEVGM KYRNLILKPG GSLDGMDMLQ NFLQREPNQK AFLMSRGLNG S 704
P47788        ---------- ---------- ---------- ---------- ---------- - 245
gi|7305353|     QIRDQVLKMFFSKKPL-------
gi|3927808|     AICKGLLRLLCQRAAWPGHAQNC
```

Endopeptidase 24.16 or mitochondrial oligopeptidase, abbreviated here as EP 24.16 (MOP), is a thiol- and metal-dependent oligopeptidase that is found in multiple intracellular compartments in mammalian cells. From an analysis of the corresponding gene, we found that the distribution of the enzyme to appropriate subcellular locations is achieved by the use of alternative sites for the initiation of transcription. The pig EP 24.16 (MOP) gene spans over 100 kilobases and is organized into 16 exons. The core protein sequence is encoded by exons 5-16 which match perfectly with exons 2-13 of the gene for endopeptidase 24.15, another member of the thimet oligopeptidase family. These two sets of 11 exons share the same splice sites, suggesting a common ancestor. Multiple species of mRNA for EP 24.16 (MOP) were detected by the 5'-rapid amplification of cDNA ends and they were shown to have been generated from a single gene by alternative choices of sites for the initiation of transcription and splicing. Two types of transcript were prepared, corresponding to transcription from distal and proximal sites. Their expression in vitro in COS-1 cells indicated that they encoded two isoforms (long and short) which differed only at their amino termini: the long form contained a cleavable mitochondrial targeting sequence and was directed to mitochondria; the short form, lacking such a signal sequence, remained in the cytosol. The complex structure of the EP 24.16 (MOP) gene thus allows, by alternative promoter usage, a fine transcriptional regulation of coordinate expression, in the different subcellular compartments, of the two isoforms arising from a single gene. PMID: 9182559, UI: 97326108 We have isolated a metallopeptidase from rat liver. The peptidase is primarily located in the mitochondrial intermembrane space, where it interacts non-covalently with the inner membrane. The enzyme hydrolyzes oligopeptides, the largest substrate molecule found being dynorphin A1-17; it has no action on proteins, and does not interact with alpha 2-macroglobulin, and can therefore be classified as an oligopeptidase. We term the enzyme oligopeptidase M. Oligopeptidase M acts similarly to thimet oligopeptidase (EC 3.4.24.15) on bradykinin and several other peptides, but hydrolyzes neurotensin exclusively at the -Pro+Tyr- bond (the symbol + is used to indicate a scissile peptide bond) rather than the -Arg+Arg- bond. The enzyme is inhibited by chelating agents and some thiol-blocking compounds, but differs from thimet oligopeptidase in not being activated by thiol compounds. The peptidase is inhibited by Pro-Ile, unlike thimet oligopeptidase, and the two enzymes are separable in chromatography on hydroxyapatite. The N-terminal amino acid sequence of rat mitochondrial oligopeptidase M contains 19 out of 20 residues identical with a segment of rabbit microsomal endopeptidase and 17 matching the corresponding segment of pig-soluble angiotensin II-binding protein. Moreover, the rat protein is recognized by a monoclonal antibody against rabbit soluble angiotensin II-binding protein, all of which is consistent with these proteins being species variants of a single protein that is a homologue of thimet oligopeptidase. The biochemical properties of the mitochondrial oligopeptidase leave us in no doubt that it is neurolysin (EC 3.4.24.16), for which no sequence has previously been reported, and which has not been thought to be mitochondrial. PMID: 7836437, UI: 95138171 We have isolated by immunological screening of a lambda ZAPII cDNA library constructed from rat brain mRNAs a cDNA clone encoding endopeptidase 3.4.24.16. The longest open reading frame encodes a 704-amino acid protein with a theoretical molecular mass of 80,202 daltons and bears the consensus sequence of the zinc metalloprotease family. The sequence exhibits a 60.2% homology with those of another zinc metallopeptidase, endopeptidase 3.4.24.15. Northern blot analysis reveals two mRNA species of about 3 and 5 kilobases in rat brain, ileum, kidney, and testis. We have transiently transfected COS-7 cells with pcDNA3 containing the cloned cDNA and established the overexpression of a 70-75-kDa immunoreactive protein. This protein hydrolyzes QFS, a quenched fluorimetric substrate of endopeptidase 3.4.24.16, and cleaves neurotensin at a single peptide bond, leading to the formation of neurotensin (1-10) and neurotensin (11-13). QFS and neurotensin hydrolysis are potently inhibited by the selective endopeptidase 3.4.24.16 dipeptide blocker Pro-Ile and by dithiothreitol, while the enzymatic activity remains unaffected by phosphoramidon and captopril, the specific inhibitors of endopeptidase 3.4.24.11 and angiotensin-converting enzyme, respectively. Altogether, these physicochemical, biochemical, and immunological properties unambiguously identify endopeptidase 3.4.24.16 as the protein encoded by the isolated cDNA clone. PMID: 7592986, UI: 96070836 A human genomic clone encompassing exons 1-3 of the neurotensin/neuromedin N gene was identified using a canine neurotensin complementary DNA probe. Sequence comparisons revealed that the 120-amino acid portion of the precursor sequence encoded by exons 1-3 is 89% identical to previously determined cow and dog sequences and that the proximal 250 bp of 5' flanking sequences are strikingly conserved between rat and human. The 5' flanking sequence contains cis-regulatory sites required for the induction of neurotensin/neuromedin N gene expression in PC12 cells, including AP1 sites and two cyclic adenosine-5'-monophosphate response elements. Oligonucleotide probes based on the human sequence were used to examine the distribution of neurotensin/neuromedin N messenger RNA in the ventral mesencephalon of schizophrenics and age- and sex-matched controls. Neurotensin/neuromedin N messenger RNA was observed in ventral mesencephalic cells some of which also contained melanin pigment or tyrosine hydroxylase messenger RNA. Neurons expressing neurotensin/neuromedin N messenger RNA were observed in the ventral mesencephalon of both schizophrenic and non-schizophrenic humans. PMID: 1436492, UI: 93063858 Neurotensin is a small neuropeptide of 13 amino acids that may function as a neurotransmitter or neuromodulator in the central nervous system. In the CNS, neurotensin is localized to the catecholamine-containing neurons. A catecholamine-producing cell line can also produce NT. Lithium salts, widely used in the treatment of manic-depressive patients, dramatically potentiate NT gene expression in this cell line. Gerhard et al. (1989) used a canine cDNA as a probe on a somatic cell hybrid panel to determine that the human gene is located on chromosome 12. The tridecapeptide neurotensin (162650) is widely distributed in various regions of the brain and in peripheral tissues. In the brain, neurotensin acts as a neuromodulator, in particular of dopamine transmission in the nigrostriatal and mesocorticolimbic systems, suggesting its possible implication in dopamine-associated behavioral neurodegenerative and neuropsychiatric disorders. Its various effects are mediated by specific membrane receptors. Vita et al. (1993) isolated a cDNA encoding the human neurotensin receptor and showed that it predicts a 418-amino acid protein that shares 84% homology with the rat protein. Le et al. (1997) also cloned the human neurotensin receptor (NTR) cDNA and its genomic DNA. The gene is encoded by 4 exons spanning more than 10 kb. The authors identified a highly polymorphic tetranucleotide repeat approximately 3 kb from the gene. Southern blot analysis revealed that the NTR gene is present in the human genome as a single-copy gene. Le et al. (1997) stated that the neurotensin receptor has 7 transmembrane spanning regions and high homology to other receptors that couple to G proteins

Neurolysin is expressed ubiquitously in the rat brain (Massarelli *et al.* Brain Res 1999 Dec 18; 851(1-2): 261-5; Dauch *et al.* J Neurochem 1992 Nov; 59(5): 1862-7). It has been suggested that this enzyme plays a role in the regulation of neurologically active peptides (Vincent *et al*: Br J Pharmacol 1997 Jun; 121(4): 705-10) and activity differs depending on the cellular source of this enzyme whether it is expressed in primary cultured neurons and astrocytes (Vincent *et al.* J Neurosci 1996 Aug 15; 16(16): 5049-59). This might play a role in nociception and signal transduction in the brain as well as central nervous system. Related endopeptidases have been shown to play a role in processing angiotensin and important regulator of blood pressure.

Uses of the Compositions of the Invention

The expression pattern, map location and protein similarity information for MOL9 suggest that it may function as neurolysin family. Therefore, the nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated, for example but not limited to, in various pathologies /disorders as described below and/or other pathologies/disorders. Potential therapeutic uses for the invention(s) are, for example but not limited to, the following: (i) Protein therapeutic, (ii) small molecule drug target, (iii) antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) diagnostic and/or prognostic marker, (v) gene therapy (gene delivery/gene ablation), (vi) research tools, and (vii) tissue regeneration *in vitro* and *in vivo* (regeneration for all these tissues and cell types composing these tissues and cell types derived from these tissues).These may also function in extracellular matrix remodeling in tissues described above.

The nucleic acids and proteins of the invention are useful in potential therapeutic applications implicated in various diseases and disorders described below and/or other pathologies and disorders. For example, but not limited to, a cDNA encoding the neurolysin -like protein may be useful in gene therapy, and the neurolysin -like protein may be useful when administered to a subject in need thereof. By way of nonlimiting example, the compositions of the present invention will have efficacy for treatment of patients suffering from Cancer, Trauma, Viral/bacterial/parasitic infections, Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation, Atherosclerosis, Aneurysms, Hypertension, Fibromuscular dysplasia, Stroke, Scleroderma, Fertility, Diabetes, Von Hippel-Lindau (VHL) syndrome , Pancreatitis, Hirschsprung's disease , Crohn's Disease, Appendicitis, Alzheimer's disease, Stroke, Hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Systemic lupus erythematosus , Autoimmune disease, Asthma, Emphysema, Scleroderma, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Renal tubular acidosis, IgA nephropathy, Hypercalceimia, Lesch-Nyhan syndrome. The novel nucleic acid encoding the neurolysin-like protein, and the neurolysin -like protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods

MOL10

MOL10a

A novel nucleic acid encoding a protein bearing sequence similarity to Cyclic-Nucleotide-Gated Olfactory Channel -like protein was identified by TblastN using CuraGen Corporation's sequence file for MOL10 probe or homolog, run against the Genomic Daily Files made available by GenBank. The nucleic acid was further predicted by the program GenScan™, including selection of exons. These were further modified by means of similarities using BLAST searches. The sequences were then manually corrected for apparent inconsistencies, thereby obtaining the sequences encoding the full-length protein. The disclosed novel MOL10a nucleic acid of 1835 nucleotides (also referred to as GM98960647_A) is shown in Table 10A. An open reading frame begins with an ATG initiation codon at nucleotides 54-56 and ends with a TGA codon at nucleotides 1788-1790. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 10A, and the start and stop codons are in bold letters.

The nucleic acid sequence has 1536 of 1733 bases (88%) identical to a *Rattus norvegicus* Cyclic-Nucleotide-Gated Olfactory Channel ocnc2 mRNA (GENBANK-ID: U12623) (Expect = $5.2e^{-108}$).

Table 10A. MOL10a Nucleotide Sequence (SEQ ID NO:27)
TACAGGCAGAGAGGGTGTGGACATCTCACACCCCAGCACCAGACCACAGAACCATGAGCCAGGACACCAAA GTGAAGACAACAGAGTCCAGTCCCCCAGCCCCATCCAAGGCCAGGAGGAAGTTGCTGCCTGTCCTGGACCC ATCTGGGGATTACTACTACTGGTGGCTGAACACAATGGTCTTCCCAGTCATGTATAACCTCATCATCCTCG TGTGCAGGGCCTGCTTCCCCGACTTGCAGCACGGTTATCTGGTGGCCTGGTTGGTGCTGGACTACACGAGT GACCTGCTATACCTACTAGACATGGTGGTGCGCTTCCACACAGGTGGATTCTTGGAACAGGGCATCCTGGT GGTGGACAAGGGTAGGATCTCGAGTCGCTACGTTCGCACCTGGAGTTTCTTCTTGGACCTGGCTTCCCTGA TGCCCACAGATGTGGTCTACGTGCGGCTGGGCCCGCACACACCCACCCTGAGGCTGAACCGCTTTCTCCGC GCGCCCCGCCTCTTCGAGGCCTTCGACCGCACAGAGACCCGCACAGCTTACCCAAATGCCTTTCGCATTGC CAAGCTGATGCTTTACATTTTTGTCGTCATCCATTGGAACAGCTGCCTATACTTTGCCCTATCCCGGTACC TGGGCTTCGGGCGTGACGCATGGGTGTACCCGGACCCCGCGCAGCCTGGCTTTGAGCGCCTGCGGCGCCAG TACCTCTATAGCTTTTACTTCTCCACGCTGATACTGACTACAGTGGGCGATACACCGCCGCCAGCCAGGGA AGAAGAGTACCTCTTCATGGTGGGCGACTTCCTGCTGGCCGTCATGGGTTTCGCCACCATCATGGGTAGCA TGAGCTCTGTCATCTACAACATGAACACTGCAGATGCGGCTTTCTACCCAGATCATGCACTGGTGAAGAAG TACATGAAGCTGCAGCACGTCAACCGCAAGCTGGAGCGGCGAGTTATTGACTGGTATCAGCACCTGCAGAT CAACAAGAAGATGACCAACGAGGTAGCCATCTTACAGCACTTGCCTGAGCGGCTGCGGGCAGAAGTGGCTG TGTCTGTGCACCTGTCCACTCTGAGCCGGGTGCAGATCTTTCAGAACTGTGAGGCCAGCCTGCTGGAGGAG CTGGTGCTGAAGCTGCAGCCCCAGACCTACTCACCAGGTGAATATGTATGCCGCAAAGGAGACATTGGCCA AGAGATGTACATCATCCGAGAGGGTCAACTGGCCGTGGTGGCAGATGATGGTATCACACAGTATGCTGTGC TCGGTGCAGGGCTCTACTTTGGGGAGATCAGCATCATCAACATCAAAGGTGGGAACATGTCTGGGAACCGC CGCACAGCCAACATCAAGAGCCTAGGTTATTCAGACCTATTCTGCCTGAGCAAGGAGGACCTGCGGGAGGT GCTGAGCGAGTATCCACAAGCACAGACCATCATGGAGGAGAAAGGACGTGAGATCCTGCTGAAAATGAACA AGTTGGACGTGAATGCTGAGGCAGCTGAGATCGCCCTGCAGGAGGCCACAGAGTCCCGGCTACGAGGCCTA GACCAGCAGCTGGATGATCTACAGACCAAGTTTGCTCGCCTCCTGGCTGAGCTGGAGTCCAGCGCACTTAA GATTGCTTACCGCATTGAACGGCTGGAGTGGCAGACTCGAGAGTGGCCAATGCCCGAGGACCTGGCTGAGG CTGATGACGAGGGTGAGCCTGAGGAGGGAACTTCCAAAGATGAAGAGGGCAGGGCCAGCCAGGAGGGACCC CCAGGTCCAGAG**TGA**CCCCATCCCCATCCCCAGGATTCCCACCTCCTAGTGAATCCAGAG

The MOL10a protein encoded by SEQ ID NO:27 has 638 amino acid residues, and is presented using the one-letter code in Table 10B (SEQ ID NO:28). PSORT analysis predicts the protein of the invention to be localized in the plasma membrane with a certainty of 0. 6000. Using the SIGNALP analysis, it is predicted that the protein of the invention has a signal peptide with most likely cleavage site between positions 57 and 58.

Table 10B. Encoded MOL10a protein sequence (SEQ ID NO:28)
MSQDTKVKTTESSPPAPSKARRKLLPVLDPSGDYYYWWLNTMVFPVMYNLIILVCRACFPDLQHGYLVAWL VLDYTSDLLYLLDMVVRFHTGGFLEQGILVVDKGRISSRYVRTWSFFLDLASLMPTDVVYVRLGPHTPTLR LNRFLRAPRLFEAFDRTETRTAYPNAFRIAKLMLYIFVVIHWNSCLYFALSRYLGFGRDAWVYPDPAQPGF ERLRRQYLYSFYFSTLILTTVGDTPPPAREEEYLFMVGDFLLAVMGFATIMGSMSSVIYNMNTADAAFYPD HALVKKYMKLQHVNRKLERRVIDWYQHLQINKKMTNEVAILQHLPERLRAEVAVSVHLSTLSRVQIFQNCE ASLLEELVLKLQPQTYSPGEYVCRKGDIGQEMYIIREGQLAVVADDGITQYAVLGAGLYFGEISIINIKGG NMSGNRRTANIKSLGYSDLFCLSKEDLREVLSEYPQAQTIMEEKGREILLKMNKLDVNAEAAEIALQEATE SRLRGLDQQLDDLQTKFARLLAELESSALKIAYRIERLEWQTREWPMPEDLAEADDEGEPEEGTSKDEEGR ASQEGPPGPE

The full amino acid sequence of the protein of the invention was found to have 1068 of 1649 amino acid residues (64%) identical to, and 1068 of 1649 residues (64%) positive with, the 575 amino acid residue Cyclic-Nucleotide-Gated Olfactory Channel ocnc2 subunit protein from *Rattus norvegicus* (ptnr:SPTREMBL-ACC: Q64359) (E value = 5.5e-^{54}), and .292 of 556 amino acid residues (52%) identical to, and 404 of 556 residues (72%) positive with, the 694 amino acid residue Cone Photoreceptor cGMP-Gated Channel Alpha Subunit *Homo sapiens* (Human) (ptnr: TREMBLNEW -ACC: AAC17440) (E value = 5.8e-^{157})

MOL10b

In the present invention, the target sequence identified previously, MOL10a Accession Number GM98960647_A (also known as CG54557-01), was subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. Usually the resulting amplicons were gel purified, cloned and sequenced to high redundancy. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported below, which is designated MOL10b (Accession Number CG54557-02). This differs from the previously identified sequence [GM98960647_A (also known as CG54557-01)] at aminoacid position 159 T->A and has deletions at positions 22 R, 93 G and 426 G.

The disclosed novel MOL10b nucleic acid of 2551 nucleotides (also referred to as CG54557-02) is shown in Table 9D. An open reading frame begins with an ATG initiation codon at nucleotides 779-781 and ends with a TGA codon at nucleotides 2504-2506. A putative untranslated region upstream from the initiation codon and downstream from the termination codon are underlined in Table 10A, and the start and stop codons are in bold letters.

The nucleic acid sequence has 11625 of 1857 bases (87%) identical to a gb:GENBANK-ID:RNU12425|acc:U12425.1 mRNA from Rattus norvegicus (Rattus norvegicus olfactory cyclic nucleotide-gated channel mRNA, complete cds) (Expect = $4.0e^{-316}$).

Table 10D. MOL10b Nucleotide Sequence (SEQ ID NO:29)
GTTTTTGTTGTTTTGATATAGGAGATATTGAAGCAGGTTCACAAAAAGAGAAAAGTTGAAAGATTGGGGAC
CATAAAACACATGGAATGGTTGGTAGGATCAGGCACTAGAAGTCACAAGAAGGATATGAGGACAAAAGCAC
CATAGGATGGCCCCTATCACACTACCTATGAGAATGGTGTGATGGGGGAAGGCGTATGTGGAGGTAGATAA
GGGTAGGAAGTAGGTTACAAAAATAGAGCTCACTTCTCATGTGAGAGGCATCTCTTTGTCCCTGGAGAATA
GTTTAGCACCTGACATAGATAAGCCATTCAGTAATAGTTGTTAAATAAATAAATAGTGAGGCCCAAATAGA
ATTTGCAAAGATAAAACAGAGTGTTTGATCCTACACTAAAACTGAGGTCTTCTGACCCAGAGGACACCTAT
GTAGCTCAGTTGCTGTGGAAAGAGGGGAGGAGGAAAACAGAGACAAGACTCAGGCTTCCCTCTGAGGCATG
CACCCCCACCTTCTCCAGGGATCTCATTAGAGGTGTTTAGCTGGGCAGGTGTAAGCCCAGGCCCTGGGAGA
CAGGGCAGAGTGCTAGAGCTAGACTGTCTCCACCCCTTCAGTAGCGCTAGCTCTGGTTGTGTTGCTAAGAG
CCCCAAAGACAAAGAAGTCACAGCAGAAGCCCAACAGCAGCCTCCTTCAGGCAGTCAGGCACTAGTGCCCA
ACTCCAGAAGTCCCCTACAGGCAGAGAGGGTGTGGACATCTCACACCCCAGCACCAGACCACAGAACCATG
AGCCAGGACACCAAAGTGAAGACAACAGAGTCCAGTCCCCCAGCCCCATCCAAGGCCAGGAAGTTGCTGCC
TGTCCTGGACCCATCTGGGGATTACTACTACTGGTGGCTGAACACAATGGTCTTCCCAGTCATGTATAACC
TCATCATCCTCGTGTGCAGAGCCTGCTTCCCCGACTTGCAGCACGGTTATCTGGTGGCCTGGTTGGTGCTG
GACTACACGAGTGACCTGCTATACCTACTAGACATGGTGGTGCGCTTCCACACAGGATTCTTGGAACAGGG
CATCCTGGTGGTGGACAAGGGTAGGATCTCGAGTCGCTACGTTCGCACCTGGAGTTTCTTCTTGGACCTGG
CTTCCCTGATGCCCACAGATGTGGTCTACGTGCGGCTGGGCCCGCACACACCCACCCTGAGGCTGAACCGC
TTTCTCCGCGCGCCCCGCCTCTTCGAGGCCTTCGACCGCGCAGAGACCCGCACAGCTTACCCAAATGCCTT
TCGCATTGCCAAGCTGATGCTTTACATTTTTGTCGTCATCCATTGGAACAGCTGCCTATACTTTGCCCTAT
CCCGGTACCTGGGCTTCGGGCGTGACGCATGGGTGTACCCGGACCCCGCGCAGCCTGGCTTTGAGCGCCTG
CGGCGCCAGTACCTCTATAGCTTTTACTTCTCCACGCTGATACTGACTACAGTGGGCGATACACCGCCGCC
AGCCAGGGAAGAAGAGTACCTCTTCATGGTGGGCGACTTCCTGCTGGCCGTCATGGGTTTCGCCACCATCA
TGGGTAGCATGAGCTCTGTCATCTACAACATGAACACTGCAGATGCGGCTTTCTACCCAGATCATGCACTG
GTGAAGAAGTACATGAAGCTGCAGCACGTCAACCGCAAGCTGGAGCGGCGAGTTATTGACTGGTATCAGCA
CCTGCAGATCAACAAGAAGATGACCAACGAGGTAGCCATCTTACAGCACTTGCCTGAGCGGCTGCGGGCAG
AAGTGGCTGTGTCTGTGCACCTGTCCACTCTGAGCCGGGTGCAGATCTTTCAGAACTGTGAGGCCAGCCTG
CTGGAGGAGCTGGTGCTGAAGCTGCAGCCCCAGACCTACTCACCAGGTGAATATGTATGCCGCAAAGGAGA

CATTGGCCAAGAGATGTACATCATCCGAGAGGGTCAACTGGCCGTGGTGGCAGATGATGGTATCACACAGT ATGCTGTGCTCGGTGCAGGGCTCTACTTTGGGGAGATCAGCATCATCAACATCAAAGGGAACATGTCTGGG AACCGCCGCACAGCCAACATCAAGAGCCTAGGTTATTCAGACCTATTCTGCCTGAGCAAGGAGGACCTGCG GGAGGTGCTGAGCGAGTATCCACAAGCACAGACCATCATGGAGGAGAAAGGACGTGAGATCCTGCTGAAAA TGAACAAGTTGGACGTGAATGCTGAGGCAGCTGAGATCGCCCTGCAGGAGGCCACAGAGTCCCGGCTACGA GGCCTAGACCAGCAGCTGGATGATCTACAGACCAAGTTTGCTCGCCTCCTGGCTGAGCTGGAGTCCAGCGC ACTTAAGATTGCTTACCGCATTGAACGGCTGGAGTGGCAGACTCGAGAGTGGCCAATGCCCGAGGACCTGG CTGAGGCTGATGACGAGGGTGAGCCTGAGGAGGGAACTTCCAAAGATGAAGAGGGCAGGGCCAGCCAGGAG GGACCCCCAGGTCCAGAGTGACCCCATCCCCATCCCCAGGATTCCCACCTCCTAGTGAATCCAGAG

The MOL9a protein encoded by SEQ ID NO:29 has 575 amino acid residues, and is presented using the one-letter code in Table 10B (SEQ ID NO:30). PSORT analysis predicts the protein of the invention to be localized in the plasma membrane with a certainty of 0. 6000. Using the SIGNALP analysis, it is predicted that the protein of the invention has a signal peptide with most likely cleavage site between positions 56 and 57 (CRA-CF)

Table 10E. Encoded MOL10b protein sequence (SEQ ID NO:30)
MSQDTKVKTTESSPPAPSKARKLLPVLDPSGDYYYWWLNTMVFPVMYNLIILVCRACFPDLQHGYLVAWLV LDYTSDLLYLLDMVVRFHTGFLEQGILVVDKGRISSRYVRTWSFFLDLASLMPTDVVYVRLGPHTPTLRLN RFLRAPRLFEAFDRAETRTAYPNAFRIAKLMLYIFVVIHWNSCLYFALSRYLGFGRDAWVYPDPAQPGFER LRRQYLYSFYFSTLILTTVGDTPPPAREEEYLFMVGDFLLAVMGFATIMGSMSSVIYNMNTADAAFYPDHA LVKKYMKLQHVNRKLERRVIDWYQHLQINKKMTNEVAILQHLPERLRAEVAVSVHLSTLSRVQIFQNCEAS LLEELVLKLQPQTYSPGEYVCRKGDIGQEMYIIREGQLAVVADDGITQYAVLGAGLYFGEISIINIKGNMS GNRRTANIKSLGYSDLFCLSKEDLREVLSEYPQAQTIMEEKGREILLKMNKLDVNAEAAEIALQEATESRL RGLDQQLDDLQTKFARLLAELESSALKIAYRIERLEWQTREWPMPEDLAEADDEGEPEEGTSKDEEGRASQ EGPPGPE

The full amino acid sequence of the protein of the invention was found to have 536 of 575 amino acid residues (93%) identical to, and 552 of 575 amino acid residues (96%) similar to, the 575 amino acid residue ptnr:SWISSPROT-ACC:Q64359 protein from Rattus norvegicus (Rat) (CYCLIC-NUCLEOTIDE-GATED OLFACTORY CHANNEL OCNC2 SUBUNIT) (E value = $4.2e^{-287}$)

Chromosomal information:

The Cyclic-nucleotide gated olfactory channel ocnc2 disclosed in this invention maps to chromosome 11. This information was assigned using OMIM, the electronic northern bioinformatic tool implemented by CuraGen Corporation, public ESTs, public literature references and/or genomic clone homologies. This was executed to derive the chromosomal mapping of the SeqCalling assemblies, Genomic clones, literature references and/or EST sequences that were included in the invention.

Tissue expression

The Cyclic-nucleotide gated olfactory channel ocnc2 disclosed in this invention is expressed in at least the following tissues: Adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain - whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea, uterus. . This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, and/or RACE sources.

In addition, the sequence is predicted to be expressed in the following tissues because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:RNU12425|acc:U12425.1) a closely related Rattus norvegicus olfactory cyclic nucleotide-gated channel mRNA, complete cds homolog in species Rattus norvegicus : olfactory neuroepithelium.

These materials are further useful in the generation of antibodies that bind immuno-specifically to the novel MOL10b substances for use in therapeutic or diagnostic methods. These antibodies may be generated according to methods known in the art, using prediction from hydrophobicity charts, as described in the "Anti-MOLX Antibodies" section below. For example the disclosed MOL10b protein has multiple hydrophilic regions, each of which can be used as an immunogen. In one embodiment, a contemplated MOL10b epitope is from about amino acids 25 to 75. In another embodiment, a MOL10b epitope is from about amino acids 1 to 30. In further embodiments, MOL10b epitopes are found in amino acids 150-250, 275-350, 375-400. and 425-560. These novel proteins can also be used to develop assay system for functional analysis.

Homology between the MOL10 isoforms and other homologous proteins is presented graphically in the multiple sequence alignment given in Table 9I (with MOL10a being shown on line 1 and MOL10b on line 2) as a ClustalW analysis comparing MOL10 with related protein sequences.

Table 10C. Information for the ClustalW proteins:

1) MOL10a (SEQ ID NO:28)
2) MOL10b (SEQ ID NO:30)
3) S35691 cyclic nucleotide-gated channel protein - rabbit (SEQ ID NO:73)
4) Q64359 Cyclic-Nucleotide-Gated Olfactory Channel ocnc2 subunit protein from *Rattus norvegicus* (SEQ ID NO:74)
5) AAC17440 Cone Photoreceptor cGMP-Gated Channel Alpha Subunit *Homo sapiens* (SEQ ID NO:75)

```
                    10         20         30         40         50         60
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  ---------- ---------- ---------- ---------- ---------- ----------  1
MOL10b Pro  ---------- ---------- ---------- ---------- ---------- ----------  1
S35691      MSSWRSCARA PLSGSAWRRS AATRRSRRCL KTKRKRWSSG KGTPMQSTQC ETRRRAQTPC  60
Q64359      ---------- ---------- ---------- ---------- ---------- ----------  1
AAC17440    MAKINTQYSH P-S----RTH LKVKTSDRDL NRAENGLSRA HSS---SEET SSVLQPGIAM  52

                    70         80         90        100        110        120
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  ---------- ---------- ---------- ---------- MSQDT----- ----------  5
MOL10b Pro  ---------- ---------- ---------- ---------- MSQDT----- ----------  5
S35691      ESTGHTWRMT EKSNGVKSSP ANNHNNHVPA TIKANGKDES RTRSR-PQSA ADDDTSSELQ  119
Q64359      ---------- ---------- ---------- ---------- MSQDG----- ----------  5
AAC17440    ETRG----LA DSGQGSFTGQ GIARLSRLIF LLRRWAARHV HHQDQGPDSF PDRFRGAELK  108

                   130        140        150        160        170        180
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  KVKTTESSPP ---------- ---------- ----APSKAR RKLLP----- ----------  26
MOL10b Pro  KVKTTESSPP ---------- ---------- ----APSKAR -KLLP----- ----------  25
S35691      RLAEMDAPQQ RRGGFRRIVR LVGVIRQWAN RNFREEEARP DSFLERFRGP ELQTVTTQQG  179
Q64359      KVKTTESTPP ---------- ---------- ----APTKAR -KWLP----- ----------  25
AAC17440    EVSSQESNAQ ---------- --------AN VGSQEPADRG RSAWP----- -LAKCNTNTS  144

                   190        200        210        220        230        240
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  ---------- ---------- VLDPSGDYYY WWLNTMVFPV MYNLIILVCR ACFPDLQHGY  66
MOL10b Pro  ---------- ---------- VLDPSGDYYY WWLNTMVFPV MYNLIILVCR ACFPDLQHGY  65
S35691      DGKGDKDGDG KGTKKKFELF VLDPAGDWYY RWLFVIAMPV LYNWCLLVAR ACFSDLQRGY  239
Q64359      ---------- ---------- VLDPSGDYYY WWLNTMVFPI MYNLIIVVCR ACFPDLQHSY  65
AAC17440    NNTEEE---- KKTKKK-DAI VVDPSSNLYY RWLTATALPV FYNWYLLICR ACFDELQSEY  199

                   250        260        270        280        290        300
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  LVAWLVLDYT SDLLYLLDMV VRFHTGGFLE QGILVVDKGR ISSRYVRTWS FFLDLASLMP  126
MOL10b Pro  LVAWLVLDYT SDLLYLLDMV VRFHTG-FLE QGILVVDKGR ISSRYVRTWS FFLDLASLMP  124
S35691      FLVWLVLDYF SDVVYIADLF IRLRTG-FLE QGLLVKDPKK LRDNYIHTLQ FKLDVASIIP  298
Q64359      LVAWFVLDYT SDLLYLLDIG VRFHTG-FLE QGILVVDKGM IASRYVRTWS FLLDLASLVP  124
AAC17440    LMLWLVLDYS ADVLYVLDVL VRARTG-FLE QGLMVSDTNR LWQHYKTTTQ FKLDVLSLVP  258

                   310        320        330        340        350        360
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  TDVVYVRLGP HTPTLRLNRF LRAPRLFEAF DRTETRTAYP NAFRIAKLML YIFVVIHWNS  186
MOL10b Pro  TDVVYVRLGP HTPTLRLNRF LRAPRLFEAF DRAETRTAYP NAFRIAKLML YIFVVIHWNS  184
S35691      TDLIYFAVGI HNPELRFNRL LHFARMFEFF DRTETRTSYP NIFRISNLVL YILVIIHWNA  358
Q64359      TDAAYVQLGP HIPTLRLNRF LRVPRLFEAF DRTETRTAYP NAFRIAKLML YIFVVIHWNS  184
AAC17440    TDLAYLKVGT NYPEVRFNRL LKFSRLFEFF DRTETRTNYP NMFRIGNLVL YILIIIHWNA  318

                   370        380        390        400        410        420
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  CLYFALSRYL GFGRDAWVYP DPAQPGFERL RRQYLYSFYF STLILTTVGD TPPPAREEEY  246
MOL10b Pro  CLYFALSRYL GFGRDAWVYP DPAQPGFERL RRQYLYSFYF STLILTTVGD TPPPAREEEY  244
S35691      CIYYAISKSI GFGVDTWVYP NITDPEYGYL AREYIYCLYW STLTLTTIGE TPPPVKDEEY  418
Q64359      CLYFALSRYL GFGRDAWVYP DPAQPGFERL RRQYLYSFYF STLILTTVGD TPLPDREEEY  244
AAC17440    CIYFAISKFI GFGTDSWVYP NISIPEHGRL SRKYIYSLYW STLTLTTIGE TPPPVKDEEY  378

                   430        440        450        460        470        480
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  LFMVGDFLLA VMGFATIMGS MSSVIYNMNT ADAAFYPDHA LVKKYMKLQH VNRKLERRVI  306
MOL10b Pro  LFMVGDFLLA VMGFATIMGS MSSVIYNMNT ADAAFYPDHA LVKKYMKLQH VNRKLERRVI  304
S35691      LFVIFDFLIG VLIFATIVGN VGSMISNMNA TRAEFQAKID AVKHYMQFRK VSKEMEAKVI  478
Q64359      LFMVGDFLLA VMGFATIMGS MSSVIYNMNT ADAAFYPDHA LVKKYMKLQH VNKRLERRVI  304
AAC17440    LFVVVDFLVG VLIFATIVGN VGSMISNMNA SRAEFQAKID SIKQYMQFRK VTKDLETRVI  438

                   490        500        510        520        530        540
```

```
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  DWYQHLQINK KMTNEVAILQ HLPERLRAEV AVSVHLSTLS RVQIFQNCEA SLLEELVLKL  366
MOL10b Pro  DWYQHLQINK KMTNEVAILQ HLPERLRAEV AVSVHLSTLS RVQIFQNCEA SLLEELVLKL  364
S35691      KWFDYLWTNK KTVDEREVLK NLPAKLRAEI AINVHLSTLK KVRIFQDCEA GLLVELVLKL  538
Q64359      DWYQHLQINK KMTNEVAILQ HLPERLRAEV AVSVHLSTLS RVQIFQNCEA SLLEELVLKL  364
AAC17440    RWFDYLWANK KTVDEKEVLK SLPDKLKAEI AINVHLDTLK KVRIFQDCEA GLLVELVLKL  498

                   550        560        570        580        590        600
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  QPQTYSPGEY VCRKGDIGQE MYIIREGQLA VVADDGITQY AVLGAGLYFG EISIINIKGG  426
MOL10b Pro  QPQTYSPGEY VCRKGDIGQE MYIIREGQLA VVADDGITQY AVLGAGLYFG EISIINIKG-  423
S35691      RPQVFSPGDY ICRKGDIGKE MYIIKEGKLA VVADDGVTQY ALLSAGSCFG EISILNIKG-  597
Q64359      QPQTYSPGEY VCRKGDIGRE MYIIREGQLA VVADDGVTQY AVLGAGLYFG EISIINIKG-  423
AAC17440    RPTVFSPGDY TCKKGDIGKE MYIINEGKLA VVADDGVTQF VVLSDGSYFG EISILNIKG-  557

                   610        620        630        640        650        660
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  NMSGNRRTAN IKSLGYSDLF CLSKEDLREV LSEYPQAQTI MEEKGREILL KMNKLDVNAE  486
MOL10b Pro  NMSGNRRTAN IKSLGYSDLF CLSKEDLREV LSEYPQAQTI MEEKGREILL KMNKLDVNAE  483
S35691      SKMGNRRTAN IRSLGYSDLF CLSKDDLMEA VTEYPDAKKV LEERGREILM KEGLLDENEV  657
Q64359      NMSGNRRTAN IKSLGYSDLF CLSKEDLREV LSEYPQAQAV MEEKGREILL KMNKLDVNAE  483
AAC17440    SKSGNRRTAN IRSIGYSDLF CLSKDDLMEA LTEYPEAKKA LEEKGRQILM KDNLIDEELA  617

                   670        680        690        700        710        720
            ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
MOL10a Pro  AAEIALQEAT ESRLRGLDQQ LDDLQTKFAR LLAELESSAL KIAYRIERLE WQTREWPMPE  546
MOL10b Pro  AAEIALQEAT ESRLRGLDQQ LDDLQTKFAR LLAELESSAL KIAYRIERLE WQTREWPMPE  543
S35691      AASMEV-DVQ EK-LKQLETN METLYTRFGR LLAEYTGAQQ KLKQRITVLE VKMKQNTEDD  715
Q64359      AAEIALQEAT ESRLKGLDQQ LDDLQTKFAR LLAELESSAL KIAYRIERLE WQTREWPMPE  543
AAC17440    RAGADPKDLE EK-VEQLGSS LDTLQTRFAR LLAEYNATQM KMKQRLSQLE SQVKG-GGDK  675

                   730        740        750
            ....|....| ....|....| ....|....| ..
MOL10a Pro  DLAEADDEGE PEEGTSKDEE GRASQEGPPG PE  578
MOL10b Pro  DLAEADDEGE PEEGTSKDEE GRASQEGPPG PE  575
S35691      YLSDGMNSPE PAAAEQP--- ---------- --  732
Q64359      DMGEADDEAE PGEGTSKDGE GKAGQAGPSG IE  575
AAC17440    PLADGEVPGD ATKTEDKQQ- ---------- --  694
```

Cyclic nucleotide-gated (CNG) channels play central roles in visual and olfactory signal transduction. In the retina, rod photoreceptors express the subunits CNCalpha1 and CNCbeta1a. In cone photoreceptors, only CNCalpha2 expression has been demonstrated so far. Rat olfactory sensory neurons (OSNs) express two homologous subunits, here designated CNCalpha3 and CNCalpha4. This paper describes the characterization of CNCbeta1b, a third subunit expressed in OSNs and establishes it as a component of the native channel. CNCbeta1b is an alternate splice form of the rod photoreceptor CNCbeta1a subunit. Analysis of mRNA and protein expression together suggest co-expression of all three subunits in sensory cilia of OSNs. From single-channel analyses of native rat olfactory channels and of channels expressed heterologously from all possible combinations of the CNCalpha3, -alpha4, and -beta1b subunits, we conclude that the native CNG channel in OSNs is composed of all three subunits. Thus, CNG channels in both rod photoreceptors and olfactory sensory neurons result from coassembly of specific alpha subunits with various forms of an alternatively spliced beta subunit.

Phototransduction is mediated by an enzymatic cascade that ultimately leads to the hydrolysis of cGMP. The photoreceptor cells, rods and cones, integrate and respond to cGMP hydrolysis via a cGMP-gated cation channel in the plasma membrane of the outer segment. Kaupp et al. (1989) cloned this channel from bovine retina. Dhallan et al. (1991) used the bovine sequence to isolate cDNA and genomic DNA encompassing the entire protein coding region of the human homolog. Assignment to chromosome 4 was achieved by study of somatic cell hybrids. Pittler et al. (1992) determined the primary structures of the human and mouse retinal rod cGMP-gated cation channel by analysis of cDNA clones and amplified DNA. The open reading frames predicted polypeptides of 690 and 683 residues, respectively, exhibiting 88% sequence similarity. Significant sequence similarity (59%) of the visual cGMP-gated channel to the olfactory cAMP-gated channel was pointed out. The RNA transcript was found to be 3.2 kb long in human, mouse, and dog. By PCR used in connection with somatic cell hybrid DNAs, Pittler et al. (1992) mapped the CNCG gene to 4p14-q13 near the centromere. By interspecific backcross haplotype analysis, the corresponding gene in the mouse, Cncg, was mapped to a site 0.9 cM proximal to the Kit locus on chromosome 5. Griffin et al. (1993) mapped the CNCG1 gene to 4p12-cen by fluorescence in situ hybridization. It is noteworthy that the rod cGMP PDE beta polypeptide (PDEB; 180072) also maps to 4p, at 4p16.3.

Uses of the Compositions of the Invention

The protein similarity information, expression pattern, and map location for MOL10 suggest that it may have important structural and/or physiological functions characteristic of the Cyclic-nucleotide gated channel family. Therefore, the nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration in vitro and in vivo (vi) biological defense weapon.

The nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications implicated in various diseases and disorders described below and/or other pathologies. For example, the compositions of the present invention will have efficacy for treatment of patients suffering from:

color blindness, CNS developmental disorders and other diseases, disorders and conditions of the like.

These materials are further useful in the generation of antibodies that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

A summary of the MOLX nucleic acids and proteins of the invention is provided in Tables 11 and 11X.

TABLE 11: Summary Of Nucleic Acids And Proteins Of The Invention

Name	Tables	Clone; Description of Homolog	Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO
MOL1a	1A, 1B,	MOL1a: GM_79960178	1	2
MOL1b	1C, 1D	MOL1b: CG54674-02	114	115
MOL1c	1E, 1F	MOL1c: 248587042	116	117
MOL1d	1G, 1H	MOL1d: 248651580	118	119
MOL1e	1I, 1K	MOL1e: 255304731	120	122
MOL1f	1L, 1M	MOL1f: 255304783	123	124
MOL1g	1N, 1P	MOL1g: 255341675	125	127
MOL1h	1Q, 1R	MOL1h: 248210503	128	129
MOL1i	1S, 1T	MOL1i: 248210481	130	131
MOL1j	1U, 1V	MOL1j: 248210473	132	133
MOL1k	1W, 1X	MOL1k: 248210474	134	135
MOL1l	1Y, 1Z	MOL1l: 246484229	136	137
MOL1m	1AAA, 1AAC	MOL1m: 258065840	158	159
MOL1n	1AAD, 1AAE	MOL1n: 263483006	160	161
MOL1o	1AAF, 1AAG	MOL1o: CG54674-01	162	163
MOL1p	1AAH, 1AAJ	MOL1p: 263676346	164	165
MOL1q	1AAK, 1AAM	MOL1q: 264289162	166	167
MOL1r	1AAN, 1AAO	MOL1r: 248651580	168	169
MOL1s	1AAP, 1AAR	MOL1s: 255304731	170	171
MOL1t	1AAS, 1AAT	MOL1t: 255304783	172	173
MOL1u	1AAU, 1AAW	MOL1u: 255341675	174	175
MOL2a	2A, 2B	MOL2a: 20466828_EXT1	3	4
MOL2b	2C, 2D	MOL2b: CG51424-02	138	139
MOL3	3A, 3B	MOL3: 82254077.0.1	5	6
MOL4a	4A, 4B	MOL4a: AC004826	7	8
MOL4b	4C, 4D	MOL4b: CG53138-05	140	141
MOL4c	4E, 4F	MOL4c: CG53138-06	142	143
MOL4d	4G, 4H	MOL4d: CG53138-04	144	145
MOL4e	4I, 4J	MOL4e: 251445570	146	147
MOL4f	4K, 4L	MOL4f: 250059708	148	149
MOL4g	4M, 4N	MOL4g: 246861879	150	151
MOL5	5A, 5B,	MOL5: AC025535	9	10
MOL6	6A, 6B	MOL6a: GM_87760758_A	11	12
	6C, 6D	NOV6b: CG54548-03	152	153
	6E, 6F	MOL6c: 246861979	154	155
	6G, 6H	MOL6d: 246862070	156	157
	6J, 6K	MOL6e: GM_87760758_A_da	13	14
	6BBA, 6BBB	MOL6f: 256801454	176	177
MOL7	7A, 7B	MOL7: 30675745.0.499	15	16

MOL8	8A, 8B	MOL8a: 11800699-0-16	17	18
	8D, 8E	MOL8b: CG56222-01	19	20
MOL9	9A, 9B	MOL9a: 19506719_B_EXT	21	22
	9D, 9E	MOL9b: 19506719_B_EXT-S773	23	24
	9F, 9G	MOL9c: CG56222-01	25	26
MOL10	10A, 10B	MOL10a GM98960647_A	27	28
	10D, 10E	MOL10b CG54557-02	29	30

TABLE 11X. Sequences and Corresponding SEQ ID Numbers

MOLX Assignment	Internal Identification	SEQ ID NO (nucleic acid)	SEQ ID NO (polypeptide)	Homology
11	2396e7_clone	183	184	Chloride ion channel
12	Cit978skb_139p6_A	185	186	Fatty acid-binding protein (FABP)
13	94115520_EXT	187	188	Insulin-like growth factor
14	GB_ACC#360_L_9_A	189	190	Cytokeratin-18
15	21426654_EXT	191	192	Metallocarboxypeptidase
16	AL031704_A	193	194	Mast cell protease-6
17	71768093_A	195	196	Sulfate anion transporter
18	416_d_14_A	197	198	Cytostatin
19	416_d_14_B	199	200	Cytostatin
20	GM_38019075_A	201	202	Chemokine receptor
21	CG54656-05	203	204	Chemokine receptor
22	32338334_1	205	206	Carboxypeptidase

MOL11 is homologous to members of the chloride channel family of proteins that are important in maintaining physiological ion balance and neuronal signal transduction. Thus, the MOL11 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders characterized by altered ion regulation and neural signaling, *e.g.* cystic fibrosis, arrythmia seen in long QT syndrome, Dent's disease, Bartter's syndrome, bronchitis and sinusitis.

Also, MOL12 is homologous to a family of fatty acid-binding proteins important in keratinocyte differentiation. Thus MOL12 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders characterized by aberrant keratinocyte differentiation, *e.g.* squamous cell carcinoma and lesional psoriatic skin.

Further, MOL13 is homologous to a family of insulin-like growth factor-binding proteins important in cell proliferation and differentiation. Thus, the MOL13 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in proliferative and apoptotic disorders, *e.g.* cancer, Alzheimer's disease, and obesity.

Also, MOL14 is homologous to the cytokeratin-18 family of proteins important in cytoskeletal stability in keratinocytes and other cell types. Thus, MOL14 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders of the liver, pancreas and intestine, *e.g.* chronic hepatitis and drug-induced hepatotoxicity.

Additionally, MOL15 and MOL22 are homologous to the carboxypeptidase family of proteins important in peptide processing. Thus MOL15 and MOL22 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in metabolic disorders of the pancreas, *e.g.* acute pancreatitis.

Also, MOL16 is homologous to the mast cell protease-6 family of proteins important in mast cell activation and migration. Thus MOL16 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders of the immune system, *e.g.* infectious inflammatory peritonitis.

Further, MOL17 is homologous to members of the sulfate anion channel family of proteins that are important in maintaining physiological ion balance and neuronal signal transduction. Thus, the MOL17 nucleic acids, polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders characterized by altered sulfate anion regulation and neural signaling, *e.g.* Pendred syndrome, diastrophic dysplasia and other skeletal dysplasias.

Still further, MOL18-19 are homologous to a family of cytostatin-like proteins that are important in modulation of cell shape and motility by controlling cell interactions with the extracellular matrix. Thus, MOL18-19 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders characterized by altered cell shape, motility, and apoptosis, *e.g.* cancer and ischemic injury.

Finally, MOL20-21 are homologous to the chemokine receptor family of proteins that are important in neuronal signal transduction and lymphocyte chemoattraction. Thus, MOL20-21 nucleic acids and polypeptides, antibodies and related compounds according to the invention will be useful in therapeutic and diagnostic applications in disorders characterized by altered immune response to injury and infection, *e.g.* AIDS, acute lung injury, adult respiratory distress syndrome, and multiple sclerosis.

MOL11

A MOL11 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the chloride channel family of proteins. A MOL11 nucleic acid is found on human chromosome 19. A MOL11 nucleic acid and its encoded polypeptide includes the sequences shown in Table 11A. The disclosed nucleic acid (SEQ ID NO:183) is 739 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 1-3 and ends with a TAA stop codon at nucleotides 737-739. The representative ORF encodes a 246 amino acid polypeptide (SEQ ID NO:184) with a predicted molecular weight of 28,017.3 daltons (Da). PSORT analysis of a MOL11 polypeptide predicts a plasma membrane protein with a certainty of 0.7900. SIGNALP analysis suggests the presence of a signal peptide with the most likely cleavage site occuring between positions 53 and 54 in SEQ ID NO.: 184.

TABLE 11A.

ATGGCATTGTCGATGCCACTGAACAAGTTGAAGGAGGAAGACAAAGAGCCCCT
CCTTGAGCTCTGGGTCAAGGCTGTCAGTGATGGTGAAAGCACAGGAATCTGCC
TTTTTCCCAGAGATTCCTCATGATTCTTTGGCTCAAAGGAGTTGTCTTCAGTGT
CACAACTGTTGATCTGAAAAGGAAACCTGCAGATCTGCAAAACAAGGCTCCTG
GGAACCACCCACCACTTATAACTTCAACAGTGAAGTCAAATAAGATTGAGGAA
GCTCCTGAAGAAGTCTTATGTCCTCCCAAGTACTTAAAGCTTTCACCAAAACAC
CCAGAATCAAATACTGCTGGAATGGACATCTTTGCCAAATTCTCTGCATACATC
AAGAATTCAAGGCCAGAGGTTAATGAAGCATTAGTGAAGCATCTCTTAAAAAC
CCTGCAGAAAATGGAATATCTGAATTCTCCTCTCCCTGATGAAATTGATGAAAA
TAGCATGCAGGACACTAAGTTTTCTACACATAAATTTCTGAATGGCAATAAAAT
GGCATTAGCTGATTGCCATCTGCTGCCCAAACTGCATATTGTCAAAAAAAAAG
AAAAATATAGAAAATATAAAAATATAGAAAAAAAAGGAATGACTGGCATCTG
GAGATACCTAACGAATACAAGTAGTAGGGATATGTTCAACAATACCTGTCCCA
ATGATAAAGAGATTGAAATAGCAGCAGAAACAGTTAATGTAG**TAA** (SEQ ID
NO.: 183)

MALSMPLNKLKEEDKEPLLELWVKAVSDGESTGICLFSQRFLMILWLKGVVFSVT
TVDLKRKPADLQNKAPGNHPPLITSTVKSNKIEEAPEEVLCPPKYLKLSPKHPESN
TAGMDIFAKFSAYIKNSRPEVNEALVKHLLKTLQKMEYLNSPLPDEIDENSMQDT
KFSTHKFLNGNKMALADCHLLPKLHIVKKKEKYRKYKNIEKKGMTGIWRYLTNT
SSRDMFNNTCPNDKEIEIAAETVNVV (SEQ ID NO.: 184)

A MOL11 nucleic acid has a high degree of homology (92% identity) with a human chloride channel protein P64-like mRNA (CC64; GenBank Accession No.:

AK001624), as is shown in Table 11B. A MOL11 polypeptide also has homology (78% identity, 85% similarity) with an intracellular human chloride channel polypeptide (ICCP; EMBL Accession No.: AAF19055), as is shown in Table 11C.

TABLE 11B.

```
MOL11: 252 aaataagattgaggaagctcctgaagaagtcttatgtcctcccaagtacttaaagctttc 311
           ||||||||||||||||  || ||||||||||||||| |||||||||||||||||||||||
CC64:  436 aaataagattgaggaatttcttgaagaagtcttatgccctcccaagtacttaaagctttc 495

MOL11: 312 accaaaacacccagaatcaaatactgctggaatggacatctttgccaaattctctgcata 371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CC64:  496 accaaaacacccagaatcaaatactgctggaatggacatctttgccaaattctctgcata 555

MOL11: 372 catcaagaattcaaggccagaggttaatgaagcattagtgaagcatctcttaaaaccct 431
            |||||||||||||||||||||| |||||||||| | | || |  |||| | ||||||||
CC64:  556 tatcaagaattcaaggccagaggctaatgaagcactggagaggggtctcctgaaaaccct 615

MOL11: 432 gcagaaaatg---gaatatctgaattctcctctccctgatgaaattgatgaaaatagcat 488
           ||||||| ||   |||||||||||||||||||||||||||||||||||||||||||| ||
CC64:  616 gcagaaactggatgaatatctgaattctcctctccctgatgaaattgatgaaaatagtat 675

MOL11: 489 gcaggacactaagttttctacacataaatttctgaatggcaataaaatggcattagctga 548
           | ||||||  ||||||||||||| |||||||||| |||||||| ||||| ||||||||||
CC64:  676 ggaggacataaagttttctacacgtaaatttctggatggcaatgaaatgacattagctga 735

MOL11: 549 ttgccatctgctgcccaaactgcatattgtc 579 (SEQ ID NO.: 207)
           |||| | ||||||||||||||||||||||||
CC64:  736 ttgcaacctgctgcccaaactgcatattgtc 766 (SEQ ID NO.: 208)
```

TABLE 11C.

```
MOL11:   1 MALSMPLNKLKEEDKEPLLELWVKAVSDGESTGICLFSQRFLMILWLKGVVFSVTTVDLK 60
           |||||||| |||||||||+||+||| ||||| | | ||||  ||||||||||||||||||
ICCP:    1 MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMILWLKGVVFSVTTVDLK 60

MOL11:  61 RKPADLQNKAPGNHPPLIT--STVKS--NKIEEAPEEVLCPPKYLKLSPKHPESNTAGMD 116
           |||||||| ||| ||| ||  | ||+  |||||  |||||||||||||||||||||||||
ICCP:   61 RKPADLQNLAPGTHPPFITFNSEVKTDVNKIEEFLEEVLCPPKYLKLSPKHPESNTAGMD 120

MOL11: 117 IFAKFSAYIKNSRPEVNEALVKHLLKTLQKM-EYLNSPLPDEIDENSMQDTKFSTHKFLN 175
           ||||||||||||||| |||| + |||||||+ ||||||||||||||||+| |||| +||+
ICCP:  121 IFAKFSAYIKNSRPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTRRFLD 180

MOL11: 176 GNKMALADCHLLPKLHIVKKKEKYRKYKNIE-KKGMTGIWRYLTNTSSRDMFNNTCPNDK 234
           |++| ||||+|||||||||   |  ||+| +  ||||||||||||  ||| | ||||+||
ICCP:  181 GDEMTLADCNLLPKLHIVKVVAK--KYRNFDIPKGMTGIWRYLTNAYSRDEFTNTCPSDK 238

MOL11: 235 EIEIAAETVNVV 246 (SEQ ID NO.: 184)
           |+|||   |
ICCP:  239 EVEIAYSDV 247 (SEQ ID NO.: 209)
Where | indicates identity and + indicates similarity.
```

Transporters, channels, and pumps that reside in cell membranes are key to maintaining the right balance of ions in cells, and are vital for transmitting signals from nerves to tissues. The consequences of defects in ion channels and transporters are diverse, depending on where they are located and what their cargo is. In the heart, defects in potassium channels do not allow proper transmission of electrical impulses, resulting in the arrythmia seen in long QT syndrome. In the lungs, failure of a sodium and chloride transporter found in epithelial cells leads to the congestion of cystic fibrosis, while one of the most common inherited forms of deafness, Pendred syndrome, looks to be associated with a defect in a sulphate transporter.

Chloride channels (CLC) perform important roles in the regulation of cellular excitability, in transepithelial transport, cell volume regulation, and acidification of intracellular organelles. This variety of functions requires a large number of different chloride channels that are encoded by genes belonging to several unrelated gene families. The CLC family of chloride channels has nine known members in mammals that show a differential tissue distribution and function both in plasma membranes and in intracellular organelles. CLC proteins have about 10-12 transmembrane domains. They probably function as dimers and may have two pores. The functional expression of channels altered by site-directed mutagenesis has led to important insights into their structure-function relationship. Their physiological relevance is obvious from three human inherited diseases (myotonia congenita, Dent's disease and Bartter's syndrome) that result from mutations in some of their members and from a knock-out mouse model (See Jentsch *et al.*,1999, Pflugers Arch. **437**:783).

Recent studies of hereditary renal tubular disorders have facilitated the identification and roles of chloride channels and cotransporters in the regulation of the most abundant anion, Cl-, in the ECF. Thus, mutations that result in a loss of function of the voltage-gated chloride channel, CLC-5, are associated with Dent's disease, which is characterized by low-molecular weight proteinuria, hypercalciuria, nephrolithiasis, and renal failure. Mutations of another voltage-gated chloride channel, CLC-Kb, are associated with a form of Bartter's syndrome, whereas other forms of Bartter's syndrome are caused by mutations in the bumetanide-sensitive sodium-potassium-chloride cotransporter (NKCC2) and the potassium channel, ROMK. Finally, mutations of the thiazide-sensitive sodium-chloride cotransporter (NCCT) are associated with Gitelman's syndrome (See Thakker,1999, Adv Nephrol. Necker Hosp. **29**:289). These studies have helped to elucidate some of the renal tubular mechanisms regulating mineral homeostasis and the role of chloride channels.

A more prominent case of chloride channel dysfunction is cystic fibrosis. Cystic fibrosis (CF) is a genetic disease with multisystem involvement in which defective chloride transport across membranes causes dehydrated secretions. Cystic fibrosis (CF) affects approximately 1 in 2000 people making it one of the commonest fatal, inherited diseases in the Caucasian population. Dysfunction of the cystic fibrosis transmembrane conductance regulator (CFTR) Cl- channel is also associated with a wide spectrum of diseases (See Hwang & Sheppard, 1999, Trends Pharmacol. Sci. **20**:448). The protein encoded by the CF gene, the cystic fibrosis transmembrane conductance regulator (CFTR), functions as a cyclic adenosine monophosphate-regulated chloride channel. The ability to detect CFTR mutations has led to the recognition of its association with a variety of conditions, including chronic bronchitis, sinusitis with nasal polyps, pancreatitis, and, in men, infertility (Choudari *et al*, 1999, Gastroenterol. Clin. North Am. **28**:543). In the search for modulators of CFTR, pharmacological agents that interact directly with the CFTR Cl- channel have been identified. Some agents stimulate CFTR by interacting with the nucleotide-binding domains that control channel gating, whereas others inhibit CFTR by binding within the channel pore and preventing Cl- permeation. Knowledge of the molecular pharmacology of CFTR might lead to new treatments for diseases caused by the dysfunction of CFTR.

MOL11 represents a new member of the chloride channel family. MOL11 can be used as a marker for human chromosome 19. MOL11 is useful in determining changes in expression of genes contained within the chloride channel protein family. MOL11 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of chloride channel-associated proteins. MOL11 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving cystic fibrosis, congenital myotonia, Dent disease, an X-linked renal tubular disorder, leukoencephalopathy, malignant hyperthermia, hypertension, arrythmia seen in long QT syndrome, Dent's disease, Bartter's syndrome, bronchitis, sinusitis and other pathologies and disorders.

MOL12

A MOL12 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the fatty acid-binding protein family of proteins. A MOL12 nucleic acid is found on human chromosome 5. A MOL12 nucleic acid and its encoded polypeptide includes the sequences shown in Table 12A. The disclosed nucleic acid (SEQ ID NO:185) is 550 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 27-29 and ends with a TAA stop codon at nucleotides 543-545. The representative ORF encodes a 172 amino acid polypeptide (SEQ ID NO:186) with a predicted molecular weight of 19,464.4 Da. PSORT analysis of a MOL12 polypeptide predicts a mitochondrial matrix protein with a certainty of 0.3600. SIGNALP analysis suggests the lack of a signal peptide.

TABLE 12A.

TCTGAGGACACAGCCACACTCTTGTC**ATG**CCATTGCCCTTCTATTCTTTCCTTA
TAACATCATGTAAGAGGGCACAGCATGTTTCCCATGCTGGACCCTGCTCTGCT
CACTCCACACACCTTCTGACACCCACCATGGACACTGTTCAGCAACTGGAAGA
AAGAGGGCACCTGATGGACAGCAAAGGCTTTGATGAAAATAAATACATGAAG
GAACTAGGAGTGGGACTAGCCCTCTGCGAAAAAAAGGGTGCTATGGCCAAAA
AAGATTGTATTAGCTTTTTTGATGGCAAAAACCTCACCATAAAAATGGAGAGT
ACTTTAAAATCATACAGTTTTCTCACACTCAGGGGAGGGAAATTCAAAGAAAC
TACAGGTGACGGCAGAAAAACTCAGACTTGCACCTTTACATATGGCACATTGG
TTCGACATCAGAAGTGGAATGGAAAGGAAGGCAAAATAAGAAAATTGAAAG
ACAGGAAATTAGTGGTGGACTGCATCATAAACAATGTCACCTGTACTCAGATC
TATGAAAAAGTAGAA**TAA**AAACT (SEQ ID NO.: 185)

MPLPFYSFLITSCKRAQHVSHAGPCSAHSTHLLTPTMDTVQQLEERGHLMDSKGF
DENKYMKELGVGLALCEKKGAMAKKDCISFFDGKNLTIKMESTLKSYSFLTLRG
GKFKETTGDGRKTQTCTFTYGTLVRHQKWNGKEGKIRKLKDRKLVVDCIINNVT
CTQIYEKVE (SEQ ID NO.: 186)

A MOL12 nucleic acid has a high degree of homology (99% identity) with an uncharacterized region of human chromosome 5, including the clone CTB-139P6 (CHR5; GenBank Accession No.: AC010293), as is shown in Table 12B. A MOL12 polypeptide has homology (71% identity, 79% similarity) with a human epidermal fatty acid-binding protein polypeptide (FABP; EMBL Accession No.: Q01469), as is shown in Table 12C. A MOL12 polypeptide also has homology (71% identity, 79% similarity) with a human melanogenic inhibitor polypeptide (hMI; PatP Accession No.: R55866) as is shown in Table 12D.

TABLE 12B.

```
MOL12:   1 tctgaggacacagccacactcttgtcatgccattgcccttctattctttccttataacat 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19410 tctgaggacacagccacactcttgtcatgccattgcccttctattctttccttataacat 19469

MOL12:  61 catgtaagagggcacagcatgtttcccatgctggaccctgctctgctcactccacacacc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19470 catgtaagagggcacagcatgtttcccatgctggaccctgctctgctcactccacacacc 19529

MOL12: 121 ttctgacacccaccatggacactgttcagcaactggaagaaagagggcacctgatggaca 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19530 ttctgacacccaccatggacactgttcagcaactggaagaaagagggcacctgatggaca 19589

MOL12: 181 gcaaaggctttgatgaa-aataaatacatgaaggaactaggagtgggactagccctctgc 239
           ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Chr5:19590 gcaaaggctttgatgaataataaatacatgaaggaactaggagtgggactagccctctgc 19649

MOL12: 240 gaaaaaaagggtgctatggccaaaaaagattgtattagctttttgatggcaaaaacctc 299
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19650 gaaaaaaagggtgctatggccaaaaaagattgtattagctttttgatggcaaaaacctc 19709

MOL12: 300 accataaaaatggagagtactttaaaatcatacagttttctcacactcaggggagggaaa 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19710 accataaaaatggagagtactttaaaatcatacagttttctcacactcaggggagggaaa 19769

MOL12: 360 ttcaaagaaactacaggtgacggcagaaaaactcagacttgcacctttacatatggcaca 419
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Chr5:19770 ttcaaagaaactacaggtgacggcagaaaaactcagac-tgcacctttacatatggcaca 19828

MOL12: 420 ttggttcgacatcagaagtggaatggaaaggaaggcaaaataagaaaattgaaagacagg 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19829 ttggttcgacatcagaagtggaatggaaaggaaggcaaaataagaaaattgaaagacagg 19888

MOL12: 480 aaattagtggtggactgcatcataaacaatgtcacctgtactcagatctatgaaaaagta 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Chr5:19889 aaattagtggtggactgcatcataaacaatgtcacctgtactcagatctatgaaaaagta 19948

MOL12: 540 gaataaaaact 550 (SEQ ID NO.: 185)
           |||||||||||
Chr5:19949 gaataaaaact 19959 (SEQ ID NO.: 210)
```

TABLE 12C.

```
MOL12:    1 MDTVQQLEERGHLMDSKGFDENKYMKELGVGLALCEKKGAMAKKDCISFFDGKNLTIKME 60
            | |||||| |  |+|||||||  ||||||||+||  | ||||| |||   |||||||| |
FABP:     1 MATVQQLEGRWRLVDSKGFDE--YMKELGVGIAL-RKMGAMAKPDCIITCDGKNLTIKTE 57

MOL12:   61 STLKSYSFLTLRGGKFKETTGDGRKTQT-CTFTYGTLVRHQKWNGKEGKI-RKLKDRKLV 118
            ||||+  |    | ||+||| ||||||| | || | ||+||+|+|||  | ||||| |||
FABP:    58 STLKTTQFSCTLGEKFEETTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLV 117

MOL12:  119 VDCIINNVTCTQIYEKVE 136 (SEQ ID NO.: 211)
            |+|++||||||+||||||
FABP:   118 VECVMNNVTCTRIYEKVE 135 (SEQ ID NO.: 212)
Where | indicates identity and + indicates similarity.
```

TABLE 12D.

```
MOL12:    1 MDTVQQLEERGHLMDSKGFDENKYMKELGVGLALCEKKGAMAKKDCISFFDGKNLTIKME 60
            | |||||| |  |+|||||||  ||||||||+||  | ||||| |||   |||||||| |
HMI:      1 MATVQQLEGRWRLVDSKGFDE--YMKELGVGIAL-RKMGAMAKPDCIITCDGKNLTIKTE 57

MOL12:   61 STLKSYSFLTLRGGKFKETTGDGRKTQT-CTFTYGTLVRHQKWNGKEGKI-RKLKDRKLV 118
            ||||+  |    | ||+||| ||||||| | || | ||+||+|+|||  | ||||| |||
HMI:     58 STLKTTQFSCTLGEKFEETTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLV 117
```

```
MOL12: 119 VDCIINNVTCTQIYEKVE 136 (SEQ ID NO.: 211)
           |+|++||||||+||||||
HMI:   118 VECVMNNVTCTRIYEKVE 135 (SEQ ID NO.: 213)
```

Where | indicates identity and + indicates similarity.

Fatty acid metabolism in mammalian cells depends on a flux of fatty acids, between the plasma membrane and mitochondria or peroxisomes for beta-oxidation, and between other cellular organelles for lipid synthesis. The fatty acid-binding protein (FABP) family consists of small, cytosolic proteins believed to be involved in the uptake, transport, and solubilization of their hydrophobic ligands. Members of this family have highly conserved sequences and tertiary structures. Fatty acid-binding proteins were first isolated in the intestine (FABP2; OMIM- 134640) and later found in liver (FABP1; OMIM- 134650), striated muscle (FABP3; OMIM- 134651), adipocytes (FABP4; OMIM- 600434) and epidermal tissues (E-FABP; GDB ID:136450).

Epidermal fatty acid binding protein (E-FABP) was cloned as a novel keratinocyte protein by Madsen and co-workers from the skin of psoriasis patients (See Madsen *et al.*,1992, J. Invest. Dermatol. **99**:299). Later using quantitative Western blot analysis, Kingma and colleagues have shown that in addition to the skin, bovine E-FABP is expressed in retina, testis, and lens (See Kingma et al., 1998, Biochemistry **37**:3250). Since E-FABP was originally identified from the skin of psoriasis patients, it is also known as psoriasis-associated fatty acid-binding protein (PA-FABP). PA-FABP is a cytoplasmic protein, and is expressed in keratinocytes. It is highly up-regulated in psoriatic skin. It shares similarity to other members of the fatty acid-binding proteins and belongs to the fabp/p2/crbp/crabp family of transporter. PA-FABP is believed to have a high specificity for fatty acids, with highest affinity for c18 chain length. Decreasing the chain length or introducing double bonds reduces the affinity. PA-FABP may be involved in keratinocyte differentiation.

Immunohistochemical localization of the expression of E-FABP in psoriasis, basal and squamous cell carcinomas has been carried out in order to obtain indirect information, at the cellular level, on the transport of the fatty acids (See Masouye *et al.,* 1996, Dermatology **192**:208). E-FABP was localized in the upper stratum spinosum and stratum granulosum in normal and non-lesional psoriatic skin. In contrast, lesional psoriatic epidermis strongly expressed E-FABP in all suprabasal layers, like nonkeratinized oral mucosa. The basal layer did not express E-FABP reactivity in any of these samples. Accordingly, basal cell carcinomas were E-FABP negative whereas only well-differentiated cells of squamous cell carcinomas expressed E-FABP. This suggests that E-

FABP expression is related to the commitment of keratinocyte differentiation and that the putative role of E-FABP should not be restricted to the formation of the skin lipid barrier. Since the pattern of E-FABP expression mimics cellular FA transport, our results suggest that lesional psoriatic skin and oral mucosa have a higher metabolism/transport for fatty acids than normal and non-lesional psoriatic epidermis.

MOL12 represents a new member of the fatty acid-binding protein family. MOL12 can be used as a marker for human chromosome 5. MOL12 is useful in determining changes in expression of genes contained within the fatty acid-binding protein family. MOL12 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of fatty acid-binding protein associated proteins. MOL12 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving psoriatic skin and cancer, *e.g.* basal and squamous cell carcinomas.

MOL13

A MOL13 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the insulin-like growth factor family of proteins. A MOL13 nucleic acid is found on human chromosome 10. A MOL13 nucleic acid and its encoded polypeptide includes the sequences shown in Table 13A. The disclosed nucleic acid (SEQ ID NO:187) is 915 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA stop codon at nucleotides 913-915. The representative ORF encodes a 304 amino acid polypeptide (SEQ ID NO:188) with a predicted molecular weight of 32,944.7 Da. A MOL13 polypeptide is likely to be detected in kidney, spleen, thyroid, brain and salivary gland. PSORT analysis of a MOL13 polypeptide predicts a secreted protein with a certainty of 0.8200. SIGNALP analysis suggests the presence of a signal peptide with the most likely cleavage site occuring between positions 30 and 31 in SEQ ID NO.: 188.

TABLE 13A.

ATGCTGCCGCCGCCGCGGCCCGCAGCTGCCTTGGCGCTGCCTGTGCTCCTGCT
ACTGCTGGTGGTGCTGACGCCGCCCCCGACCGGCGCAAGGCCATCCCCAGGCC
CAGATTACCTGCGGCGCGGCTGGATGCGGCTGCTAGCGGAGGGCGAGGGCTG
CGCTCCCTGCCGGCCAGAAGAGTGCGCCGCGCCGCGGGGCTGCCTGGCGGGC

AGGGTGCGCGACGCGTGCGGCTGCTGCTGGGAATGCGCCAACCTCGAGGGCC
AGCTCTGCGACCTGGACCCCAGTGCTCACTTCTACGGGCACTGCGGCGAGCAG
CTTGAGTGCCGGCTGGACACAGGCGGCGACCTGAGCCGCGGAGAGGTGCCGG
AACCTCTGTGTGCCTGTCGTTCGCAGAGTCCGCTCTGCGGGTCCGACGGTCAC
ACCTACTCCCAGATCTGCCGCCTGCAGGAGGCGGCCCGCGCTCGGCCCGATGC
CAACCTCACTGTGGCACACCCGGGGCCCTGCGAATCGGGGCCCCAGATCGTGT
CACATCCATATGACACTTGGAATGTGACAGGGCAGGATGTGATCTTTGGCTGT
GAAGTGTTTGCCTACCCCATGGCCTCCATCGAGTGGAGGAAGGATGGCTTGGA
CATCCAGCTGCCAGGGGATGACCCCCACATCTCTGTGCAGTTTAGGGGTGGAC
CCCAGAGGTTTGAGGTGACTGGCTGGCTGCAGATCCAGGCTGTGCGTCCCAGT
GATGAGGGCACTTACCGCTGCCTTGGCCGCAATGCCCTGGGTCAAGTGGAGGC
CCCTGCTAGCTTGACAGTGCTCACACCTGACCAGCTGAACTCTACAGGCATCC
CCCAGCTGCGATCACTAAACCTGGTTCCTGAGGAGGAGGCTGAGAGTGAAGA
GAATGACGATTACTAC**TAG**(SEQ ID NO.: 187)

MLPPPRPAAALALPVLLLLLVVLTPPPTGARPSPGPDYLRRGWMRLLAEGEGCAP
CRPEECAAPRGCLAGRVRDACGCCWECANLEGQLCDLDPSAHFYGHCGEQLECR
LDTGGDLSRGEVPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAH
PGPCESGPQIVSHPYDTWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDP
HISVQFRGGPQRFEVTGWLQIQAVRPSDEGTYRCLGRNALGQVEAPASLTVLTPD
QLNSTGIPQLRSLNLVPEEEAESEENDDYY (SEQ ID NO.:188)

A MOL13 nucleic acid has a high degree of homology (100% identity) with an uncharacterized region of human chromosome 10, including the clone RP11-108L7 (CHR10; GenBank Accession No.: AL133215), as is shown in Table 13B. A MOL13 polypeptide has a high degree of homology (99% identity) with a human prostacyclin-stimulating factor-2 polypeptide (PSF2; PATP Accession No.: Y93650), as is shown in Table 13C. The expression patterns of a MOL13 nucleic acid were analyzed by expression profiling, as is shown in Example 4.

TABLE 13B.

```
MOL13: 1     atgctgccgccgccgcggcccgcagctgccttggcgctgcctgtgctcctgctactgctg 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35670 atgctgccgccgccgcggcccgcagctgccttggcgctgcctgtgctcctgctactgctg 35611

MOL13: 61    gtggtgctgacgccgcccccgaccggcgcaaggccatccccaggcccagattacctgcgg 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35610 gtggtgctgacgccgcccccgaccggcgcaaggccatccccaggcccagattacctgcgg 35551

MOL13: 121   cgcggctggatgcggctgctagcggagggcgagggctgcgctccctgccggccagaagag 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35550 cgcggctggatgcggctgctagcggagggcgagggctgcgctccctgccggccagaagag 35491

MOL13: 181   tgcgccgcgccgcggggctgcctggcgggcagggtgcgcgacgcgtgcggctgctgctgg 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35490 tgcgccgcgccgcggggctgcctggcgggcagggtgcgcgacgcgtgcggctgctgctgg 35431

MOL13: 241   gaatgcgccaacctcgagggccagctctgcgacctggaccccagtgctcacttctacggg 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35430 gaatgcgccaacctcgagggccagctctgcgacctggaccccagtgctcacttctacggg 35371
```

```
MOL13: 301   cactgcggcgagcagcttgagtgccggctggacacaggcggcgacctgagccgcggagag 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35370 cactgcggcgagcagcttgagtgccggctggacacaggcggcgacctgagccgcggagag 35311

MOL13: 361   gtgccggaacctctgtgtgcctgtcgttcgcagagtccgctctgcgggtccgacggtcac 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35310 gtgccggaacctctgtgtgcctgtcgttcgcagagtccgctctgcgggtccgacggtcac 35251

MOL13: 421   acctactcccagatctgccgcctgcaggaggcggcccgcgctcggcccgatgccaacctc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR10: 35250 acctactcccagatctgccgcctgcaggaggcggcccgcgctcggcccgatgccaacctc 35191

MOL13: 481   actgtggcacacccggggccctgcgaatcggg 512 (SEQ ID NO.: 214)
             ||||||||||||||||||||||||||||||||
CHR10: 35190 actgtggcacacccggggccctgcgaatcggg 35159 (SEQ ID NO.: 215)
```

TABLE 13C.

```
MOL13:    1 MLPPPRPAAALALPVLLLLLVVLTPPPTGARPSPGPDYLRRGWMRLLAEGEGCAPCRPEE 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PSF2:     1 MLPPPRPAAALALPVLLLLLVVLTPPPTGARPSPGPDYLRRGWMRLLAEGEGCAPCRPEE 60

MOL13:   61 CAAPRGCLAGRVRDACGCCWECANLEGQLCDLDPSAHFYGHCGEQLECRLDTGGDLSRGE 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PSF2:    61 CAAPRGCLAGRVRDACGCCWECANLEGQLCDLDPSAHFYGHCGEQLECRLDTGGDLSRGE 120

MOL13:  121 VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPCESGPQIVSHPYD 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PSF2:   121 VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPCESGPQIVSHPYD 180

MOL13:  181 TWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTGWLQI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PSF2:   181 TWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFEVTGWLQI 240

MOL13:  241 QAVRPSDEGTYRCLGRNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEEN 300
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
PSF2:   241 QAVRPSDEGTYRCLARNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEEN 300

MOL13:  301 DDYY 304 (SEQ ID NO.: 188)
            ||||
PSF2:   301 DDYY 304 (SEQ ID NO.: 216)
Where | indicates identity and + indicates similarity.
```

MOL13 nucleotide sequence showed 99% homology with AAA46731 DNA-encoding sequence for human prostacyclin-stimulating factor-2 (WO 200036105-A1 to Human Genome Sciences, Inc.); 96% homology with AAA46752 Clone HOABR24R, related to human prostacyclin-stimulating factor-2 (WO 200036105-A1 to Human Genome Sciences, Inc.); 87% homology with human FKSG40 mRNA (GenBank ID: AF333487, acc:AF333487.1); 87% homology with human FKSG28 mRNA (GenBank ID: AYO14217, acc:AY)14271.1); 62% homology with Sequence 17 (2036 bp) from U.S. Pat. No.6004794; and 73 % homology with AAA46756 Clone AI075710, also related to human prostacyclin-stimulating factor-2 (WO 200036105-A1 to Human Genome Sciences, Inc.). MOL13 protein sequence displayed 100% homology with human hypothetical 32.9 Kda protein (Tremblnew-Acc:AAH07758); 100% homology with human novel insulin-like growth factor binding-type protein with Kazal-type serine protease inhibitor domain (Sptrembl-Acc:Q9NTP5 BA108L7.1); 100% homology with human 252 amino acid long polypeptide (Tremblnew-Acc:AAG50291 FKSG40); 99% homology with the AAY93650 amino acid sequence of human prostacyclin-stimulating factor-2 (WO 200036105-A1 to Human Genome Sciences, Inc.); and 38% homology with human AAR79101 Prostaglandin I2 (PGI2) production promoter (WO 9429448 to H. Nawata).

The insulin-like growth factor binding protein (IGFBP) family comprises six structurally distinct, but highly homologous proteins. They have been identified in serum and other biological fluids, tissue extracts, and cell culture media. cDNAs encoding human IGFBP-4, -5, and -6 have been cloned and expressed these BPs in yeast as ubiquitin (Ub)-IGFBP fusion proteins. Western ligand blotting with 125I-IGF II under non-reducing conditions of recombinant human (rh) IGFBP-containing yeast lysates reveals specific binding bands for IGFBP-4, -5, and -6 at apparent molecular masses of 24-26, 30-32, and 24-26 kDa, respectively, indicating processing of the fusion proteins. High-performance liquid chromatography-purified rhIGFBPs have virtually the same amino acid composition, amino acid number, and NH2-terminal sequences as the native BPs. Except for the affinity of rhIGFBP-6 for IGF I (Ka = 8.5 x 10(8) M-1), the affinity constants of the three IGFBPs for IGF I and II lie between 1.7 and 3.3 x 10(10) M-1, i.e. 25-100 times higher than the IGF I and II affinities of the type I IGF receptor. When present in excess, rhIGFBP-4, -5, and -6 inhibit IGF I- and II-stimulated DNA and glycogen synthesis in human osteoblastic cells, but rhIGFBP-6 has only a weak inhibitory effect on IGF I in agreement with its relatively lower IGF I affinity constant. IGFBPs contribute to the control of IGF-mediated cell growth and metabolism. (See Kiefer *et al.*, 1992, J. Biol. Chem. 267:12692.).

Insulin-like growth factor proteins are associated with cancer progression. The down-regulation of T1A12/mac25, a novel insulin-like growth factor binding-like protein related gene, is associated with disease progression in breast carcinomas. To define genes that are essential to the initiation and progression of breast cancer Burger and colleagues utilized subtractive hybridization and differential display cloning techniques and isolated over 950 cDNAs from breast cell-lines derived from matched normal and tumor tissue. Of these, 102 cDNAs were characterized by DNA sequencing and Northern blot analysis. GenBank searches showed that one of these genes, T1A12 is identical to mac25, an insulin-like growth factor-binding protein related gene. Antibodies generated against the

C-terminal region of the T1A12/mac25 protein were used to investigate its expression in 60 primary breast tissues. Sections of 12 benign, 16 ductal carcinoma in situ and 32 infiltrating ductal carcinoma specimens were examined. Strong immunoperoxidase staining was observed in luminal epithelial cells of normal lobules and ducts, in apocrine cells of cysts and fibroadenomas. Moderate to weak protein expression was found in hyperplastic and DCIS cells, but no specific staining was detected in invasive carcinoma cells. FISH mapping using a PAC clone localized the T1A12/mac25 gene to 4q12-13. Microsatellite length polymorphism was studied using markers for 4q in paired normal and tumor breast tissues. Thirty-three per cent (10/30) of the samples were found to be polymorphic with D4S189 and D4S231 microsatellite markers and LOH was detected in 50% (5/10) of these informative samples. The data indicate that T1A12/mac25 expression is abrogated during breast cancer progression concomitant with loss of heterozygosity on chromosome 4q. T1A12/mac25 may therefore have a tumor suppressor-like function and its expression could indicate a disease with a more favorable status, having a better prognosis (See Burger *et al.*, Oncogene **16**:2459).

Gupta et al. provide evidence from genetic and pharmacologic studies to suggest that cyclooxygenase-2 (COX-2) enzyme plays a role in the development of colorectal cancer (Gupta et al., *PNAS* 97(24):13275-80, November 21, 2000. However, little is known about the identity or role of the eicosanoid receptor pathways that are activated by COX-derived prostaglandins (PGs). Gupta et al. report that COX-2-derived prostacyclin promotes embryo implantation in mouse uterus via activation of the nuclear hormone receptor peroxisome proliferator-activated receptor (PPAR) delta. Analysis of PPARdelta mRNA in matched normal and tumor samples revealed that, similar to COX-2, the expression of PPARdelta is upregulated in colorectal carcinomas (Id.). Moreover, mRNA of both COX-2 and PPARdelta localize to the same region within a tumor. Transfection assays indicate that endogenously synthesized prostacyclin (PGI(2)) can serve as a ligand for PPARdelta. Carbaprostacyclin, a stable PGI(2) analog and a synthetic PPARdelta agonist, has been found to induce transactivation of endogenous PPARdelta in human colon carcinoma cells. Thus, it appears that PPARdelta behaves similarly to COX-2, is aberrantly expressed in colorectal tumors, and is transcriptionally responsive to PGI(2).

MOL13 represents a new member of the insulin-like growth factor family. MOL13 can be used as a marker for human chromosome 10. MOL13 is useful in determining changes in expression of genes contained within the insulin-like growth factor protein family. MOL13 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of insulin-like growth factor-like protein associated proteins. MOL13 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving cell proliferative disorders, *e.g.* cancer.

MOL14

A MOL14 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the cytokeratin-18 family of proteins. A MOL14 nucleic acid and its encoded polypeptide includes the sequences shown in Table 14A. The disclosed nucleic acid (SEQ ID NO:189) is 1,299 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 5-7 and ends with a TAA stop codon at nucleotides 1,286-1,288. The representative ORF encodes a 427 amino acid polypeptide (SEQ ID NO:190) with a predicted molecular weight of 48,096.8 Da. PSORT analysis of a MOL14 polypeptide predicts localization in the endoplasmic reticulum membrane with a certainty of 0.5500. SIGNALP analysis suggests the lack of a signal peptide. Putative untranslated regions upstream and downstream of the coding sequence are underlined in SEQ ID NO.: 190.

TABLE 14A.

CAGC**ATG**AGCTTCACCACTCCCTCCACCTTCTCCACCAACTACCAGTCCCTGG
GCTCTGTCCAGCCGCCCAGCTATGGCACCTGGCCGGTCAGCAGCGCAGCCAGC
ATCTATGCAGGCACTGGGGGGCTTGGGTCCCAGATCTCCATGTCCTGTTCTAC
CAGTTTCTGGGGCGGCTTGGGGTCTGGGGGCCTGGCCACAGAGATGGCTGGG
GGTCTGGCAGAAATGGGGGGCATCCAGAATGAGAAGGAGACCATGCAAAGCC
TGAACGACCACCTGGACTACCTGGACAGAGTGAGGAACCTGGAGACCGAGAA
CTGGAGGCTGGAGAGCAAAATCCAGGAGTATCTGGAGAAGAGACCCCATGTC
AGAGACTGGGGCCATTACTTCAAGACCATCAAGGAACTGAGGGCTCAGATCTT
CGCAAATACTGTGGACAATGTCCACATCATTCTGCAGATCGACAATGCCCGTC
TTGCTGCTGATGACTTCAGAGTCAAGTATGAGACAGAGCTGGCCATGCGCCAG
TCTGTGGAGAGCAACATCCATGGGCTCTGCAAGGTCATTGATGACACCAATGT
CACTCTGCTGCAGCTGGAGACAGAGATGGGCGCTCTCAAGGAGGAGCTGCTC
CTCATGAAGAAGAACCATGAAGAGGAAGTAAAAGGCTTGCAAGTCCAGATTG
CCAACTCTGGGTTGGCCGTGGAGGTAGATGCCCCCAAATCTCAAGTCCTCGCC
AAGGTCATGGCAGACATCAGGGCCCAATATGATGAGCTGTCTCAGAAGAACT
CAGAGAAGCTAGGCAAGTACTGGTCTCAGCAGACTGAGGAGAGCACCACAGT
GGTCACCACACACTCTGCCAAGGTCAGAGCTGCTGAGATGACAACGGAGCTG
AGACGTACAGTCCAGTGCTTGGAGATTGACCTGGACTCAATGAGAAATCTGAA
GACCAGCTTGGAGAACAGCCTGAGGGAGGTGGAGGCCCGCTACGCCCTGCAG
ATGGAGCAGCTCAACAGAATCCTGCTGTACTTGGAGTCAAAGCTGGCACAGA
ACTGGGCAGAGGGCCAGCGCAAGGTCCAGGAGTACAAGGACTTGCTGAACAT
CAGGGTCAAGCTGGAGGCTGAGATCGCCACCTACCGCCGCCTGCTGGAAGAC
AGCGAGGGCCTCAATCTTGGTGATGCCCTGGACAGCAGCAACTCCATGCAAAC
CATCCAAAAGACCACCACCCGCCAGATAGTGGATAGCAAAGTGGTGTCTGAG
ATCAGTGACACCAAAGTTCTGAGACAT**TAA**GCCAGCAGAAG (SEQ ID NO.: 189)

MSFTTPSTFSTNYQSLGSVQPPSYGTWPVSSAASIYAGTGGLGSQISMSCSTSFWG
GLGSGGLATEMAGGLAEMGGIQNEKETMQSLNDHLDYLDRVRNLETENWRLES
KIQEYLEKRPHVRDWGHYFKTIKELRAQIFANTVDNVHIILQIDNARLAADDFRVK
YETELAMRQSVESNIHGLCKVIDDTNVTLLQLETEMGALKEELLLMKKNHEEEV
KGLQVQIANSGLAVEVDAPKSQVLAKVMADIRAQYDELSQKNSEKLGKYWSQQ
TEESTTVVTTHSAKVRAAEMTTELRRTVQCLEIDLDSMRNLKTSLENSLREVEAR
YALQMEQLNRILLYLESKLAQNWAEGQRKVQEYKDLLNIRVKLEAEIATYRRLLE
DSEGLNLGDALDSSNSMQTIQKTTTRQIVDSKVVSEISDTKVLRH (SEQ ID NO.: 190)

A MOL14 nucleic acid has a high degree of homology (90% identity) with a human keratin-18 mRNA (K-18; GenBank Accession No.: M26326), as is shown in Table 14B. A MOL14 polypeptide has homology (82% identity, 89% similarity) with a human keratin 18 polypeptide (hK18; GenBank Accession No.: S05481), as is shown in Table 14C.

TABLE 14B.

```
MOL14:     1 CAGCATGAGCTTCACCACTCCCTCCACCTTCTCCACCAACTACCAGTCCCTGGGCTCTGT 60
             |||||||||||||||||||| ||||||||||||||||||||||| |||||||||||||||
K-18:     48 CAGCATGAGCTTCACCACTCGCTCCACCTTCTCCACCAACTACCGGTCCCTGGGCTCTGT 107

MOL14:    61 CCAGCCGCCCAGCTATGGCACCTGGCCGGTCAGCAGCGCAGCCAGCATCTATGCAGGCAC 120
             |||| |||||||||| ||| || |||||||||||||||| |||||| ||||||||||| |
K-18:    108 CCAGGCGCCCAGCTACGGCGCCCGGCCGGTCAGCAGCGCGGCCAGCGTCTATGCAGGCGC 167

MOL14:   121 TGGGGGGCT-TGGGTCCCAGATCTCCATGTCCTGTTCTACCAGTTTCTGGGGCGGCTTGG 179
             |||||| || ||| |||| ||||||| ||||| | || ||||| ||| |||||||| |||
K-18:    168 TGGGGG-CTCTGGTTCCCGGATCTCCGTGTCCCGCTCCACCAGCTTCAGGGGCGGCATGG 226

MOL14:   180 GGTCTGGGGGCCTGGCCACAGAGATGGCTGGGGGTCTGGCAGAAATGGGGGGCATCCAGA 239
             |||| |||||||||||||| | ||| || ||||||||||||| |||||| ||||||||||
K-18:    227 GGTCCGGGGGCCTGGCCACCGGGATAGCCGGGGGTCTGGCAGGAATGGGAGGCATCCAGA 286

MOL14:   240 ATGAGAAGGAGACCATGCAAAGCCTGAACGACCACCTGGACT---ACCTGGACAGAGTGA 296
             | ||||||||||||||||||||||||||||||| ||||| ||   |||||||||||||||
K-18:    287 ACGAGAAGGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGA 346

MOL14:   297 GGAACCTGGAGACCGAGAACTGGAGGCTGGAGAGCAAAATCCAGGAGTATCTGGAGAAGA 356
             ||| |||||||||||||||| ||||||||||||||||||||| |||| |  |||||||||
K-18:    347 GGAGCCTGGAGACCGAGAACCGGAGGCTGGAGAGCAAAATCCGGGAGCACTTGGAGAAGA 406

MOL14:   357 -G--ACCCCATGTCAGAGACTGGGGCCATTACTTCAAGACCATCAAGGAACTGAGGGCTC 413
              |  |||||| |||||||||||| ||||||||||||||| |||| |||| ||||||||||
K-18:    407 AGGGACCCCAGGTCAGAGACTGGAGCCATTACTTCAAGATCATCGAGGACCTGAGGGCTC 466

MOL14:   414 AGATCTTCGCAAATACTGTGGACAATGTCCACATCATTCTGCAGATCGACAATGCCCGTC 473
             ||||||||||||||||||||||||||| || |||| |||||||||| |||||||||||||
K-18:    467 AGATCTTCGCAAATACTGTGGACAATGCCCGCATCGTTCTGCAGATTGACAATGCCCGTC 526

MOL14:   474 TTGCTGCTGATGACTTCAGAGTCAAGTATGAGACAGAGCTGGCCATGCGCCAGTCTGTGG 533
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
K-18:    527 TTGCTGCTGATGACTTTAGAGTCAAGTATGAGACAGAGCTGGCCATGCGCCAGTCTGTGG 586

MOL14:   534 AGAGCAACATCCATGGGCTCTGCAAGGTCATTGATGACACCAATGTCACTCTGCTGCAGC 593
             ||| | |||||||||||||| ||||||||||||||||||||||| |||| |  |||||||
K-18:    587 AGAACGACATCCATGGGCTCCGCAAGGTCATTGATGACACCAATATCACACGACTGCAGC 646

MOL14:   594 TGGAGACAGAGATGGGCGCTCTCAAGGAGGAGCTGCTCCTCATGAAGAAGAACCATGAAG 653
             ||||||||||||| |  ||||||||||||||||||||| |||||||||||||||| ||||
K-18:    647 TGGAGACAGAGATCGAGGCTCTCAAGGAGGAGCTGCTCTTCATGAAGAAGAACCACGAAG 706

MOL14:   654 AGGAAGTAAAAGGCTTGCAAGTCCAGATTGCCAACTCTGGGTTGGCCGTGGAGGTAGATG 713
             |||||||||||||| | |||| ||||||||||| |||||||||| |||||||||||||||
K-18:    707 AGGAAGTAAAAGGCCTACAAGCCCAGATTGCCAGCTCTGGGTTGACCGTGGAGGTAGATG 766

MOL14:   714 CCCCCAAATCTCAAGTCCTCGCCAAGGTCATGGCAGACATCAGGGCCCAATATGATGAGC 773
             ||||||||||||| | |||||||||| |||||||||||||| ||||||||||||| ||||
K-18:    767 CCCCCAAATCTCAGGACCTCGCCAAGATCATGGCAGACATCCGGGCCCAATATGACGAGC 826

MOL14:   774 TGTCTCAGAAGAACTCAGAGAAGCTAGGCAAGTACTGGTCTCAGCAGACTGAGGAGAGCA 833
             || ||| |||||||  |||| |||||| |||||||||||||||||||| |||||||||||
K-18:    827 TGGCTCGGAAGAACCGAGAGGAGCTAGACAAGTACTGGTCTCAGCAGATTGAGGAGAGCA 886

MOL14:   834 CCACAGTGGTCACCACACACTCTGCCAAGGTCAGAGCTGCTGAGATGACA---ACGGAGC 890
             ||||||||||||||||||| |||||  ||||  |||||||||||| |||    || ||||
K-18:    887 CCACAGTGGTCACCACACAGTCTGCTGAGGTTGGAGCTGCTGAGACGACGCTCACAGAGC 946

MOL14:   891 TGAGACGTACAGTCCAGTGCTTGGAGATTGACCTGGACTCAATGAGAAATCTGAAGACCA 950
             |||||||||||||||||| ||||||||| ||||||||||| ||||||||||||||| |||
K-18:    947 TGAGACGTACAGTCCAGTCCTTGGAGATCGACCTGGACTCCATGAGAAATCTGAAGGCCA 1006

MOL14:   951 GCTTGGAGAACAGCCTGAGGGAGGTGGAGGCCCGCTACGCCCTGCAGATGGAGCAGCTCA 1010
```

```
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
K-18:   1007 GCTTGGAGAACAGCCTGAGGGAGGTGGAGGCCCGCTACGCCCTACAGATGGAGCAGCTCA 1066

MOL14:  1011 ACAGAATCCTGCTGTACTTGGAGTCAAAGCTGGCACAGAACTGGGCAGAGGGCCAGCGCA 1070
             || | ||||||||| || | |||||| |||||||||||| | |||||||||| ||||||
K-18:   1067 ACGGGATCCTGCTGCACCTTGAGTCAGAGCTGGCACAGACCCGGGCAGAGGGACAGCGCC 1126

MOL14:  1071 AGGTCCAGGAGTACAAGGACTTGCTGAACATCAGGGTCAAGCTGGAGGCTGAGATCGCCA 1130
             ||| |||||||||  ||| | |||||||||||| ||||||||||||||||||||||||||
K-18:   1127 AGGCCCAGGAGTATGAGGCCCTGCTGAACATCAAGGTCAAGCTGGAGGCTGAGATCGCCA 1186

MOL14:  1131 CCTACCGCCGCCTGCTGGAAGACAGCGAGGGCCTCAATCTTGGTGATGCCCTGGACAGCA 1190
             ||||||||||||||||||||||  |||||| | | ||||||||||||||| |||||||||
K-18:   1187 CCTACCGCCGCCTGCTGGAAGATGGCGAGGACTTTAATCTTGGTGATGCCTTGGACAGCA 1246

MOL14:  1191 GCAACTCCATGCAAACCATCCAAAAGACCACCACCCGCCAGATAGTGGATAGCAAAGTGG 1250
             ||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||||
K-18:   1247 GCAACTCCATGCAAACCATCCAAAAGACCACCACCCGCCGGATAGTGGATGGCAAAGTGG 1306

MOL14:  1251 TGTCTGAGATCAGTGACACCAAAGTTCTGAGACATTAAGCCAGCAGAAG 1299(SEQ ID NO.:
189)
             ||||||||| || |||||||||||||||||| |||||||||||||||||
K-18:   1307 TGTCTGAGACCAATGACACCAAAGTTCTGAGGCATTAAGCCAGCAGAAG 1355 (SEQ ID NO.:
217)
```

TABLE 14C.

```
MOL14:     1 MSFTTPSTFSTNYQSLGSVQPPSYGTWPVSSAASIYAGTGGLGSQISMSCSTSFWGGLGS 60
             ||||| |||||||+|||||| ||||  |||||||+||| || ||+||+| |||| ||+||
HK18:      1 MSFTTRSTFSTNYRSLGSVQAPSYGARPVSSAASVYAGAGGSGSRISVSRSTSFRGGMGS 60

MOL14:  61   GGLATEMAGGLAEMGGIQNEKETMQSLNDHL-DYLDRVRNLETENWRLESKIQEYLEKR- 118
             ||||| +||||| |||||||||||||||| |  ||||||+||||| ||||||+|+|||+
HK18:     61 GGLATGIAGGLAGMGGIQNEKETMQSLNDRLASYLDRVRSLETENRRLESKIREHLEKKG 120

MOL14:   119 PHVRDWGHYFKTIKELRAQIFANTVDNVHIILQIDNARLAADDFRVKYETELAMRQSVES 178
             | |||| |||| |++||||||||||||  |+||||||||||||||||||||||||||||+
HK18:    121 PQVRDWSHYFKIIEDLRAQIFANTVDNARIVLQIDNARLAADDFRVKYETELAMRQSVEN 180

MOL14:   179 NIHGLCKVIDDTNVTLLQLETEMGALKEELLLMKKNHEEEVKGLQVQIANSGLAVEVDAP 238
             +|||| |||||||+| ||||||+ ||||||| ||||||||||||| |||+||| ||||||
HK18:    181 DIHGLRKVIDDTNITRLQLETEIEALKEELLFMKKNHEEEVKGLQAQIASSGLTVEVDAP 240

MOL14:   239 KSQVLAKVMADIRAQYDELSQKNSEKLGKYWSQQTEESTTVVTTHSAKVRAAEMT-TELR 297
             ||| |||+|||||||||||++|| |+| |||||| ||||||||| ||+| ||| | ||||
HK18:    241 KSQDLAKIMADIRAQYDELARKNREELDKYWSQQIEESTTVVTTQSAEVGAAETTLTELR 300

MOL14:   298 RTVQCLEIDLDSMRNLKTSLENSLREVEARYALQMEQLNRILLYLESKLAQNWAEGQRKV 357
             |||| |||||||||||| ||||||||||||||||||||| |||+|||+|||  |||||+
HK18:    301 RTVQSLEIDLDSMRNLKASLENSLREVEARYALQMEQLNGILLHLESELAQTRAEGQRQA 360

MOL14:   358 QEYKDLLNIRVKLEAEIATYRRLLEDSEGLNLGDALDSSNSMQTIQKTTTRQIVDSKVVS 317
             |||+ ||||+|||||||||||||||| |  |||||||||||||||||||||+||| ||||
HK18:    361 QEYEALLNIKVKLEAEIATYRRLLEDGEDFNLGDALDSSNSMQTIQKTTTRRIVDGKVVS 420

MOL14: 318   EISDTKVLRH 328 (SEQ ID NO.: 190)
             | +|||||||
HK18:    421 ETNDTKVLRH 430 (SEQ ID NO.: 218)
Where | indicates identity and + indicates similarity.
```

Intermediate filaments (IFs) are a structurally related family of cellular proteins that appear to be intimately involved with the cytoskeleton. The common structural motif shared by all IFs is a central alpha-helical 'rod domain' flanked by variable N- and C-terminal domains. The rod domain, the canonical feature of IFs, has been highly conserved during evolution. The variable terminals, however, have allowed the known IFs to be classified into 6 distinct types by virtue of their differing amino acid sequences (See Steinert and Roop, 1988, Annu. Rev. Biochem. **57**:593). Keratins compose types I and II; intermediate filaments desmin, vimentin, GFAP, and peripherin, type III; neurofilaments, type IV, and nuclear lamins, type V. Nestin (600915) has been classed as type VI (See Lendahl *et al.*, 1990, Cell **60**:585).The acidic keratins are coded by genes KRT9 to KRT19. These genes are located on mouse chromosome 11 and human chromosome 17, except for KRT18 which may be located on human chromosome 12 (see later). The basic keratins are coded by genes KRT1 to KRT8, which are located on mouse chromosome 15 and human chromosome 12.

Ku and colleagues described transgenic mice that express point-mutant K18 and develop chronic hepatitis and hepatocyte fragility in association with disruption of hepatocyte keratin filaments. They showed that transgenic mice expressing mutant K18 are highly susceptible to hepatotoxicity after acute administration of acetaminophen or chronic ingestion of griseofulvin. The authors concluded that the predisposition to hepatotoxicity results directly from the keratin mutation since nontransgenic or transgenic mice that express normal human K18 are more resistant. Hepatotoxicity was manifested by a significant difference in lethality, liver histopathology, and biochemical serum testing. Keratin glycosylation decreased in all griseofulvin-fed mice, whereas keratin phosphorylation increased dramatically preferentially in mice expressing normal K18. The phosphorylation increase in normal K18 after griseofulvin feeding appeared to involve sites that are different from those that increased after partial hepatectomy. Ku and co-workers stated that this dramatic phosphorylation increase in nonmutant keratins could provide survival advantage to hepatocytes (See Ku *et al.*, J. Cell Biol. **131**:1305).

K8/18 is the major keratin pair in epithelia of the type found in liver, pancreas, and intestine. Transgenic mice that express mutant keratin 18, as already noted, develop chronic hepatitis, and have an increased susceptibility to drug-induced hepatotoxicity. By studying patients with liver disease of unknown cause for mutations in KRT18, Ku and colleagues described a his127leu (H127L) KRT mutation in a patient with cryptogenic cirrhosis that was germline transmitted. The mutant KRT18 isolated from the liver explant, or after expression in bacteria, showed an altered migration on 2-dimensional gel analysis as compared with normal human liver or bacterially expressed KRT18. Electron microscopy of in vitro assembled mutant KRT18 and wildtype KRT8 showed an assembly defect as compared with normal KRT8/18 assembly. The results suggested that mutations in KRT18 predispose to cryptogenic cirrhosis in humans (See Ku *et al.*, 1997, J. Clin. Invest. 99:19).

MOL14 represents a new member of the cytokeratin-18 family. MOL14 is useful in determining changes in expression of genes contained within the cytokeratin-18 protein family. MOL14 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of cytokeratin-18-like protein-associated proteins. MOL14 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving hepatic disorders, *e.g.* cryptogenic cirrhosis.

MOL15

A MOL15 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the metallocarboxypeptidase family of proteins. A MOL15 nucleic acid maps to human chromosome 20. A MOL15 nucleic acid and its encoded polypeptide includes the sequences shown in Table 15A. A MOL15 nucleic acid is likely to be expressed in testis, spleen, salivary gland, brain, heart, thyroid, bone marrow, lung, kidney, uterus, ovary and germ cells. The disclosed nucleic acid (SEQ ID NO:191) is 2,202 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA stop codon at nucleotides 2,200-2,200. The representative ORF encodes a 733 amino acid polypeptide (SEQ ID NO:192) with a predicted molecular weight of 81,573.8 Da. PSORT analysis of a MOL15 polypeptide predicts a lysosomal localization with a certainty of 0.5487 and a secreted protein with a certainty of 0.5469. SIGNALP analysis suggests the presence of a signal peptide, with the most likely cleavage site between position 20 and 21 of SEQ ID NO.: 192.

TABLE 15A.

ATGTGGGGGCTCCTGCTCGCCCTGGCCGGCTTCGCGCCGGCCGTCGGCCCGGC
TCTGGGGGCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACC
AAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGTCGG
CGGAGACAGCTAACACCTCAGAACAGCATGTCCGGATTCGAGTCATCAAGAA
GAAAAAGGTCATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACC

CCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACTCCAGCAGGGACCCTCGA
CCCCGCTGAGAAACAAGAACCAGGCTGTCCTCCTTTGGGTCTGGAGTCCCTGC
GAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTTGGA
CCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTAT
ATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTG
GACGCTGGGCACCCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTC
TGTCTGGAGGTATGACTGGGTCACATCATACAAGGTCCAGTTCAGCAATGACA
GTCGGACCTGGTGGGGAAGTAGGAACCACAGCAGTGGGATGGACGCAGTGTT
TCCTGCCAATTCAGACCCAGAAACTCCAGTGCTGAACCTCCTGCCGGAGCCCC
AGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTCCAGGGAGGCGCG
CCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAATGACCT
ATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCA
CAATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCC
AACATTACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTA
TGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAGCTGGGTGAGCCTGAG
GTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGC
TTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGG
GTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTGCCCTCCATGAACCCT
GATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCTGGTGGGCTGGGCCG
AGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC
AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCC
CCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTG
GCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCT
AAGTGCCAACCTCCACGGGGGTGAGCTCGTGGTGTCCTACCCATTCGACATGA
CTCGCACCCCGTGGGCTGCCCGCGAGCTCACGCCCACACCAGATGATGCTGTG
TTTCGCTGGCTCAGCACTGTCTATGCTGGCAGTAATCTGGCCATGCAGGACAC
CAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGTGCACGGCAACATCATCA
ACGGGGCTGACTGGCACACGGTCCCCGGGAGTATGAATGACTTCAGCTACCTA
CACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCCTCA
CGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACC
TACCTGGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACA
CGGAGCTTGGGATTGCTGACGCTGTCATTGCCGTGGATGGGATTAACCATGAC
GTGACCACGGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCCCAGGGGACT
ACATGGTGACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGGAACTGTCGG
GTCACTTTGAAGAGGGGCCCCTTCCCCTGCAATTTCGTGCTCACCAAGACTCC
CAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGAC
CTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGAT**TGA**(SEQ ID NO.: 191)

MWGLLLALAGFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPSAET
ANTSEQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQE
PGCPPLGLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQ
DADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRN
HSSGMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPV
SDPNDLFLEAPASGSSDPLDFQHHNYKAMRKLMKQVQEQCPNITRIYSIGKSYQG
LKLYVMEMSDKPGEHELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRG
NPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVGWAEGRWNNQSIDLNHNFA
DLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETRAVIKWMKRIPFVL
SANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTS
RRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENE

LPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAW GGDYWRLLTPGDYMVTASAEGYHSVTRNCRVTLKRGPFPCNFVLTKTPKQRLRE LLAAGAKVPPDLRRRLERLRGQKD (SEQ ID NO.: 192)

A MOL15 polypeptide has homology (84% identity, 89% similarity) with a mouse metallocarboxypeptidase CPX-1 polypeptide (CPX1; EMBL Accession No.: Q9Z100), as is shown in Table 15B. Also, a MOL15 polypeptide has a high degree of homology with an uncharacterized human protein APG04 (AGP04; PatP Accession No.: B36174), as is shown in Table 15C.

TABLE 15B.

```
MOL15:    1 MWGLLLALAGFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPSAETANTSE 60
            |||||||+  |||+||  ||||  || |||       |||| | ||| |||| +   |||
CPX1:     1 MWGLLLAVTAFAPSVGLGLGAPSASVPGLA-------PGSTLAPHSSVAQPSTKANETSE 53

MOL15:   61 QHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQEPGCPPLGLE 120
            +|||+|||||||+++||||||    | || || |+|   || ||   |||||||||||||
CPX1:    54 RHVRLRVIKKKKIVVKKRKKLR--HPGPLGTARPVVPTHPAKTLTLPEKQEPGCPPLGLE 111

MOL15:  121 SLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGHP 180
            |||||||+|||||||||||| ||||||||||||||||||||||||+|| +|| |||| +|
CPX1:   112 SLRVSDSQLEASSSQSFGLGAHRGRLNIQSGLEDGDLYDGAWCAEQQDTEPWLQVDAKNP 171

MOL15:  181 TRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVLN 240
             ||+|++|||||||||||||||+||||||||+||| ||| |+||| ||||||| ||||||
CPX1:   172 VRFAGIVTQGRNSVWRYDWVTSFKVQFSNDSQTWWKSRN-STGMDIVFPANSDAETPVLN 230

MOL15:  241 LLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHHN 300
            |||||||||||||||||| ||| ||||||||||||||||||| ||   |||+ |||+|||
CPX1:   231 LLPEPQVARFIRLLPQTWFQGGVPCLRAEILACPVSDPNDLFPEAHTLGSSNSLDFRHHN 290

MOL15:  301 YKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMHG 360
            ||||||||||| |||||||||||||||+|||||||||||| |||||||||||||||||||
CPX1:   291 YKAMRKLMKQVNEQCPNITRIYSIGKSHQGLKLYVMEMSDHPGEHELGEPEVRYVAGMHG 350

MOL15:  361 NEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVGW 420
            |||||||||||||||||||||||+|||||||+| |||||||||||||| |||||||||||
CPX1:   351 NEALGRELLLLLMQFLCHEFLRGDPRVTRLLTETRIHLLPSMNPDGYETAYHRGSELVGW 410

MOL15:  421 AEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETRA 480
            ||||| +| |||||||||||| || |+||| ||  ||||||||||||||||||||||| |
CPX1:   411 AEGRWTHQGIDLNHNFADLNTQLWYAEDDGLVPDTVPNHHLPLPTYYTLPNATVAPETWA 470

MOL15:  481 VIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNL 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||+| 
CPX1:   471 VIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGTNR 530

MOL15:  541 AMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHEN 600
            ||||| ||||||||||+|||+|||||||||||||||||||||||||||||||||||||| 
CPX1:   531 AMQDTDRRPCHSQDFSLHGNVINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHEK 590

MOL15:  601 ELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYW 660
            |||||||||||||||||||||||| |||||||||||||||||||+|||||||||||||||
CPX1:   591 ELPQEWENNKDALLTYLEQVRMGITGVVRDKDTELGIADAVIAVEGINHDVTTAWGGDYW 650

MOL15:  661 RLLTPGDYMVTASAEGYHSVTRNCRVTLKRGPFPCNFVLTKTPKQRLRELLAAGAKVPPD 720
            ||||||||+|||||||||+| ++|+|| + || ||||+||||||+|||||||   |+|||
CPX1:   651 RLLTPGDYVVTASAEGYHTVRQHCQVTFEEGPVPCNFLLTKTPKERLRELLATRGKLPPD 710
```

```
MOL15: 721 LRRRLERLRGQKD 733 (SEQ ID NO.: 192)
           |||+|||||||||
CPX1:  711 LRRKLERLRGQK 722 (SEQ ID NO.: 219)
Where | indicates identity and + indicates similarity.
```

TABLE 15C.

```
MOL15:     1 MWGLLLALAGFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPSAETAN-TS 59
             ||||||||| ||||||||||||||||||||||||||||||||||||||||| ||||| ||
AGP04:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

MOL15:    60 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQEPGCPPLGL 119
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
AGP04:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

MOL15:   120 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 179
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

MOL15:180    PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

MOL15:240    NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

MOL15:300    NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

MOL15:360    GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 419
             ||||||||||||||||||||||||||+|||||||||||||||||||||||||||||||||
AGP04:   361 GNEALGRELLLLLMQFLCHEFLRGNPQVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

MOL15:420    WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:421    WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

MOL15:480    AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 539
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

MOL15:540    LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:541    LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

MOL15:600    NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGP04:   601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

MOL15:660    WRLLTPGDYMVTASAEGYHSVTRNCRVTLKRGPFPCNFVLTKTPKQRLRELLAAGAKVPP 719
             |||||||||||||||||||||||||||| + |||||||||||||||||||||||||||||
AGP04:661    WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

MOL15:720      DLRRRLERLRGQKD 733 (SEQ ID NO.: 192)
               ||||||||||||||
AGP04:     721 DLRRRLERLRGQKD 734 (SEQ ID NO.: 220)
```

Where | indicates identity and + indicates similarity.

Metallocarboxypeptidases are members of a gene family with broad gene expression patterns and *in vivo* functions. The recent finding that Cpe(fat)/Cpe(fat) mice, which lack carboxypeptidase E (CPE) activity because of a point mutation, are still capable of a reduced amount of neuroendocrine peptide processing suggested that additional carboxypeptidases (CPs) participate in this processing reaction. Searches for novel members of the CPE gene family led to the discovery of CPD, CPZ, AEBP1, and CPX-2. Like AEBP1 and CPX-2, CPX-1 contains an N-terminal region of 160 amino acids with sequence similarity to the discoidin domain of a variety of proteins. The 410-residue CP-like domain of CPX-1 has 54% to 62% amino acid sequence identity with AEBP1 and CPX-2 and 33% to 49% amino acid identity with other members of the CPE subfamily. However, several active-site residues that are important for catalytic activity of other CPs are not conserved in CPX-1. Furthermore, CPX-1 expressed in either the baculovirus system or the mouse AtT-20 cell line does not cleave standard CP substrates. Northern blot analysis shows the highest levels of CPX-1 mRNA in testis and spleen and lower levels in salivary gland, brain, heart, lung, and kidney. *In situ* hybridization of CPX-1 mRNA in embryonic and fetal mouse tissue showed expression throughout the head and thorax, with abundance in primordial cartilage and skeletal structures. In the head, high levels of CPX-1 mRNA are associated with the nasal mesenchyme, primordial cartilage structures in the ear, and the meninges. In the thorax, CPX-1 mRNA is expressed in multiple developing skeletal structures, including chondrocytes and perichondrial cells of the rib, vertebral, and long-bone primordia. CPX-1 may have a role in development, possibly mediating cell interactions via its discoidin domain. (See Lei *et al.*, 1999, DNA Cell Biology **18**:175).

MOL15 represents a new member of the metallocarboxypeptidase family of proteins. MOL15 is useful in determining changes in expression of genes contained within the metallocarboxypeptidase protein family. MOL15 will be useful in identifying testis, spleen, salivary gland, brain, heart, thyroid, bone marrow, lung, kidney, uterus, ovary tissue and germ cells. MOL15 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of the metallocarboxypeptidase-associated protein family of proteins. MOL15 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving metabolic disorders of the pancreas, *e.g.* acute pancreatitis.

MOL16

A MOL16 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the mast cell protease-6 family of proteins. A MOL16 nucleic acid and its encoded polypeptide includes the sequences shown in Table 16A. The disclosed nucleic acid (SEQ ID NO: 193) is 846 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 6-8 and ends with a TGA stop codon at nucleotides 840-842. The representative ORF encodes a 278 amino acid polypeptide (SEQ ID NO:194) with a predicted molecular weight of 30,570.1 Da. PSORT analysis of a MOL16 polypeptide predicts a lysosomal localization with a certainty of 0.8650. SIGNALP analysis suggests the presence of a signal peptide, with the most likely cleavage site between position 17 and18 of SEQ ID NO.: 194). Putative untranslated regions upstream and downstream of the open reading frame are underlined in SEQ ID NO.: 193.

TABLE 16A.

CGCAG**ATG**CTGTGGCTGCTATTCCTGACCCTCCCCTGCCTGGGGGGCTCCATG
TCCAAGACCCCAGTGCCCGTCCCAGAGAATGACCTGGTGGGCATTGTGGGGG
GCCACAATGCCCCCCCGGGGAAGTGGCCGTGGCAGGTCAGCCTGAGGGTCTA
CAGCTACCACTGGGCCTCCTGGGCGCACATCTGTGGGGGCTCCCTCATCCACC
CCCAGTGGGTGCTGACTGCTGCCCACTGCATTTTCTGGAAGGACACCGACCCG
TCCATCTACCGGATCCACGCTGGGGACGTGTATCTCTACGGGGGCCGGGGGCT
GCTGAACGTCAGCCGGATCATCGTCCACCCCAACTATGTCACTGCGGGGCTGG
GTGCGGATGTGGCCCTGCTCCAGCTGGTGAGCCCCATGATCGGAGCCGCTAAT
GTCAGGACGGTCAAGCTCTCCCCGGTCTCGCTGGAGCTCACCCCGAAGGACCA
GTGCTGGGTGACTGGCTGGGGAGCGATCAGGATGTTCGAGTCGCTGCCGCCGC
CCTACCGCCTGCAGCAGGCGAGTGTGCAGGTGCTGGAGAACGCCGTCTGTGA
GCAGCCCTACCGCAACGCCTCAGGGCACACTGGCGACCGGCAGCTCATCCTGG
ATGACATGCTGTGTGCCGGCAGCGAGGGCCGAGACTCCTGTCAGGGTGACTCC
GGCGGCCCTCTGGTCTGCAGGCTGCGGGGGTCCTGGCGCCTGGTGGGGGTGGT
CAGCTGGGGCTACGGCTGTACCCTGCGGGACTTTCCCGGCGTCTACACCCACG
TCCAGATCTACGTGCTCTGGATCCTGCAGCAAGTCGGGGAGTTGCCC**TGAGCA**
G (SEQ ID NO.: 193)

MLWLLFLTLPCLGGSMSKTPVPVPENDLVGIVGGHNAPPGKWPWQVSLRVYSYH
WASWAHICGGSLIHPQWVLTAAHCIFWKDTDPSIYRIHAGDVYLYGGRGLLNVS
RIIVHPNYVTAGLGADVALLQLVSPMIGAANVRTVKLSPVSLELTPKDQCWVTG
WGAIRMFESLPPPYRLQQASVQVLENAVCEQPYRNASGHTGDRQLILDDMLCAG
SEGRDSCQGDSGGPLVCRLRGSWRLVGVVSWGYGCTLRDFPGVYTHVQIYVLWI
LQQVGELP (SEQ ID NO.: 194)

A MOL16 nucleic acid has homology (99% identity) with an uncharacterized region of human chromosome 16 including clone LA16-303A1 (CHR16; GenBank Accession No.: HS303A1), as is shown in table 16B. A MOL16 polypeptide has homology (51% identity, 89% similarity) with a mouse mast cell protease-6 precursor polypeptide (MCP6; SwissProt Accession No.: P21845), as is shown in Table 16C. Also, a MOL16 polypeptide has homology with a human beta-tryptase precursor polypeptide (HBTP; SwissProt Accession No.: P20231), as is shown in Table 16D. Expression profiling of a MOL16 nucleic acid is described in Example 5.

TABLE 16B.

```
MOL16:247    ggaaggacaccgacccgtccatctaccggatccacgctggggacgtgtatctctacgggg 306
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR16: 21749 ggaaggacaccgacccgtccatctaccggatccacgctggggacgtgtatctctacgggg 21690

MOL16:307    gccgggggctgctgaacgtcagccggatcatcgtccaccccaactatgtcactgcggggc 366
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR16: 21689 gccgggggctgctgaacgtcagccggatcatcgtccaccccaactatgtcactgcggggc 21630

MOL16:367    tgggtgcggatgtggccctgctccagctggtgagccccatgatcggagccgctaatgtca 426
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
CHR16: 21629 tgggtgcggatgtggccctgctccagctggtgagccccatgatctgagccgctaatgtca 21570

MOL16:427    ggacggtcaagctctccccggtctcgctggagctcaccccgaaggaccagtgctgggtga 486
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CHR16: 21569 ggacggtcaagctctccccggtctcgctggagctcaccccgaaggaccagtgctgggtga 21510

MOL16:   487 ctggctggggagcgatcaggatgttcg 513 (SEQ ID NO.: 221)
             |||||||||||||||||||||||||||
CHR16: 21509 ctggctggggagcgatcaggatgttcg 21483 (SEQ ID NO.: 222)
```

TABLE 16C.

```
MOL16:    69 PVPENDLVGIVGGHNAPPGKWPWQVSLRVYSYHWASWAHICGGSLIHPQWVLTAAHCIFW 248
             | | |  ||||||| |   ||||||||| +  ++  | | |||||||||||||||||+
MCP6:     23 PRPANQRVGIVGGHEASESKWPWQVSLR-FKLNY--WIHFCGGSLIHPQWVLTAAHCVGP 79

MOL16:   249 KDTDPSIYRIHAGDVYLYGGRGLLNVSRIIVHPNYVTAGLGADVALLQLVSPMIGAANVR 428
                 | ++|+   + ||| |  ||+++||+|||+| ||  |||||||+|  |+  + ++
MCP6:     80 HIKSPQLFRVQLREQYLYYGDQLLSLNRIVVHPHYYTAEGGADVALLELEVPVNVSTHIH 139

MOL16:   429 TVKLSPVSLELTPKDQCWVTGWGAIRMFESLPPPYRLQQASVQVLENAVCEQPYRNASGH 608
              + | | |    |   ||||||| |   | ||||| |+|  | ++||++|++ |     +
MCP6:    140 PISLPPASETFPPGTSCWVTGWGDIDNDEPLPPPYPLKQVKVPIVENSLCDRKYHTGL-Y 198

MOL16:   609 TGDR-QLILDDMLCAGSEGRDSCQGDSGGPLVCRLRGSWRLVGVVSWGYGCTLRDFPGVY 785
             |||   ++ | |||||+  ||||||||||||||+++|+|   |||||| ||   + ||+|
MCP6:    199 TGDDFPIVHDGMLCAGNTRRDSCQGDSGGPLVCKVKGTWLQAGVVSWGEGCAQPNKPGIY 258

MOL16:   786 THVQIYVLWILQQVGE 833 (SEQ ID NO.: 223)
             | |  |+ || + | |
MCP6:    259 TRVTYYLDWIHRYVPE 274 (SEQ ID NO.: 224)
Where | indicates identity and + indicates similarity.
```

TABLE 16D.

```
MOL16:     1 MLWLLFLTLPCLGGSMSKTPVPVPENDLVGIVGGHNAPPGKWPWQVSLRVYSYHWASWAH 60
             || || | || |       | |      ||||||  ||  ||||||||||   |   | |
HBTP:      1 MLNLLLLALPVLASRAYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRV---HGPYWMH 57

MOL16:    61 ICGGSLIHPQWVLTAAHCIFWKDTDPSIYRIHAGDVYLYGGRGLLNVSRIIVHPNYVTAG 120
              |||||||||||||||||+     | +  |+   + +||    || |||||||| + ||
HBTP:     58 FCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQ 117

MOL16:   121 LGADVALLQLVSPMIGAANVRTVKLSPVSLELTPKDQCWVTGWGAIRMFESLPPPYRLQQ 180
```

```
             +|||+|||+|  |+  +++| || | | |    |   ||||||| +   | ||||+ |+|
HBTP:    118 IGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQ 177

MOL16:   546 ASVQVLENAVCEQPYRNASGHTGDR-QLILDDMLCAGSEGRDSCQGDSGGPLVCRLRGSW 722
               | ++|| +|+  | +   +|||  +++ |||||||+  ||||||||||||||++ |+|
HBTP:    178 VKVPIMENHICDAKY-HLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTW 236

MOL16:   181 RLVGVVSWGYGCTLRDFPGVYTHVQIYVLWILQQVGELP 220 (SEQ ID NO.: 225)
                |||||| ||   + ||+|| |  |+ ||   | + |
HBTP:    237 LQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKKP 275 (SEQ ID NO.: 226)
```

Where | indicates identity and + indicates similarity.

The term mastocytosis denotes a heterogenous group of disorders characterized by abnormal growth and accumulation of mast cells in one or more organs. Cutaneous and systemic variants of the disease have been described. Mast cell disorders have also been categorized according to other aspects, such as family history, age, course of disease, or presence of a concomitant myeloid neoplasm. However, so far, generally accepted disease criteria are missing. Recently, a number of diagnostic (disease-related) markers have been identified in mastocytosis research. These include the mast cell enzyme tryptase, CD2, and mast cell growth factor receptor c-kit (CD117). The mast cell enzyme tryptase is increasingly used as a serum- and immunohistochemical marker to estimate the actual spread of disease (burden of neoplastic mast cells). The clinical significance of novel mastocytosis markers is currently under investigation. First results indicate that they may be useful to define reliable criteria for the delineation of the disease.

MOL16 represents a new member of the mast cell protease-6 family of proteins. MOL16 is useful in determining changes in expression of genes contained within the mast cell protease-6 protein family. MOL16 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of the mast cell protease-6-associated protein family of proteins. MOL16 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in potential therapeutic applications implicated in disorders characterized by abnormal growth and accumulation of mast cells in one or more organs including, but not limited to skin, ear and brain as well as other pathologies and disorder such as hemophilia, idiopathic thrombocytopenic purpura, autoimmume disease, allergies, immunodeficiencies, transplantation, graft vesus host, anemia, ataxia-telangiectasia, lymphedema, tonsilitis, hypercoagulation, and sudden infant death syndrome.

The MOL16 nucleic acid and protein of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the MOL16 nucleic acid or the protein are to be assessed.

MOL17

A MOL17 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the sulfate anion transporter family of proteins. A MOL17 nucleic acid is likely to be expressed in the adrenal gland. A MOL17 nucleic acid and its encoded polypeptide includes the sequences shown in Table 17A. The disclosed nucleic acid (SEQ ID NO:195) is 2,145 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 70-72 and ends with a TAG stop codon at nucleotides 1969-1971. The representative ORF encodes a 633 amino acid polypeptide (SEQ ID NO:196) with a predicted molecular weight of 67,472.4 Da. PSORT analysis of a MOL17 polypeptide predicts a peroxisomal localization with a certainty of 0.8000 . SIGNALP analysis suggests the lack of a signal peptide. Putative untranslated regions upstream and downstream of the ORF are underlined in SEQ ID NO.: 195).

TABLE 17A.

GATCCGGGGGCTCCTGTGACCATGCCCTCTTCTCGCCCGCAGGTCGGCCACGG
GACCTGACGCAACAGG**ATG**GACGAGTCCCCTGAGCCTCTGCAGCAGGGCAGA
GGGCCGGTGCCGGTCCGACGCCAGCGCCCAGCACCCCGGGGTCTGCGTGAGA
TGCTGAAGGCCAGGCTGTGGTGCAGCTGCTCGTGCAGTGTGCTGTGCGTCCGG
GCGCTGGTGCAGGACCTGCTCCCCGCCACGCGCTGGCTGCGTCAGTACCGCCC
GCGGGAGTACCTGGCAGGCGACGTCATGTCTGGGCTGGTCATCGGCATCATCC
TGGTCCCGCAGGCCATCGCCTACTCATTGCTGGCCGGGCTGCAGCCCATCTAC
AGCCTCTATACGTCCTTCTTCGCCAACCTCATCTACTTCCTCATGGGCACCTCA
CGGCATGTCTCCGTGGGCATCTTCAGCCTGCTTTGCCTCATGGTGGGGCAGGT
GGTGGACCGGGAGCTCCAGCTGGCCGGCTTTGACCCCTCCCAGGACGGCCTGC
AGCCCGGAGCCAACAGCAGCACCCTCAACGGCTCGGCTGCCATGCTGGACTG
CGGGCGTGACTGCTACGCCATCCGTGTCGCCACCGCCCTCACGCTGATGACCG
GGCTTTACCAGGTCCTCATGGGCGTCCTCCGGCTGGGCTTCGTGTCCGCCTACC
TCTCACAGCCACTGCTCGATGGCTTTGCCATGGGGGCCTCCGTGACCATCCTG
ACCTCGCAGCTCAAACACCTGCTGGGCGTGCGGATCCCGCGGCACCAGGGGC
CCGGCATGGTGGTCCTCACATGGCTGAGCCTGCTGCGCGGCGCCGGGCAGGCC
AACGTGTGCGACGTGGTCACCAGCACGGTGTGCCTGGCGGTGCTGCTAGCCGC
GAAGGAGCTCTCAGACCGCTACCGACACCGCCTGAGGGTGCCGCTGCCCACG
GAGCTGCTGGTCATCGTGGTGGCCACACTCGTGTCGCACTTCGGGCAGCTCCA
CAAGCGCTTTGGCTCGAGCGTGGCTGGCGACATCCCCACGGGTTTCATGCCCC

CTCAGGTCCCAGAGCCCAGGCTGATGCAGCGTGTGGCTTTGGATGCCGTGGCC
CTGGCCCTCGTGGCTGCCGCCTTCTCCATCTCGCTGGCGGAGATGTTCGCCCGC
AGTCACGGCTACTCTGTGCGTGCCAACCAGGAGCTGCTGGCTGTGCATCGTGG
TCACCTGCGGGGGGCCTGCCAAGGTGTGGGACTCCCGGGCTGTGGCGGA**TCA**
CCGGCTGACGCGCTGGTCTGGGCAGGCACGGGCACCTGTATGCTGGTCAGCAC
AGAGGCCGGGCTGCTGGCTGGCGTCATCCTCTCGCTGCTCAGCCTGGCCGGCC
GCACCCAAAAGCCACGCACCGCCCTGCTGGCCCGCATCGGGGACACGGCCTTC
TACGAGGATGCCACAGAGTTCGAGGGCCTCGTCCCTGAGCCCGGCGTGCGGGT
GTTCCGCTTTGGGGGGCCGCTGTACTATGCCAACAAGGACTTCTTCCTGCAGT
CACTCTACAGCCTCACGGGGCTGGACGCAGGGTGCATGGCTGCCAGGAGGAA
GGAGGGGGGCTCAGAGACGGGGGTCGGTGAGGGAGGCCCTGCCCAGGGCGA
GGACCTGGGCCCGGTTAGCACCAGGGCTGCGCTGGTGCCCGCAGCGGCCGGC
TTCCACACAGTGGTCATCGACTGCGCCCCGCTGCTGTTCCTAGACGCAGCCGG
TGTGAGCACGCTGCAGGACCTGCGCCGAGACTACGGGGCCCTGGGCATCAGC
CTGCTGCTAGCCTGCTGCAGCCCGCCTGTGAGAGACATTCTGAGCAGAGGAGG
CTTCCTCGGGGAGGGCCCCGGGGACACGGCTGAGGAGGAGCAGCTGTTCCTC
AGTGTGCACGATGCCGTGCAGACAGCACGAGCCCGCCACAGGGAGCTGGAGG
CCACCGATGCCCATCTG**TAG**CAGGGCCAGGCCTGCCCAGCAGCCTCTGCTCCC
TCCTGGGGACCCACAGCAGACGTCTGCAAGCCACTGCTGAGACCCTTCCCAGG
GAGGAGCCACCCAAGAGCTGCACTCTTGTGCCACAGCTGCCCTGGGAAACC
GGGGAACCCCAACTGGGAAAGGAGGCCCTCTGATCA (SEQ ID NO.: 195)

MDESPEPLQQGRGPVPVRRQRPAPRGLREMLKARLWCSCSCSVLCVRALVQDLL
PATRWLRQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLI
YFLMGTSRHVSVGIFSLLCLMVGQVVDRELQLAGFDPSQDGLQPGANSSTLNGSA
AMLDCGRDCYAIRVATALTLMTGLYQVLMGVLRLGFVSAYLSQPLLDGFAMGA
SVTILTSQLKHLLGVRIPRHQGPGMVVLTWLSLLRGAGQANVCDVVTSTVCLAVL
LAAKELSDRYRHRLRVPLPTELLVIVVATLVSHFGQLHKRFGSSVAGDIPTGFMPP
QVPEPRLMQRVALDAVALALVAAAFSISLAEMFARSHGYSVRANQELLAVHRGH
LRGACQGVGLPGCGGSPADALVWAGTGTCMLVSTEAGLLAGVILSLLSLAGRTQ
KPRTALLARIGDTAFYEDATEFEGLVPEPGVRVFRFGGPLYYANKDFFLQSLYSLT
GLDAGCMAARRKEGGSETGVGEGGPAQGEDLGPVSTRAALVPAAAGFHTVVIDC
APLLFLDAAGVSTLQDLRRDYGALGISLLLACCSPPVRDILSRGGFLGEGPGDTAE
EEQLFLSVHDAVQTARARHRELEATDAHL (SEQ ID NO.: 196)

A MOL17 nucleic acid has a high degree of homology (99% identity) with human sulfate anion transporter mRNA (SAT1; GenBank Accession No.: AF297659), as is shown in Table 17B. A MOL17 polypeptide has homology (74% identity, 81% similarity) with a rat sulfate anion transporter 1 polypeptide (SAT1; SwissProt Accession No.: P45380), as is shown in Table 17C.

TABLE 17B.

```
MOL17:40 caggtcggccacgggacctgacgcaacaggatggacgagtcccctgagcctctgcagcag 99
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 93 caggtcggccacgggacctgacgcaacaggatggacgagtcccctgagcctctgcagcag 152

MOL17:100 ggcagagggccggtgccggtccgacgccagcgcccagcaccccggggtctgcgtgagatg 159
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
SAT1: 153 ggcagagggccggtgccggtccgacggcagcgcccagcaccccggggtctgcgtgagatg 212
```

```
MOL17:160 ctgaaggccaggctgtggtgcagctgctcgtgcagtgtgctgtgcgtccgggcgctggtg 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 213 ctgaaggccaggctgtggtgcagctgctcgtgcagtgtgctgtgcgtccgggcgctggtg 272

MOL17:220 caggacctgctccccgccacgcgctggctgcgtcagtaccgcccgcgggagtacctggca 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 273 caggacctgctccccgccacgcgctggctgcgtcagtaccgcccgcgggagtacctggca 332

MOL17:280 ggcgacgtcatgtctgggctggtcatcggcatcatcctggtcccgcaggccatcgcctac 339
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
SAT1: 333 ggcgacgtcatgtctgggctggtcatcggcatcatcctggtgccgcaggccatcgcctac 392

MOL17:340 tcattgctggccgggctgcagcccatctacagcctctatacgtccttcttcgccaacctc 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 393 tcattgctggccgggctgcagcccatctacagcctctatacgtccttcttcgccaacctc 452

MOL17:400 atctacttcctcatgggcacctcacggcatgtctccgtgggcatcttcagcctgctttgc 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 453 atctacttcctcatgggcacctcacggcatgtctccgtgggcatcttcagcctgctttgc 512

MOL17:460 ctcatggtggggcaggtggtggaccgggagctccagctggccggctttgacccctcccag 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 513 ctcatggtggggcaggtggtggaccgggagctccagctggccggctttgacccctcccag 572

MOL17:520 gacggcctgcagcccggagccaacagcagcaccctcaacggctcggctgccatgctggac 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 573 gacggcctgcagcccggagccaacagcagcaccctcaacggctcggctgccatgctggac 632

MOL17:580 tgcgggcgtgactgctacgccatccgtgtcgccaccgccctcacgctgatgaccgggctt 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 633 tgcgggcgtgactgctacgccatccgtgtcgccaccgccctcacgctgatgaccgggctt 692

MOL17:640 taccaggtcctcatgggcgtcctccggctgggcttcgtgtccgcctacctctcacagcca 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 693 taccaggtcctcatgggcgtcctccggctgggcttcgtgtccgcctacctctcacagcca 752

MOL17:700 ctgctcgatggctttgccatgggggcctccgtgaccatcctgacctcgcagctcaaacac 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 753 ctgctcgatggctttgccatgggggcctccgtgaccatcctgacctcgcagctcaaacac 812

MOL17:760 ctgctgggcgtgcggatcccgcggcaccaggggcccggcatggtggtcctcacatggctg 819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 813 ctgctgggcgtgcggatcccgcggcaccaggggcccggcatggtggtcctcacatggctg 872

MOL17:820 agcctgctgcgcggcgccgggcaggccaacgtgtgcgacgtggtcaccagcacggtgtgc 879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 873 agcctgctgcgcggcgccgggcaggccaacgtgtgcgacgtggtcaccagcacggtgtgc 932

MOL17:880 ctggcggtgctgctagccgcgaaggagctctcagaccgctaccgacaccgcctgagggtg 939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 933 ctggcggtgctgctagccgcgaaggagctctcagaccgctaccgacaccgcctgagggtg 992

MOL17:940 ccgctgcccacggagctgctggtcatcgtggtggccacactcgtgtcgcacttcgggcag 999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 993 ccgctgcccacggagctgctggtcatcgtggtggccacactcgtgtcgcacttcgggcag 1052

MOL17:1000 ctccacaagcgctttggctcgagcgtggctggcgacatccccacgggtttcatgccccct 1059
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 1053 ctccacaagcgctttggctcgagcgtggctggcgacatccccacgggtttcatgccccct 1112

MOL17:1060 caggtcccagagcccaggctgatgcagcgtgtggctttggatgccgtggccctggccctc 1119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 1113 caggtcccagagcccaggctgatgcagcgtgtggctttggatgccgtggccctggccctc 1172

MOL17:1120 gtggctgccgccttctccatctcgctggcggagatgttcgcccgcagtcacggctactct 1179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1: 1173 gtggctgccgccttctccatctcgctggcggagatgttcgcccgcagtcacggctactct 1232
```

```
MOL17:1180 gtgcgtgccaaccaggagctgctggctgtg 1209 (SEQ ID NO.: 227)
           ||||||||||||||||||||||||||||||
SAT1: 1233 gtgcgtgccaaccaggagctgctggctgtg 1262 (SEQ ID NO.: 228)
```

TABLE 17C.

```
MOL17:   70 MDESPEPLQQGRGPVPVRRQRPAPRGLREMLKARLWCSCSCSVLCVRALVQDLLPATRWL 249
            || |||| |+|   | |||| |  +|| | |||||  ||+||+ | +|||| | |  |||
SAT1:     1 MDASPEPPQKGGTLVLVRRQPPVSQGLLETLKARLKKSCTCSMPCAQALVQGLFPVIRWL 60

MOL17:  250 RQYRPREYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 429
             ||| +||||||||||||||||||||||||||||||||||||||||||||||||||||||
SAT1:    61 PQYRLKEYLAGDVMSGLVIGIILVPQAIAYSLLAGLQPIYSLYTSFFANLIYFLMGTSRH 120

MOL17:  430 VSVGIFSLLCLMVGQVVDRELQLAGFDPSQDGLQPGANSSTLNGSAAML----DCGRDCY 597
            |+||||||||||||||||||||||||||||| | || | |||| +| +     ||||||+
SAT1:   121 VNVGIFSLLCLMVGQVVDRELQLAGFDPSQDSLGPGNNDSTLNNTATLTVGLQDCGRDCH 180

MOL17:  598 AIRVATALTLMTGLYQVLMGVLRLGFVSAYLSQPLLDGFAMGASVTILTSQLKHLLGVRI 777
            |||+||||||| ||||||||+||||||| |||||||||||||||||||||| ||||||||
SAT1:   181 AIRIATALTLMAGLYQVLMGILRLGFVSTYLSQPLLDGFAMGASVTILTSQAKHLLGVRI 240

MOL17:  778 PRHQGPGMVVLTWLSLLRGAGQANVCDVVTSTVCLAVLLAAKELSDRYRHRLRVPLPTEL 957
            ||||| |||+ ||||||+  ||||+|||||| ||||||| |||||||||| |+||+||||
SAT1:   241 PRHQGLGMVIHTWLSLLQNVGQANLCDVVTSAVCLAVLLTAKELSDRYRHYLKVPVPTEL 300

MOL17:958 LVIVVATLVSHFGQLHKRFGSSVAGDIPTGFMPPQVPEPRLMQRVALDAVALALVAAAFS 1137
          |||||||+ ||||||| ||||||||+|||||+ ||+|+|++|  |||||++|||| +|||
SAT1: 301 LVIVVATIASHFGQLHTRFGSSVAGNIPTGFVAPQIPDPKIMWSVALDAMSLALVGSAFS 360

MOL17:1138 ISLAEMFARSHGYSVRANQELLAVHRGHLRGACQGVGLPG---CGGSPA---DALVWAGT 1299
            ||||||||||||||| ||||||||      | |    ||    |  + |     ||   |
SAT1:   361 ISLAEMFARSHGYSVSANQELLAV------GCCNV--LPAFFHCFATSAALSKTLVKIAT 412

MOL17: 1300 GTCMLVSTEAGLLAGVILSLLSLA 1371 (SEQ ID NO.: 229)
            | |    +     | |+| || ||
SAT1:   413 G-CQTQLSSVVSAAVVLLVLLVLA 435 (SEQ ID NO.: 230)
Where | indicates identity and + indicates similarity.
```

Sulfate anion transporter proteins are members of the superfamily of anion exchangers. Two vertebrate sulfate transporters that play a role in sulfate incorporation in tissues are members of the superfamily of anion exchangers: the diastrophic dysplasia sulfate transporter, which is mutant in diastrophic dysplasia and certain other skeletal dysplasias, and downregulated in adenoma, which is mutant in familial chloride diarrhea. By subtractive hybridization, Schweinfest and co-workers isolated a cDNA for a tumor suppressor candidate gene, which they called DRA (downregulated in adenoma), from a normal colon tissue cDNA library. Its expression, which appeared to be limited to the mucosa of normal colon, was significantly decreased in adenomas and adenocarcinomas of the colon and was downregulated early in tumorigenesis (See Schweinfest *et al.*, 1993, Proc. Nat. Acad. Sci. U.S.A. 90:4166). These two sulfate transporters contain twelve membrane-spanning domains and are sensitive to the anion-exchanger inhibitor DIDS.

Girard and colleagues demonstrated that HEVECs express 2 functional classes of sulfate transporters defined by their differential sensitivity to the DIDS anion-exchanger inhibitor. They reported the molecular characterization of a DIDS-resistant sulfate transporter from human HEVECs, designated SUT1 (See Girard *et al.*, 1999, Proc. Nat. Acad. Sci. U.S.A. **96**:12772). SUT1 belongs to the family of sodium-coupled anion transporters and exhibits 40 to 50% amino acid identity with the rat renal sodium/sulfate cotransporter NaSi1, as well as with the human and rat sodium/dicarboxylate cotransporters NADC1/SDCT1 and NADC3/SDCT2. Functional expression studies in cRNA-injected Xenopus laevis oocytes showed that SUT1 mediates high levels of sodium-dependent sulfate transport, which is resistant to DIDS inhibition. Northern blot analysis showed that SUT1 exhibits a highly restricted tissue distribution, with abundant expression in placenta. Reverse transcription-PCR analysis indicated that SUT1 and DTDST were coexpressed in HEVECs. SUT1 and DTDST may correspond, respectively, to the DIDS-resistant and DIDS-sensitive components of sulfate uptake in HEVEC (See Girard *et al.*, 1999, Proc. Nat. Acad. Sci. U.S.A. **96**:12772).

Girard and colleagues also mapped the SUT1 gene to 7q33 by finding a sequence tagged site (STS) corresponding to nucleotides 2579-2833 of the SUT1 cDNA. This STS mapped to chromosome 7 at D7S509, which maps to 7q33 close to 7q32. They confirmed these mapping data by identifying ESTs with sequence identity to SUT1 cDNA that mapped between markers D7S500 and D7S509 on 7q33 (See Girard *et al.*, 1999, Proc. Nat. Acad. Sci. U.S.A. **96**:12772).

MOL17 represents a new member of the sulfate anion transporter family of proteins. MOL17 is useful in determining changes in expression of genes contained within the sulfate anion transporter protein family. MOL17 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of the sulfate anion transporter-associated protein family of proteins. MOL17 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving disorders such as Pendred syndrome, skeletal dysplasias, diastrophic dysplasia, cancer, adenoma.

MOL18

A MOL18 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the cytostatin family of proteins. A MOL18 nucleic acid was identified on human chromosome 1. A MOL18 nucleic acid and its encoded polypeptide includes the sequences shown in Table 18A. The disclosed nucleic acid (SEQ ID NO:197) is 406 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 1-3 and ends with a TAA stop codon at nucleotides 397-399. The representative ORF encodes a 132 amino acid polypeptide (SEQ ID NO:198) with a predicted molecular weight of 15,599.6 Da. PSORT analysis of a MOL18 polypeptide predicts a peroxisomal localization with a certainty of 0.6400. SIGNALP analysis suggests the lack of a signal peptide. Putative untranslated regions downstream of the ORF are underlined in SEQ ID NO.: 197).

TABLE 18A.

GTGGAGGAGGCTTTCTGTAATACCTGGAAGCTGACCGACCAGAACTTTGATG
AGTACATGAAGGCTCTAGGGATGGGCTTTGTCACTAGGCAGGTGGGAAATGT
GGACAAACCAAGAGTGATTATCAGTCAAGAAGAAGACAAGGTGGTGATCAGG
ATTCAAAGTATGTTCAAGAACACAGAGGTTAGTTTCCATCTGGGAGAAGAGTT
TGATGAAACCACTACAGATGACAGAAACTGCAAGTTTGTTGTTAGTCTGGACA
GAGACAAACTCATTCACATACAGAAATGGGATGACAAAGAAACATATTTTAT
AAGAGAAATTAAGTATGGTGAAATGGTTATGACCTTTACTTTTGGTGATGATG
TGGTTGCCGTTCACCACTATAAGAAGGCA**TAA**<u>AAATGTT</u> (SEQ ID NO.: 197)

VEEAFCNTWKLTDQNFDEYMKALGMGFVTRQVGNVDKPRVIISQEEDKVVIRIQS
MFKNTEVSFHLGEEFDETTTDDRNCKFVVSLDRDKLIHIQKWDDKETYFIREIKYG
EMVMTFTFGDDVVAVHHYKKA (SEQ ID NO.: 198)

A MOL18 nucleic acid has homology (88% identity) with a human cytostatin II mRNA (CYT2; Patn Accession No.: T74751), as is shown in Table 18B. A MOL18 polypeptide has homology (80% identity, 86% similarity) with a human cytosatin II polypeptide (CYT2; PatP Accession No.: W22408), as is shown in Table 18C. A MOL18 polypeptide also has homology (80% identity, 86% similarity) with a human fatty acid-binding protein (FABP; SwissProt. Accession No.: O15540), as is shown in Table 18D. Expression profiling of a MOL18 nucleic acid is described in Example 7.

TABLE 18B.

```
MOL18:    2 TGGAGGAGGCTTTCTGTAATACCTGGAAGCTGACCGAC---CAGAACTTTGATGAGTACA 58
            ||| |||||||||||||   |||||||||||||||| ||   |||||||||||||||||||
CYT2:    17 TGGTGGAGGCTTTCTGTGCTACCTGGAAGCTGACCAACAGTCAGAACTTTGATGAGTACA 76

MOL18:   59 TGAAGGCTCTAGGGATGGGCTTTGTCACTAGGCAGGTGGGAAATGTGGACAAACCAAGAG 118
            |||||||||||||  ||||||||| ||||||||||||||||||||||  ||||||||  |
CYT2:    77 TGAAGGCTCTAGGCGTGGGCTTTGCCACTAGGCAGGTGGGAAATGTGACCAAACCAACGG 136
```

```
MOL18: 119 TGATTATCAGTCAAGAAGAAGACAAGGTGGTGATCAGGATTCAAAGTATGTTCAAGAACA 178
           | |||||||||||||||| |||||| ||||| ||||||| ||  || |  ||||||||||
CYT2:  137 TAATTATCAGTCAAGAAGGAGACAAAGTGGTCATCAGGACTCTCAGCACATTCAAGAACA 196

MOL18: 179 CAGAGGTTAGTTTCCATCTGGGAGAAGAGTTTGATGAAACCACTACAGATGACAGAAACT 238
           | ||| |||||||||| ||||||||||||||||||||||||||| ||||||| |||||||
CYT2:  197 CGGAGATTAGTTTCCAGCTGGGAGAAGAGTTTGATGAAACCACTGCAGATGATAGAAACT 256

MOL18: 239 GCAAGTTTGTTGTTAGTCTGGACAGAGACAAACTCATTCACATACAGAAATGGGATGACA 298
           | |||| ||||||||| |||||  ||||||||||  ||||||||||||||||||||| ||
CYT2:  257 GTAAGTCTGTTGTTAGCCTGGATGGAGACAAACTTGTTCACATACAGAAATGGGATGGCA 316

MOL18: 299 AAGAAACATATTTTATAAGAGAAATTAAGTATGGTGAAATGGTTATGACCTTTACTTTTG 358
           |||||||| ||||| |||||||||||||| ||||  |||||||||||||| |||||||||
CYT2:  317 AAGAAACAAATTTTGTAAGAGAAATTAAGGATGGCAAAATGGTTATGACCCTTACTTTTG 376

MOL18:359 GTGATGATGTGGTTGCCGTTCACCACTATAAGAAGGCATAAAAATGT 405(SEQ ID NO.: 231)
          |||||| || | |||| |||| ||||||| |||||||||||||||||
CYT2: 377 GTGATG-TG-G-TTGCTGTTCGCCACTATGAGAAGGCATAAAAATGT 420(SEQ ID NO.: 232)
```

TABLE 18C.

```
MOL18:    7 EAFCNTWKLTD-QNFDEYMKALGMGFVTRQVGNVDKPRVIISQEEDKVVIRIQSMFKNTE 183
            |||| |||||+ |||||||||||+|| ||||||| || |||||| ||||||  | |||||
CYT2:     3 EAFCATWKLTNSQNFDEYMKALGVGFATRQVGNVTKPTVIISQEGDKVVIRTLSTFKNTE 62

MOL18:  184 VSFHLGEEFDETTTDDRNCKFVVSLDRDKLIHIQKWDDKETYFIREIKYGEMVMTFTFGD 363
            +|| ||||||||| |||||| ||||| |||+|||||| ||| |+|||| |+|||| ||||
CYT2:    63 ISFQLGEEFDETTADDRNCKSVVSLDGDKLVHIQKWDGKETNFVREIKDGKMVMTLTFGD 122

MOL18:  364 DVVAVHHYKKA 396 (SEQ ID NO.: 233)
             |||| ||+||
CYT2:   123 -VVAVRHYEKA 132 (SEQ ID NO.: 234)
```

Where | indicates identity and + indicates similarity.

TABLE 18D.

```
MOL18:    7 EAFCNTWKLTD-QNFDEYMKALGMGFVTRQVGNVDKPRVIISQEEDKVVIRIQSMFKNTE 183
            |||| |||||+ |||||||||||+|| ||||||| || |||||| ||||||  | |||||
FABP:     3 EAFCATWKLTNSQNFDEYMKALGVGFATRQVGNVTKPTVIISQEGDKVVIRTLSTFKNTE 62

MOL18:  184 VSFHLGEEFDETTTDDRNCKFVVSLDRDKLIHIQKWDDKETYFIREIKYGEMVMTFTFGD 363
            +|| ||||||||| |||||| ||||| |||+|||||| ||| |+|||| |+|||| ||||
FABP:    63 ISFQLGEEFDETTADDRNCKSVVSLDGDKLVHIQKWDGKETNFVREIKDGKMVMTLTFGD 122

MOL18:  364 DVVAVHHYKKA 396 (SEQ ID NO.: 235)
             |||| ||+||
FABP:   123 -VVAVRHYEKA 132 (SEQ ID NO.: 236)
```

Where | indicates identity and + indicates similarity.

MOL19

A MOL19 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the cytostatin family of proteins. A MOL19 nucleic acid was identified on human chromosome 1. A MOL19 nucleic acid and its encoded polypeptide includes the sequences shown in Table 19. The disclosed nucleic acid (SEQ ID NO:199) is 418 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 4-6 and ends with a TAA stop codon at nucleotides 409-411. The representative ORF encodes a 135 amino acid polypeptide (SEQ ID NO:200). Putative untranslated regions upstream and downstream of the ORF are underlined in SEQ ID NO.: 199.

TABLE 19A.

ATA**ATG**GTAAGGGTGGAGGAGGCTTTCTGTAATACCTGGAAGCTGACCGACC
AGAACTTTGATGAGTACATGAAGGCTCTAGGGATGGGCTTTGTCACTAGGCAG
GTGGGAAATGTGGACAAACCAAGAGTGATTATCAGTCAAGAAGAAGACAAGG
TGGTGATCAGGATTCAAAGTATGTTCAAGAACACAGAGGTTAGTTTCCATCTG
GGAGAAGAGTTTGATGAAACCACTACAGATGACAGAAACTGCAAGTTTGTTG
TTAGTCTGGACAGAGACAAACTCATTCACATACAGAAATGGGATGACAAAGA
AACATATTTTATAAGAGAAATTAAGTATGGTGAAATGGTTATGACCTTTACTT
TTGGTGATGATGTGGTTGCCGTTCACCACTATAAGAAGGCA**TAA**AAATGTT
(SEQ ID NO.: 199)

MVRVEEAFCNTWKLTDQNFDEYMKALGMGFVTRQVGNVDKPRVIISQEEDKVVI
RIQSMFKNTEVSFHLGEEFDETTTDDRNCKFVVSLDRDKLIHIQKWDDKETYFIRE
IKYGEMVMTFTFGDDVVAVHHYKKA (SEQ ID NO.: 200)

A MOL19 nucleic acid has homology (88% identity) with a human cytostatin II mRNA (CYT2; Patn Accession No.: T74751). A MOL19 polypeptide has homology (80% identity, 86% similarity) with a human cytosatin II polypeptide (CYT2; PatP Accession No.: W22408). A MOL19 polypeptide also has homology (80% identity, 86% similarity) with a human fatty acid-binding protein (FABP; SwissProt. Accession No.: O15540). A region of a MOL19 polypeptide also has a high degree of homology (100%) with MOL18, as is shown in Table 19B.

TABLE 19B.

```
MOL19:4  VEEAFCNTWKLTDQNFDEYMKALGMGFVTRQVGNVDKPRVIISQEEDKVVIRIQSMFKNT 63
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MOL18:1  VEEAFCNTWKLTDQNFDEYMKALGMGFVTRQVGNVDKPRVIISQEEDKVVIRIQSMFKNT 60

MOL19:64 EVSFHLGEEFDETTTDDRNCKFVVSLDRDKLIHIQKWDDKETYFIREIKYGEMVMTFTFG
123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MOL18:61 EVSFHLGEEFDETTTDDRNCKFVVSLDRDKLIHIQKWDDKETYFIREIKYGEMVMTFTFG
120

MOL19: 124 DDVVAVHHYKKA 135 (SEQ ID NO.: 237)
            ||||||||||||
MOL18: 121 DDVVAVHHYKKA 132 (SEQ ID NO.: 238)
Where | indicates identity.
```

Cytostatin, which was originally isolated from a microbial cultured broth as a low molecular weight inhibitor of cell adhesion to extracellular matrix (ECM), has anti-metastatic activity against B16 melanoma cells in vivo. Inhibition of cell adhesion to ECM by cytostatin has been evaluated (See Kawada *et al*., 1999, Biochim. Biophys. Acta **1452**:209). Cytostatin inhibited tyrosine phosphorylation of focal adhesion kinase (FAK) and paxillin upon B16 cell adhesion to fibronectin. While the amount of FAK was not affected by cytostatin, electrophoretically slow-migrating paxillin appeared. Alkaline phosphatase treatment diminished cytostatin-induced slow-migrating paxillin. Furthermore, cytostatin increased intracellular serine/threonine-phosphorylated proteins and was found to be a selective inhibitor of protein phosphatase 2A (PP2A). Cytostatin inhibited PP2A with an IC(50) of 0.09 microgram/ml in a non-competitive manner against a substrate, p-nitrophenyl phosphate, but it had no apparent effect on other protein phosphatases including PP1, PP2B and alkaline phosphatase even at 100 microgram/ml. On the contrary, dephosphocytostatin, a cytostatin analogue, without inhibitory effect on PP2A did not affect B16 cell adhesion including FAK and paxillin. These results indicate that cytostatin inhibits cell adhesion through modification of focal contact proteins such as paxillin by inhibiting a PP2A type protein serine/threonine phosphatase.

Differential induction of apoptosis by cytostatin vis-à-vis another apoptosis inducer- bactobolin has been analyzed. Since, most solid tumor cells are less sensitive to apoptosis induced by anticancer drugs than hematopoietic cancer cells, Kawada and co-workers used B16 melanoma and EL-4 lymphoma cells as models for solid tumor- and hematopoietic cancer-derived cell lines respectively. It was found that apoptosis in B16 cells was induced strongly by bactobolin, but weakly by cytostatin. In contrast, apoptosis in EL-4 cells was induced strongly by cytostatin, but weakly by bactobolin. (See Kawada et al., 1999, Jpn. J. Cancer Res. **90**:219).

The nucleotide sequence encoding Human cytostatin can be used for inhibiting cell growth and modulate cellular differentiation. The cytostatin II polypeptides encoded by the gene can be used for inhibiting tumour growth in a subject, for stimulating growth of or protecting nervous system cells from toxic agents or for protecting against or treating viral or microbial infections in mammals. The activity of haematopoiesis by cytostatins indicate a possible immunosuppressive activity or a lineage specific stimulation of haematopoiesis. Cytostatins thus could be used for treating conditions requiring immunosuppression. Antagonists to cytostatin may be used in vitro or in vivo to induce deficiencies or enhancement in the immune or in the haematopoietic systems. They may be used e.g. to treat cardiac myocyte hypertrophy or leukemia. The cytostatin gene product can also be used to modulate angiogenesis, to inhibit metastasis of various cancers including but not limited to breast cancer, brain and other tumors. The cytostatin polypeptide can be used amongst other things to modulate breast development and milk production. The retinoid binding potential of cytostatin derived polypetides may be used on photo receptor cells in vivo or in vitro. The cytostatin polypeptides might also be used in cerebella granular cells and photo receptor cells to provide protection from lipid peroxidation associated with the oxidative stress induced during early stages of ischemia, apoptosis, and excitatory amino acid induced cell death.

MOL18-9 represent two new members of the cytostatin family of proteins. The high degree of homology between MOL18 and MOL19 indicates that MOL18-9 consitute a new sub-family of the cytostatin family of proteins, and are useful to identify sub-family-specific binding proteins. MOL18-9 are useful in determining changes in expression of genes contained within the cytostatin protein family. MOL18-9 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of the cytostatin-associated protein family of proteins. MOL18-9 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving disorders characterized by altered cell shape, motility, and apoptosis, *e.g.* cancer and ischemic injury.

MOL20

MOL20 encodes two proteins related to the chemokine receptor family which are discussed below. The disclosed proteins have been named MOL20 and MOL20.

MOL20a

A MOL20a sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the chemokine receptor family of proteins. A MOL20 nucleic acid was identified on human chromosome 1. A MOL20 nucleic acid and its encoded polypeptide includes the sequences shown in Table 20A. The disclosed nucleic acid (SEQ ID NO:201) is 1,119 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA stop codon at nucleotides 1,117-1,119. The representative ORF encodes a 372 amino acid polypeptide (SEQ ID NO:202) with a predicted molecular weight of 42,793.9 Da. PSORT analysis of a MOL20 polypeptide predicts a plasma membrane protein with a certainty of

0.6400. SIGNALP analysis suggests the presence of a signal peptide with the most likely cleavage site occuring between positions 47 and 48 of SEQ ID NO.: 202.

TABLE 20A.

ATGGAGCACACGCACGCCCACCTCGCAGCCAACAGCTCGCTGTCTTGGTGGTC
CCCCGGCTCGGCCTGCGGCTTGGGTTTCGTGCCCGTGGTCTACTACAGCCTCTT
GCTGTGCCTCGGTTTACCAGCAAATATCTTGACAGTGATCATCCTCTCCCAGCT
GGTGGCAAGAAGACAGAAGTCCTCCTACAACTATCTCTTGGCACTCGCTGCTG
CCGACATCTTGGTCCTCTTTTTCATAGTGTTTGTGGACTTCCTGTTGGAAGATT
TCATCTTGAACATGCAGATGCCTCAGGTCCCCGACAAGATCATAGAAGTGCTG
GAATTCTCATCCATCCACACCTCCATATGGATTACTGTACCGTTAACCATTGAC
AGGTATATCGCTGTCTGCCACCCGCTCAAGTACCACACGGTCTCATACCCAGC
CCGCACCCGGAAAGTCATTGTAAGTGTTTACATCACCTGCTTCCTGACCAGCA
TCCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTCT
GTGCATCACGTCCTCATCTGGATCCACTGCTTCACCGTCTACCTGGTGCCCTGC
TCCATCTTCTTCATCTTGAACTCAATCATTGTGTACAAGCTC
AGGAGGAAGAGCAATTTTCGTCTCCGTGGCTACTCCACGGGGAAGACCACCG
CCATCTTGTTCACCATTACCTCCATCTTTGCCACACTTTGGGCCCCCCGCATCA
TCATGATTCTTTACCACCTCTATGGGGCGCCCATCCAGAACCGCTGGCTGGTA
CACATCATGTCCGACATTGCCAACATGCTAGCCCTTCTGAACACAGCCATCAA
CTTCTTCCTCTACTGCTTCATCAGCAAGCGGTTCCGCACCATGGCAGCCGCCAC
GCTCAAGGCTTTCTTCAAGTGCCAGAAGCAACCTGTACAGTTCTACACCAATC
ATAACTTTTCCATAACAAGTAGCCCCTGGATCTCGCCGGCAAACTCACACTGC
ATCAAGATGCTGGTGTACCAGTATGACAAAAATGGAAAACCTATAAAAAGTC
GTAATGACAGCAAAAGCTCCTACCAGTTTGAAGATGCCATTGGAGCTTGTGTC
ATCATCCTG**TGA** (SEQ ID NO.: 201)

MEHTHAHLAANSSLSWWSPGSACGLGFVPVVYYSLLLCLGLPANILTVIILSQLVA
RRQKSSYNYLLALAAADILVLFFIVFVDFLLEDFILNMQMPQVPDKIIEVLEFSSIHT
SIWITVPLTIDRYIAVCHPLKYHTVSYPARTRKVIVSVYITCFLTSIPYYWWPNIWT
EDYISTSVHHVLIWIHCFTVYLVPCSIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAIL
FTITSIFATLWAPRIIMILYHLYGAPIQNRWLVHIMSDIANMLALLNTAINFFLYCFI
SKRFRTMAAATLKAFFKCQKQPVQFYTNHNFSITSSPWISPANSHCIKMLVYQYD
KNGKPIKSRNDSKSSYQFEDAIGACVIIL (SEQ ID NO.: 202)

A MOL20 polypeptide has homology (29% identity, 51% similarity) with a human chemokine receptor type I (HCR1; SwissProt Accession No.: P32246), as is shown in Table 20B.

TABLE 20B.

```
MOL20:    22 ACGLGFVPVVYYSLLLCLGLPANILTVIILSQLVARRQKSSYNYLLALAAADILVLFFIV 81
             | |   +| +| ||+  +||  ||| |++| |    +  +|  ||| || +|+| || +
HCR1:     31 AFGAQLLPPLY-SLVFVIGLVGNILVVLVLVQYKRLKNMTSI-YLLNLAISDLLFLFTLP 88

MOL20:     82 F-VDFLL-EDFILNMQMPQVPDKIIEVLEFSSIHTSIWITVPLTIDRYIAVCHP---LKY 137
              | +|+ | +|++    |     ||+    ++ +++ |+  + ||||||+|+ |    |+
HCR1:      89 FWIDYKLKDDWVFGDAMC----KILSGFYYTGLYSEIFFIILLTIDRYLAIVHAVFALRA 144

MOL20:    138 HTVSYPARTRKVIVSVYITCFLTSIP-YYWWPNIWTEDYISTSVH--HVLI--W------ 186
               ||++   |  +| ++ |   | |+|  |+    |   + + |+|  |  +  |
```

```
HCR1:    145  RTVTFGVITSIIIWALAI---LASMPGLYFSKTQWEFTHHTCSLHFPHESLREWKLFQAL 201

MOL20:    187 -IHCFTVYLVPCSIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAILFTITSIFATLWAPR 244
               ++ | + | |  +  |  + |+  | |+ | +       |   ++| |  ||   | |
HCR1:    202  KLNLFGLVL-PLLVMIICYTGIIKILLRRPNEK-----KSKAVRLIFVIMIIFFLFWTPY 255

MOL20:245 IIMILYHLYGAPI------QNRWLVHIMSDIANMLALLNTAINFFLYCFISKRFR 294 (SEQ ID
NO.: 239)
           + ||  ++   +      |+| |  +   +  ++|  +  +|  +| |+ +|||
HCR1: 256 NLTILISVFQDFLFTHECEQSRHL-DLAVQVTEVIAYTHCCVNPVIYAFVGERFR 309 (SEQ ID
NO.: 240)
```

Where | indicates identity and + indicates similarity.

MOL20b

A MOL20b sequence according to the invention includes a nucleic acid sequence encoding a polypeptide (also referred to as GM_38019075_A_Cura_348) related to the chemokine receptor family of proteins. A MOL20b nucleic acid and its encoded polypeptide includes the sequences shown in Table 20C. The disclosed nucleic acid (SEQ ID NO:310) is 957 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 1-3 and ends with a TGA stop codon at nucleotides 955-957. The representative ORF encodes a 372 amino acid polypeptide (SEQ ID NO:311).

Table 20C

ATGAGCACACCAGGTTTTGCAGCAAATATCTTGACAGTGATCATCCTCTCCCAGCTGGTGGCAAGAAGACAGAAGTCCTC
CTACAACTATCTCTTGGCACTCGCTGCTGCCGACATCTTGGTCCTCTTTTTCATAGTGTTTGTGGACTTCCTGTTGGAAG
ATTTCATCTTGAACATGCAGATGCCTCAGGTCCCCGACAAGATCATAGAAGTGCTGGAATTCTCATCCATCCACACCTCC
ATATGGATTACTGTACCGTTAACCATTGACAGGTATATCGCTGTCTGCCACCCGCTCAAGTACCACACGGTCTCATACCC
AGCCCGCACCCGGAAAGTCATTGTAAGTGTTTACATCACCTGCTTCCTGACCAGCATCCCCTATTACTGGTGGCCCAACA
TCTGGACTGAAGACTACATCAGCACCTCTGTGCATCACGTCCTCATCTGGATCCACTGCTTCACCGTCTACCTGGTGCCC
TGCTCCATCTTCTTCATCTTGAACTCAATCATTGTGTACAAGCTCAGGAGGAAGAGCAATTTTCGTCTCCGTGGCTACTC
CACGGGGAAGACCACCGCCATCTTGTTCACCATTACCTCCATCTTTGCCACACTTTGGGCCCCCCGCATCATCATGATTC
TTTACCACCTCTATGGGGCGCCCATCCAGAACCGCTGGCTGGTACACATCATGTCCGACATTGCCAACATGCTAGCCCTT
CTGAACACAGCCATCAACTTCTTCCTCTACTGCTTCATCAGCAAGCGGTTCCGCACCATGGCAGCCGCCACGCTCAAGGC
TTTCTTCAAGTGCCAGAAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCCATAACAAGTAGCCCCTGGATCTCGC
CGGCAAACTCACACTGCATCAAGATGCTGGTGTACCAGTATGACAAAAATGGAAAACCTATAAAAGTATCCCCGTGA
(SEQ ID NO:310)

MSTPGFAANILTVIILSQLVARRQKSSYNYLLALAAADILVLFFIVFVDFLLEDFILN
MQMPQVPDKIIEVLEFSSIHTSIWITVPLTIDRYIAVCHPLKYHTVSYPARTRKVIVS
VYITCFLTSIPYYWWPNIWTEDYISTSVHHVLIWIHCFTVYLVPCSIFFILNSIIVYKL
RRKSNFRLRGYSTGKTTAILFTITSIFATLWAPRIIMILYHLYGAPIQNRWLVHIMSD
IANMLALLNTAINFFLYCFISKRFRTMAAATLKAFFKCQKQPVQFYTNHNFSITSSP
WISPANSHCIKMLVYQYDKNGKPIKVSP (SEQ ID NO:311)

MOL21

A MOL21 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the chemokine receptor family of proteins. A MOL21 nucleic acid was identified on human chromosome 1. A MOL21 nucleic acid and its encoded polypeptide includes the sequences shown in Table 21A. The disclosed nucleic acid (SEQ ID NO:203) is 1,343 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 2-4 and ends with a TGA stop codon at nucleotides 1.061-1,063. The representative ORF encodes a 353 amino acid polypeptide (SEQ ID NO:204). PSORT analysis of a MOL21 polypeptide predicts a plasma membrane protein with a certainty of 0.6400. SIGNALP analysis suggests the presence of a signal peptide with the most likely cleavage site occuring between positions 47 and 48 of SEQ ID NO.: 204. Putative untranslated regions upstream and downstream of the ORF are underlined in SEQ ID NO.: 203.

TABLE 21A.

T**ATG**GAGCACACGCACGCCCACCTCGCAGCCAACAGCTCGCTGTCTTGGTGGT
CCCCCGGCTCGGCCTGCGGCTTGGGTTTCGTGCCCGTGGTCTACTACAGCCTCT
TGCTGTGCCTCGGTTTACCAGCAAATATCTTGACAGTGATCATCCTCTCCCAGC
TGGTGGCAAGAAGACAGAAGTCCTCCTACAACTATCTCTTGGCACTCGCTGCT
GCCGACATCTTGGTCCTCTTTTTCATAGTGTTTGTGGACTTCCTGTTGGAAGAT
TTCATCTTGAACATGCAGATGCCTCAGGTCCCCGACAAGATCATAGAAGTGCT
GGAATTCTCATCCATCCACACCTCCATATGGATTACTGTACCGTTAACCATTGA
CAGGTATATCACTGTCTGCCACCCGCTCAAGTACCACACGGTCTCATACCCAG
CCCGCACCCGGAAAGTCATTGTAAGTGTTTACATCACCTGCTTCCTGACCAGC
ATCCCCTATTACTGGTGGCCCAACATCTGGACTGAAGACTACATCAGCACCTC
TGTGCATCACGTCCTCATCTGGATCCACTGCTTCACCGTCTACCTGGTGCCCTG
CTCCATCTTCTTCATCTTGAACTCAATCATTGTGTACAAGCTCAGGAGGAAGA
GCAATTTTCGTCTCCGTGGCTACTCCACGGGGAAGACCACCGCCATCTTGTTC
ACCATTACCTCCATCTTTGCCACACTTTGGGCCCCCCGCATCATCATGATTCTT
TACCACCTCTATGGGGCGCCCATCCAGAACCGCTGGCTGGTACACATCATGTC
CGACATTGCCAACATGCTAGCCCTTCTGAACACAGCCATCAACTTCTTCCTCTA
CTGCTTCATCAGCAAGCGGTTCCGCACCATGGCAGCCGCCACGCTCAAGGCTT
TCTTCAAGTGCCAGAAGCAACCTGTACAGTTCTACACCAATCATAACTTTTCC
ATAACAAGTAGCCCCTGGATCTCGCCGGCAAACTCACACTGCATCAAGATGCT
GGTGTACCAGTATGACAAAAATGGAAAACCTATAAAAGTATCCCCG**TGA**TTC
CATAGGTGTGGCAACTACTGCCTCTGTCTAATCCATTTCCAGATGGAAGGTG
TCCCATCCTATGGCTGAGCAGCTCTCCTTAAGAGTGCTAATCCGATTTCCTGTC
TCCCGCAGACTGGGCAATTCTCAGACTGGTAGATGAGAAGAGATGGAAGAGA
AGAAAGGAGAGCATGAAGCTTGTTTTTACTTATGCATTTATTTCCACAGAGTC
GTAATGACAGCAAAAGCTCCTACCAGTTTGAAGATGCCATTGGAGCTTGTGTC
ATCATCCTGTGA (SEQ ID NO.: 203)

MEHTHAHLAANSSLSWWSPGSACGLGFVPVVYYSLLLCLGLPANILTVIILSQLVA
RRQKSSYNYLLALAAADILVLFFIVFVDFLLEDFILNMQMPQVPDKIIEVLEFSSIHT
SIWITVPLTIDRYITVCHPLKYHTVSYPARTRKVIVSVYITCFLTSIPYYWWPNIWTE
DYISTSVHHVLIWIHCFTVYLVPCSIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAILF
TITSIFATL
WAPRIIMILYHLYGAPIQNRWLVHIMSDIANMLALLNTAINFFLYCFISKRFRTMA
AATLKAFFKCQKQPVQFYTNHNFSITSSPWISPANSHCIKMLVYQYDKNGKPIKVS
P (SEQ ID NO.: 204)

A MOL21 polypeptide has homology (29% identity, 51% similarity) with a human chemokine receptor type I (HCR1; SwissProt Accession No.: P32246). MOL21 also has a high degree of homology (99% identity) with a MOL20 polypeptide, as is shown in Table 21B. Expression profiling of a MOL21 nucleic acid is described in Example 6.

TABLE 21B.

```
MOL21: 1 MEHTHAHLAANSSLSWWSPGSACGLGFVPVVYYSLLLCLGLPANILTVIILSQLVARRQK 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MOL20: 1 MEHTHAHLAANSSLSWWSPGSACGLGFVPVVYYSLLLCLGLPANILTVIILSQLVARRQK 60

MOL21: 61 SSYNYLLALAAADILVLFFIVFVDFLLEDFILNMQMPQVPDKIIEVLEFSSIHTSIWITV 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MOL20: 61 SSYNYLLALAAADILVLFFIVFVDFLLEDFILNMQMPQVPDKIIEVLEFSSIHTSIWITV 120

MOL21: 121 PLTIDRYITVCHPLKYHTVSYPARTRKVIVSVYITCFLTSIPYYWWPNIWTEDYISTSVH 180
           |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
MOL20: 121 PLTIDRYIAVCHPLKYHTVSYPARTRKVIVSVYITCFLTSIPYYWWPNIWTEDYISTSVH 180

MOL21: 181 HVLIWIHCFTVYLVPCSIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAILFTITSIFATL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MOL20: 181 HVLIWIHCFTVYLVPCSIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAILFTITSIFATL 240

MOL21: 241 WAPRIIMILYHLYGAPIQNRWLVHIMSDIANMLALLNTAINFFLYCFISKRFRTMAAATL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MOL20: 241 WAPRIIMILYHLYGAPIQNRWLVHIMSDIANMLALLNTAINFFLYCFISKRFRTMAAATL 300

MOL21: 301 KAFFKCQKQPVQFYTNHNFSITSSPWISPANSHCIKMLVYQYDKNGKPIK 350 (SEQ ID NO.:
241)
           ||||||||||||||||||||||||||||||||||||||||||||||||||
MOL20: 301 KAFFKCQKQPVQFYTNHNFSITSSPWISPANSHCIKMLVYQYDKNGKPIK 350 (SEQ ID NO.:
242)
```

Where | indicates identity.

Chemokine receptors are G protein-coupled receptors that mediate migration and activation of leukocytes as an important part of a protective immune response to injury and infection (See Rojo *et al.*, 1999 Biol. Res. **32**:263). In addition, chemokine receptors are used by HIV-1 to infect CD4 positive cells. The structural bases of chemokine receptor recognition and signal transduction are currently being investigated. High-resolution X-ray diffraction and NMR spectroscopy of chemokines indicate that all these peptides exhibit a common folding pattern, in spite of its low degree of primary-sequence homology. Chemokines' functional motifs have been identified by mutagenesis studies, and a possible mechanism for receptor recognition and activation is proposed, but high-resolution structure data of chemokine receptors is not yet available. Studies with receptor chimeras have identified the putative extracellular domains as the major selectivity determinants. Single-amino acid substitutions in the extracellular domains produce profound changes in receptor specificity, suggesting that motifs in these domains operate as a restrictive barrier to a common activation motif. Similarly HIV-1 usage of chemokine receptors involve interaction of one or more extracellular domains of the receptor with conserved and variable domains on the viral envelope protein gp 120, indicating a highly complex interaction. Elucidating the structural requirements for receptor interaction with chemokines and with HIV-1 will provide important insights into understanding the mechanisms of chemokine recognition and receptor activation. In addition, this information can greatly facilitate the design of effective immunomodulatory and anti-HIV-1 therapeutic agents.

Chemokines are a superfamily of small cytokine-like molecules which have been described primarily on the basis of their ability to mediate the migration of various cell types, particularly those of lymphoid origin (See Zlotnick A, *et.al.*; 1999, Crit Rev Immunol. 19:1). The receptors for these molecules are all seven-transmembrane domain G protein-coupled receptors that have historically been excellent targets for small-molecule drugs. This fact, coupled with the advent of large-scale DNA database mining and the recognition that chemokine receptors are also coreceptors for HIV, has driven discovery in this field at a tremendous rate. This process has included not just an expansion of the number of known chemokines and chemokine receptors, but also a greater appreciation for the variety of functions that chemokines are involved in.

Chemokines and chemokine receptors have emerged as crucial factors controlling the development and function of leukocytes (See Pelchen-Matthews A, *et.al.*; 1999, Immunol Rev. **168**:33). Recent studies have indicated that, in addition to these essential roles, both chemokines and chemokine receptors play critical roles in viral infection and replication. Not only are chemokine receptors key components of the receptor/fusion complexes of primate immunodeficiency viruses, but chemokines can also influence virus entry and infection. Many viruses, in particular herpesviruses, encode chemokines and chemokine receptors that influence the replication of both the parent virus and other unrelated viruses. The cell surface expression of the chemokine receptors is regulated through their interaction with membrane trafficking pathways. Ligands induce receptor internalization and downmodulation through endocytosis, and recycling is regulated within endosomes. Part of the mechanism through which chemokines protect cells from HIV infection is through ligand-induced internalization of the specific chemokine receptor co-receptors. In addition, mechanisms may exist to regulate the trafficking of newly synthesized receptors to the cell surface..

Eosinophils play a central role in the pathophysiology of allergic disease (See Simon L, *et al.,* 2000, Immunol Cell Biol **78**:415). The mechanisms that regulate eosinophil migration are complex; however, chemokines and cytokines produced in both the early and late phases of the asthmatic response appear to cooperate in eosinophil recruitment. In particular, there exists a unique synergy between eotaxin and IL-5. The role of chemokine/cytokine cooperativity has been investigated in the extracellular matrix, adhesion molecule/integrin interactions, receptor polarization and aggregation and the convergence and divergence of intracellular signalling pathways. Understanding the mechanisms whereby eosinophils migrate will allow the development of specific therapeutic strategies aimed at attenuating specific components of the allergic response.

New information about the role of tissue inflammation in the pathogenesis of multiple sclerosis (MS) has driven a search for effective and specific therapeutics that address leukocyte trafficking (See Ransohoff RM, *et.al.*; 2000, Expert Opin Investig Drugs 9:1079). These developments in understanding MS are complemented by advances in clarifying the molecular mechanisms of leukocyte extravasation and providing the knowledge base needed to modulate tissue inflammation. Of particular interest are the chemokines and their receptors. Chemokines constitute a large family of chemoattractant peptides that regulate the vast spectrum of leukocyte migration events

MOL20 and MOL21 represent a new subfamily of the chemokine family of proteins. MOL20-21 are useful in determining changes in expression of genes contained within the chemokine protein family. MOL20-21 satisfy a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of the chemokine-associated protein family of proteins. MOL20-21 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving disorders characterized by altered response to pathogens, *e.g.* HIV and hepatitis, and neuroepithelial disorders, *e.g.* dysplasia, carcinoma, and injury resulting from trauma and surgery.

The invention further includes a method of using antibodies that are specific for a MOL20 and 21 polypeptide to treat a disease. The method includes treating a patient with an effective amount of the antibody to block the mechamisn of their pathology. Pathologies that are blocked by the use of MOL20 and 21 antibodies include metastatic potential and invasion in kidney and gastric tumors; cell growth and cell survival in colon, breast, liver and gastric tumors; cell growth and cell survival in colon, breast, liver and gastric tumors; metastasis in breast and brain tumors; metastasis and chemotherapy resistance in colon, gastric, ovarian and lung tumors; and angiogenesis and tumor growth in liver cancer.

MOL22

A MOL22 sequence according to the invention includes a nucleic acid sequence encoding a polypeptide related to the carboxypeptidase family of proteins. A MOL22 nucleic acid and its encoded polypeptide includes the sequences shown in Table 22A. The disclosed nucleic acid (SEQ ID NO:205) is 2,392 nucleotides in length and contains an open reading frame (ORF) that begins with an ATG initiation codon at nucleotides 233-235 and ends with a TGA stop codon at nucleotides 2,283-2,185. The representative ORF encodes a 650 amino acid polypeptide (SEQ ID NO:206) with a predicted molecular weight of 74,326.3 Da. PSORT analysis of a MOL22 polypeptide predicts a mitochondrial matrix localization with a certainty of 0.4513. SIGNALP analysis suggests the lack of a signal peptide.

TABLE 22A.

TCGGCGCGAGGATTCAGTGGATGAAGAGTACTTATTGCTAGAATGTTCTTCCTCATATGAACTTGACAACGTTCTGCTCT
CTAATTCCATTTATTTAGCTGTTTCGAATTGATGAGGATGCAGCGAGGAGCTGCCATCTGTGAAATGGGCCCTCACCAGA
CTCCGAATCTGCCAGTATCTTGCTCTTGGGACTTCCAGCCTCCGGAACTGTAAACACAGCAACAAAAAGTTATGAGAAC
CAAGAGCTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCCGTGAAGATGTCAGAGAGAGTTGCCCACCTC
TTGGTCTGGAAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCACATCGA
GGGAGACTCAACATCCAGGCGGGCATTAATGAAAATGATTTTTATGACGGAGCGTGGTGCGCGGGAAGAAATGACCTCCA
GCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCATCACTCAAGGGAGGAACTCCCTCTGGCTGA
GTGACTGGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACACGTGGGTCACTGTTAAGAATGGATCTGGAGAC
ATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCCCCATGGTGGCCCGCTACATCCG
CATAAACCCTCAGTCCTGGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGGCTGCCCACTGCCAGATCCTA
ATAATTATTATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAAGCACCACAATTATAAGGAAATGCGC
CAGGTACAGTTGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAATTTACAACATTGGAAAAAGCCACCAGGG
CCTGAAGCTGTATGCTGTGGAGATCTCAGATCACCCTGGGGAGCATGAAGTCGGTGAGCCCGAGTTCCACTACATCGCGG
GGGCCCACGGCAATGAGGTGCTGGGCCGGGAGCTGCTGCTGCTGCTGGTGCAGTTCGTGTGTCAGGAGTACTTGGCCCGG
AATGCGCGCATCGTCCACCTGGTGGAGGAGACGCGGATTCACGTCCTCCCCTCCCTCAACCCCGATGGCTACGAGAAGGC
CTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACTTTC
CTGATTTAAACACGCTGCTCTGGGAGGCAGAGGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATC
CCTGAGTGGTTTCTGTCGGAAAATGCCACGGTGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAAAAATCCC
TTTTGTGCTGGGCGGCAACCTGCAGGGCGGCGAGCTGGTGGTGGCGTACCCCTACGACCTGGTGCGGTCCCCCTGGAAGA
CGCAGGAACACACCCCCACCCCCGACGACCACGTGTTCCGCTGGCTGGCCTACTCCTATGCCTCCACACACCGCCTCATG
ACAGACGCCCGGAGGAGGGTGTGCCACACGGAGGACTTCCAAAAGGAGGAGGGCACTGTCAATGGGGCCTCCTGGCACAC
CGTCGCTGGAAGTCTGAACGATTTCAGCTACCTTCATACAAACTGCTTCGAACTGTCCATCTACGTGGGCTGTGATAAAT
ACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTCATCGT
GGCATTAAAGGCTTGGTGAGAGATTCACATGGAAAAGGAATCCCAAACGCCATTATCTCCGTAGAAGGCATTAACCATGA
CATCCGAACAGCCAACGATGGGGATTACTGGCGCCTCCTGAACCCTGGAGAGTATGTGGTCACAGCAAAGGCCGAAGGTT
TCACTGCATCCACCAAGAACTGTATGGTTGGCTATGACATGGGGGCCACAAGGTGTGACTTCACACTTAGCAAAACCAAC
ATGGCCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCCCGTCAGCCTGCCAGCCAGGCGGCTGAAGCTGCGGGG
GCGGAAGAGACGACAGCGTGGGTGACCCTCCTGGGCCCTTGAGACTCGTCTGGGACCCATGCAAATTAAACCAACCTGGT
AGTAGCTCCATAGTGGACTCACTCACTGTTGTTTCCTCTGTAATTCAAGAAGTGCCTGGAAGAGAGGGTGCATTGTGAGG
CAGGTCCCAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTTCTTTGTTCCCATTTATCCAAATAACTTG (SEQ ID NO.: 205)

```
MRTKSSEKAANDDHSVRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCAGRN
DLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIFEGNSEKEIPVLNELPVPMVAR
YIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTTTDDLDFKHHNYKEMRQVQLMKVVNEMCPNITRIYNIGKS
HQGLKLYAVEISDHPGEHEVGEPEFHYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGY
EKAYEGGSELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVVAAETRAVIAWME
KIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYASTHRLMTDARRRVCHTEDFQKEEGTVNGAS
WHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGI
NHDIRTANDGDYWRLLNPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARRLK
LRGRKRRQRG  (SEQ ID NO.: 206)
```

A MOL22 polypeptide has a high degree of homology (99% identity, 99% similarity) with a human membrane-bound protein PRO1310 polypeptide (P1310; PatP Accession No.: Y66645), as is shown in Table 22B. Also, a MOL22 polypeptide has a high degree of homology (94% identity, 97% similarity) with a human lung tumor-specific antigen polypeptide (HLTA; PatP Accession No.: B44409), as is shown in Table 22C.

TABLE 22B

```
MOL22:   212 KHSNKKVMRTKSSEKAANDDHSVRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLG 391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   103 KHSNKKVMRTKSSEKAANDDHSVRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLG 162

MOL22:   392 AHRGRLNIQAGINENDFYDGAWCAGRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWV 571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   163 AHRGRLNIQAGINENDFYDGAWCAGRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWV 222

MOL22:   572 TSYKVMVSNDSHTWVTVKNGSGDMIFEGNSEKEIPVLNELPVPMVARYIRINPQSWFDNG 751
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   223 TSYKVMVSNDSHTWVTVKNGSGDMIFEGNSEKEIPVLNELPVPMVARYIRINPQSWFDNG 282

MOL22:   752 SICMRMEILGCPLPDPNNYYHRRNEMTTTDDLDFKHHNYKEMRQVQLMKVVNEMCPNITR 931
             ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
P1310:   283 SICMRMEILGCPLPDPNNYYHRRNEMTTTDDLDFKHHNYKEMRQ--LMKVVNEMCPNITR 340

MOL22:   932 IYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGAHGNEVLGRELLLLLVQFVCQEY 1111
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   341 IYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGAHGNEVLGRELLLLLVQFVCQEY 400

MOL22:  1112 LARNARIVHLVEETRIHVLPSLNPDGYEKAYEGGSELGGWSLGRWTHDGIDINNNFPDLN 1291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   401 LARNARIVHLVEETRIHVLPSLNPDGYEKAYEGGSELGGWSLGRWTHDGIDINNNFPDLN 460

MOL22:  1292 TLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVVAAETRAVIAWMEKIPFVLGGNLQGG 1471
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
P1310:   461 TLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATV-AAETRAVIAWMEKIPFVLGGNLQGG 519

MOL22:  1472 ELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYASTHRLMTDARRRVCHTEDFQKEE 1651
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   520 ELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYASTHRLMTDARRRVCHTEDFQKEE 579

MOL22:  1652 GTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNRESLIVFMEQ 1831
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   580 GTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHESQLPEEWENNRESLIVFMEQ 639

MOL22:  1832 VHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKAEGFTAS 2011
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   640 VHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKAEGFTAS 699

MOL22:  2012 TKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARRLKLRGRKRRQRG 2182 (SEQ
ID NO.: 243)
```

```
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
P1310:   700 TKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARRLKLRGRKRRQRG 756(SEQ
ID NO.: 244)
Where | indicates identity and + indicates similarity.
```

TABLE 22C.

```
MOL22:   656 NSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT 835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
HLTA:      1 NSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT 60

MOL22:   836 TDDLDFKHHNYKEMRQVQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVG 1015
             ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
HLTA:     61 TDDLDFKHHNYKEMRQ--LMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVG 118

MOL22:  1016 EPEFHYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYE 1195
             ||||||||||||||||||||||||+ |+|||| |+||||| ||||||||+||||||||||
HLTA:    119 EPEFHYIAGAHGNEVLGRELLLLLLHFLCQEYSAQNARIVRLVEETRIHILPSLNPDGYE 178

MOL22:  1196 KAYEGGSELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFL 1375
             ||||||||||||||||||||||||||||||||+|||||||+|| ||||||||||||||||
HLTA:    179 KAYEGGSELGGWSLGRWTHDGIDINNNFPDLNSLLWEAEDQQNAPRKVPNHYIAIPEWFL 238

MOL22:  1376 SENATVVAAETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHV 1555
             |||||| | ||||||||||||||||||||||||||||||||+||| ||||||||||||||
HLTA:    239 SENATV-ATETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDMVRSLWKTQEHTPTPDDHV 297

MOL22:  1556 FRWLAYSYASTHRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFEL 1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
HLTA:    298 FRWLAYSYASTHRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFEL 357

MOL22:  1736 SIYVGCDKYPHESQLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGIN 1915
             |||||||||||||+|||||||||||||||||||||||||+|||  |||| ||+|||||+|
HLTA:    358 SIYVGCDKYPHESELPEEWENNRESLIVFMEQVHRGIKGIVRDLQGKGISNAVISVEGVN 417

MOL22:  1916 HDIRTANDGDYWRLLNPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARIR 2095
             ||||||+||||||||||||||||||||||  ||||||||||||||||||||+|||+||||
HLTA:    418 HDIRTASDGDYWRLLNPGEYVVTAKAEGFITSTKNCMVGYDMGATRCDFTLTKTNLARIR 477

MOL22:  2096 EIMEKFGKQPVSLPARRLKLRGRKRRQRG 2182 (SEQ ID NO.: 245)
             |||| |||||||||+||||||||||||||
HLTA:    478 EIMETFGKQPVSLPSRRLKLRGRKRRQRG 506 (SEQ ID NO.: 246)
```

Where | indicates identity and + indicates similarity.

Carboxypeptidase-like proteins are important in cell differentiation. Layne and co-workers found that the aortic carboxypeptidase-like protein, a novel protein with discoidin and carboxypeptidase-like domains, is up-regulated during vascular smooth muscle cell differentiation. Phenotypic modulation of vascular smooth muscle cells plays an important role in the pathogenesis of arteriosclerosis. In a screen of proteins expressed in human aortic smooth muscle cells, they identified a novel gene product designated aortic carboxypeptidase-like protein (ACLP). The approximately 4-kilobase human cDNA and its mouse homologue encode 1158 and 1128 amino acid proteins, respectively, that are 85% identical. ACLP is a nonnuclear protein that contains a signal peptide, a lysine- and proline-rich 11-amino acid repeating motif, a discoidin-like domain, and a C-terminal domain with 39% identity to carboxypeptidase E. By Western blot analysis and in situ hybridization, Layne et al. detected abundant ACLP expression in the adult aorta. ACLP was expressed predominantly in the smooth muscle cells of the adult mouse aorta but not in the adventitia or in several other tissues. In cultured mouse aortic smooth muscle cells, ACLP mRNA and protein were up-regulated 2-3-fold after serum starvation. Using a recently developed neural crest cell to smooth muscle cell in vitro differentiation system, Layne and co-workers found that ACLP mRNA and protein were not expressed in neural crest cells but were up-regulated dramatically with the differentiation of these cells. These results indicate that ACLP may play a role in differentiated vascular smooth muscle cells (See Layne *et al.*, 1998, J Biol Chem **273**:15654).

MOL22 represents a new member of the carboxypeptidase family of proteins. MOL22 is useful in determining changes in expression of genes contained within the carboxypeptidase protein family. MOL22 satisfies a need in the art by providing new diagnostic or therapeutic compositions useful in the treatment of disorders associated with alterations in the expression of members of the carboxypeptidase-associated protein family of proteins. MOL22 nucleic acids, polypeptides, antibodies, and other compositions of the present invention are useful in the treatment and/or diagnosis of a variety of diseases and pathologies, including by way of nonlimiting example, those involving disorders of vascular smooth muscle cell differentiation, *e.g.* heart failure, atherosclerosis, hypertension and stroke.

MOLX Nucleic Acids and Polypeptides

One aspect of the invention pertains to isolated nucleic acid molecules that encode MOLX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify MOLX-encoding nucleic acids (*e.g.*, MOLX mRNAs) and fragments for use as PCR primers for the amplification and/or mutation of MOLX nucleic acid molecules. As used herein, the term “nucleic acid molecule” is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised double-stranded DNA.

An MOLX nucleic acid can encode a mature MOLX polypeptide. As used herein, a "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product, encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an ORF described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

The term "probes", as utilized herein, refers to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as approximately, *e.g.*, 6,000 nt, depending upon the specific use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are generally obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as utilized herein, is one, which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MOLX nucleic acid molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, etc.). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 as a hybridization probe, MOLX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to MOLX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue.

Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an MOLX polypeptide). A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, thereby forming a stable duplex.

As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of MOLX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an MOLX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human MOLX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, as well as a polypeptide possessing MOLX biological activity. Various biological activities of the MOLX proteins are described below.

An MOLX polypeptide is encoded by the open reading frame ("ORF") of an MOLX nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted by a stop codon. An ORF that represents the coding sequence for a full protein begins with an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA, TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human MOLX genes allows for the generation of probes and primers designed for use in identifying and/or cloning MOLX homologues in other cell types, *e.g.* from other tissues, as well as MOLX homologues from other vertebrates. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205; or an anti-sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205; or of a naturally occurring mutant of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205.

Probes based on the human MOLX nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an MOLX protein, such as by measuring a level of an MOLX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting MOLX mRNA levels or determining whether a genomic MOLX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of an MOLX polypeptide" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of MOLX" can be prepared by isolating a portion SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 that encodes a polypeptide having an MOLX biological activity (the biological activities of the MOLX proteins are described below), expressing the encoded portion of MOLX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of MOLX.

MOLX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 due to degeneracy of the genetic code and thus encode the same MOLX proteins as that encoded by the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206.

In addition to the human MOLX nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the MOLX polypeptides may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the MOLX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an MOLX protein, preferably a vertebrate MOLX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the MOLX genes. Any and all such nucleotide variations and resulting amino acid polymorphisms in the MOLX polypeptides, which are the result of natural allelic variation and that do not alter the functional activity of the MOLX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding MOLX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the MOLX cDNAs of the invention can be isolated based on their homology to the human MOLX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205. In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding MOLX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well-known within the art. See, *e.g.*, Ausubel, et *al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990; GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* **78**: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of MOLX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 thereby leading to changes in the amino acid sequences of the encoded MOLX proteins, without altering the functional ability of said MOLX proteins. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the MOLX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the MOLX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding MOLX proteins that contain changes in amino acid residues that are not essential for activity. Such MOLX proteins differ in amino acid sequence from SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206 yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45% homologous to the amino acid sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206. Preferably, the protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206; more preferably at least about 70% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206; still more preferably at least about 80% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206; even more preferably at least about 90% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206; and most preferably at least about 95% homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206.

An isolated nucleic acid molecule encoding an MOLX protein homologous to the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the MOLX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MOLX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for MOLX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK, NEQHRK, VLIM, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant MOLX protein can be assayed for (*i*) the ability to form protein:protein interactions with other MOLX proteins, other cell-surface proteins, or biologically-active portions thereof, (*ii*) complex formation between a mutant MOLX protein and an MOLX ligand; or (*iii*) the ability of a mutant MOLX protein to bind to an intracellular target protein or biologically-active portion thereof; (*e.g.* avidin proteins).

In yet another embodiment, a mutant MOLX protein can be assayed for the ability to regulate a specific biological function (*e.g.*, regulation of insulin release).

Antisense Nucleic Acids

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire MOLX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of an MOLX protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or antisense nucleic acids complementary to an MOLX nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MOLX protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the MOLX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the MOLX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MOLX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of MOLX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MOLX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MOLX protein to thereby inhibit expression of the protein (*e.g.*, by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (*e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other. See, *e.g.*, Gaultier, *et al.*, 1987. *Nucl. Acids*

Res. **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (see, *e.g.,* Inoue, *et al.* 1987. *Nucl. Acids Res.* **15**: 6131-6148) or a chimeric RNA-DNA analogue (see, *e.g.,* Inoue, *et al.*, 1987. *FEBS Lett.* **215**: 327-330.

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave MOLX mRNA transcripts to thereby inhibit translation of MOLX mRNA. A ribozyme having specificity for an MOLX-encoding nucleic acid can be designed based upon the nucleotide sequence of an MOLX cDNA disclosed herein (*i.e.*, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MOLX-encoding mRNA. See, *e.g.*, U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* MOLX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, MOLX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the MOLX nucleic acid (*e.g.*, the MOLX promoter and/or enhancers) to form triple helical structures that prevent transcription of the MOLX gene in target cells. *See, e.g.,* Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the MOLX nucleic acids can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. *See, e.g.*, Hyrup, *et al.*, 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, *et al.*, 1996. *supra*; Perry-O'Keefe, *et al.*, 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of MOLX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of MOLX can also be used, for example, in the analysis of single base pair mutations in a gene (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S_1 nucleases (*see,* Hyrup, *et al.,* 1996.*supra*); or as probes or primers for DNA sequence and hybridization (*see,* Hyrup, *et al.*, 1996, *supra*; Perry-O'Keefe, *et al.,* 1996. *supra*).

In another embodiment, PNAs of MOLX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of MOLX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (*see,* Hyrup, et al., 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.,* 1996. *supra* and Finn, *et al.*, 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the

PNA and the 5' end of DNA. *See, e.g.*, Mag, *et al.*, 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.*, Finn, *et al.*, 1996. *supra.* Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.*, Petersen, *et al.*, 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.*, Letsinger, *et al.*, 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.*, 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.*, Krol, *et al.*, 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g.*, Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

MOLX Polypeptides

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of MOLX polypeptides whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206 while still encoding a protein that maintains its MOLX activities and physiological functions, or a functional fragment thereof.

In general, an MOLX variant that preserves MOLX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

One aspect of the invention pertains to isolated MOLX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-MOLX antibodies. In one embodiment, native MOLX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, MOLX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, an MOLX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the MOLX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MOLX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MOLX proteins having less than about 30% (by dry weight) of non-MOLX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MOLX proteins, still more preferably less than about 10% of non-MOLX proteins, and most preferably less than about 5% of non-MOLX proteins. When the MOLX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the MOLX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of MOLX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MOLX proteins having less than about 30% (by dry weight) of chemical precursors or non-MOLX chemicals, more preferably less than about 20% chemical precursors or non-MOLX chemicals, still more preferably less than about 10%

chemical precursors or non-MOLX chemicals, and most preferably less than about 5% chemical precursors or non-MOLX chemicals.

Biologically-active portions of MOLX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the MOLX proteins (*e.g.*, the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206) that include fewer amino acids than the full-length MOLX proteins, and exhibit at least one activity of an MOLX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the MOLX protein. A biologically-active portion of an MOLX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native MOLX protein.

In an embodiment, the MOLX protein has an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206. In other embodiments, the MOLX protein is substantially homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the MOLX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, and retains the functional activity of the MOLX proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206.

Determining Homology Between Two or More Sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. *See,* Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205.

The term “sequence identity” refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term “percentage of sequence identity” is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides MOLX chimeric or fusion proteins. As used herein, an MOLX "chimeric protein" or "fusion protein" comprises an MOLX polypeptide operatively-linked to a non-MOLX polypeptide. An "MOLX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MOLX protein (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206), whereas a "non-MOLX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the MOLX protein, *e.g.*, a protein that is different from the MOLX protein and that is derived from the same or a different organism. Within an MOLX fusion protein the MOLX polypeptide can correspond to all or a portion of an MOLX protein. In one embodiment, an MOLX fusion protein comprises at least one biologically-active portion of an MOLX protein. In another embodiment, an MOLX fusion protein comprises at least two biologically-active portions of an MOLX protein. In yet another embodiment, an MOLX fusion protein comprises at least three biologically-active portions of an MOLX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the MOLX polypeptide and the non-MOLX polypeptide are fused in-frame with one another. The non-MOLX polypeptide can be fused to the N-terminus or C-terminus of the MOLX polypeptide.

In one embodiment, the fusion protein is a GST-MOLX fusion protein in which the MOLX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant MOLX polypeptides.

In another embodiment, the fusion protein is an MOLX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of MOLX can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an MOLX-immunoglobulin fusion protein in which the MOLX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The MOLX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between an MOLX ligand and an MOLX protein on the surface of a cell, to thereby suppress MOLX-mediated signal transduction *in vivo*. The MOLX-immunoglobulin fusion proteins can be used to affect the bioavailability of an MOLX cognate ligand. Inhibition of the MOLX ligand/MOLX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the MOLX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-MOLX antibodies in a subject, to purify MOLX ligands, and in screening assays to identify molecules that inhibit the interaction of MOLX with an MOLX ligand.

An MOLX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (*see, e.g.,* Ausubel, *et al.* (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MOLX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MOLX protein.

MOLX Agonists and Antagonists

The invention also pertains to variants of the MOLX proteins that function as either MOLX agonists (*i.e.*, mimetics) or as MOLX antagonists. Variants of the MOLX protein can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the MOLX protein). An agonist of the MOLX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the MOLX protein. An antagonist of the MOLX protein can inhibit one or more of the activities of the naturally occurring form of the MOLX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the MOLX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the MOLX proteins.

Variants of the MOLX proteins that function as either MOLX agonists (*i.e.*, mimetics) or as MOLX antagonists can be identified by screening combinatorial libraries of mutants (*e.g.*, truncation mutants) of the MOLX proteins for MOLX protein agonist or antagonist activity. In one embodiment, a variegated library of MOLX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MOLX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MOLX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MOLX sequences therein. There are a variety of methods which can be used to produce libraries of potential MOLX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MOLX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.*, Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.*, 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.*, 1984. *Science* 198: 1056; Ike, *et al.*, 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the MOLX protein coding sequences can be used to generate a variegated population of MOLX fragments for screening and subsequent selection of variants of an MOLX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MOLX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S_1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the MOLX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MOLX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MOLX variants. *See, e.g.,* Arkin and Yourvan, 1992. *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, *et al.*, 1993. *Protein Engineering* 6:327-331.

Anti-MOLX Antibodies

The invention encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the MOLX polypeptides of said invention.

An isolated MOLX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind to MOLX polypeptides using standard techniques for polyclonal and monoclonal antibody preparation. The full-length MOLX proteins can be used or, alternatively, the invention provides antigenic peptide fragments of MOLX proteins for use as immunogens. The antigenic MOLX peptides comprises at least 4 amino acid residues of the amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206 and encompasses an epitope of MOLX such that an antibody raised against the peptide forms a specific immune complex with MOLX. Preferably, the antigenic peptide comprises at least 6, 8, 10, 15, 20, or 30 amino acid residues. Longer antigenic peptides are sometimes preferable over shorter antigenic peptides, depending on use and according to methods well known to someone skilled in the art.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of MOLX that is located on the surface of the protein (*e.g.*, a hydrophilic region). As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation (*see, e.g.*, Hopp and Woods, 1981. *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle, 1982. *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety).

As disclosed herein, MOLX protein sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically-active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically-binds (immunoreacts with) an antigen, such as MOLX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human MOLX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to an MOLX protein sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or a derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed MOLX protein or a chemically-synthesized MOLX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against MOLX can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of MOLX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular MOLX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular MOLX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (*see, e.g.*, Kohler & Milstein, 1975. *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (*see, e.g.*, Kozbor, *et al.*, 1983. *Immunol. Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (*see, e.g.*, Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the invention and may be produced by using human hybridomas (*see, e.g.*, Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (*see, e.g.*, Cole, *et al.*, 1985. In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations is incorporated herein by reference in their entirety.

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an MOLX protein (*see, e.g.,* U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (*see, e.g.,* Huse, *et al.,* 1989. *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for an MOLX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. *See, e.g.,* U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to an MOLX protein may be produced by techniques known in the art including, but not limited to: (*i*) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (*ii*) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (*iii*) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent; and (*iv*) F_v fragments.

Additionally, recombinant anti-MOLX antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Patent No. 4,816,567; U.S. Pat. No. 5,225,539; European Patent Application No. 125,023; Better, *et al.*, 1988. *Science* 240: 1041-1043; Liu, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 3439-3443; Liu, *et al.*, 1987. *J. Immunol.* 139: 3521-3526; Sun, *et al.*, 1987. *Proc. Natl. Acad. Sci. USA* 84: 214-218; Nishimura, *et al.*, 1987. *Cancer Res.* 47: 999-1005; Wood, *et al.*, 1985. *Nature* 314 :446-449; Shaw, *et al.*, 1988. *J. Natl. Cancer Inst.* 80: 1553-1559); Morrison(1985) *Science* 229:1202-1207; Oi, *et al.* (1986) *BioTechniques* 4:214; Jones, *et al.*, 1986. *Nature* 321: 552-525; Verhoeyan, *et al.*, 1988. *Science* 239: 1534; and Beidler, *et al.*, 1988. *J. Immunol.* 141: 4053-4060. Each of the above citations are incorporated herein by reference in their entirety.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an

MOLX protein is facilitated by generation of hybridomas that bind to the fragment of an MOLX protein possessing such a domain. Thus, antibodies that are specific for a desired domain within an MOLX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-MOLX antibodies may be used in methods known within the art relating to the localization and/or quantitation of an MOLX protein (*e.g.*, for use in measuring levels of the MOLX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for MOLX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds (hereinafter "Therapeutics").

An anti-MOLX antibody (*e.g.*, monoclonal antibody) can be used to isolate an MOLX polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-MOLX antibody can facilitate the purification of natural MOLX polypeptide from cells and of recombinantly-produced MOLX polypeptide expressed in host cells. Moreover, an anti-MOLX antibody can be used to detect MOLX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the MOLX protein. Anti-MOLX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

MOLX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MOLX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell).

The term "regulatory sequence" is intended to includes promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MOLX proteins, mutant forms of MOLX proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MOLX proteins in prokaryotic or eukaryotic cells. For example, MOLX proteins can be expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (*i*) to increase expression of recombinant protein; (*ii*) to increase the solubility of the recombinant protein; and (*iii*) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION

TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. *See, e.g.,* Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (*see, e.g.,* Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MOLX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerivisae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, MOLX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see, *e.g.*, Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and the α-fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3: 537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to MOLX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes *see, e.g.*, Weintraub, *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, MOLX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding MOLX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) MOLX protein. Accordingly, the invention further provides methods for producing MOLX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding MOLX protein has been introduced) in a suitable medium such that MOLX protein is produced. In another embodiment, the method further comprises isolating MOLX protein from the medium or the host cell.

Transgenic MOLX Animals

The host cells of the invention can also be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which MOLX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous MOLX sequences have been introduced into their genome or homologous recombinant animals in which endogenous MOLX sequences have been altered. Such animals are useful for studying the function and/or activity of MOLX protein and for identifying and/or evaluating modulators of MOLX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous MOLX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing MOLX-encoding nucleic acid into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human MOLX cDNA sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homologue of the human MOLX gene, such as a mouse MOLX gene, can be isolated based on hybridization to the human MOLX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the MOLX transgene to direct expression of MOLX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the MOLX transgene in its genome and/or expression of MOLX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding MOLX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of an MOLX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MOLX gene. The MOLX gene can be a human gene (*e.g.*, the cDNA of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205), but more preferably, is a non-human homologue of a human MOLX gene. For example, a mouse homologue of human MOLX gene of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 can be used to construct a homologous recombination vector suitable for altering an endogenous MOLX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous MOLX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MOLX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MOLX protein). In the homologous recombination vector, the altered portion of the MOLX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the MOLX gene to allow for homologous recombination to occur between the exogenous MOLX gene carried by the vector and an endogenous MOLX gene in an embryonic stem cell. The additional flanking MOLX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g.,* Thomas, *et al.*, 1987. *Cell* 51: 503 for a description of homologous recombination vectors. The vector is ten introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced MOLX gene has homologously-recombined with the endogenous MOLX gene are selected. *See, e.g.*, Li, *et al.*, 1992. *Cell* 69: 915.

The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras. *See, e.g.*, Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, *See, e.g.*, Lakso, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae. See,* O'Gorman, *et al.*, 1991. *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, *et al.*, 1997. *Nature* 385: 810-813. In brief, a cell (*e.g.*, a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (*e.g.*, the somatic cell) is isolated.

Pharmaceutical Compositions

The MOLX nucleic acid molecules, MOLX proteins, and anti-MOLX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.*, topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an MOLX protein or anti-MOLX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.,* U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Screening and Detection Methods

The isolated nucleic acid molecules of the invention can be used to express MOLX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect MOLX mRNA (*e.g.*, in a biological sample) or a genetic lesion in an MOLX gene, and to modulate MOLX activity, as described further, below. In addition, the MOLX proteins can be used to screen drugs or compounds that modulate the MOLX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of MOLX protein or production of MOLX protein forms that have decreased or aberrant activity compared to MOLX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with obesity, the metabolic syndrome X as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease(possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-MOLX antibodies of the invention can be used to detect and isolate MOLX proteins and modulate MOLX activity. In yet a further aspect, the invention can be used in methods to influence appetite, absorption of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to MOLX proteins or have a stimulatory or inhibitory effect on, *e.g.*, MOLX protein expression or MOLX protein activity. The invention also includes compounds identified in the screening assays described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of an MOLX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the “one-bead one-compound” library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds. *See, e.g.*, Lam, 1997. *Anticancer Drug Design* 12: 145.

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.*, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*, 1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992. *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382; Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of MOLX protein, or a biologically-active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to an MOLX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the MOLX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the MOLX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of MOLX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds MOLX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an MOLX protein, wherein determining the ability of the test compound to interact with an MOLX protein comprises determining the ability of the test compound to preferentially bind to MOLX protein or a biologically-active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of MOLX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the MOLX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of MOLX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the MOLX protein to bind to or interact with an MOLX target molecule. As used herein, a "target molecule" is a molecule with which an MOLX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses an MOLX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. An MOLX target molecule can be a non-MOLX molecule or an MOLX protein or polypeptide of the invention. In one embodiment, an MOLX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound MOLX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with MOLX.

Determining the ability of the MOLX protein to bind to or interact with an MOLX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the MOLX protein to bind to or interact with an MOLX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+}, diacylglycerol, IP_3, etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising an MOLX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting an MOLX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the MOLX protein or biologically-active portion thereof. Binding of the test compound to the MOLX protein can be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the MOLX protein or biologically-active portion thereof with a known compound which binds MOLX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an MOLX protein, wherein determining the ability of the test compound to interact with an MOLX protein comprises determining the ability of the test compound to preferentially bind to MOLX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting MOLX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the MOLX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of MOLX can be accomplished, for example, by determining the ability of the MOLX protein to bind to an MOLX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of MOLX protein can be accomplished by determining the ability of the MOLX protein further modulate an MOLX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the MOLX protein or biologically-active portion thereof with a known compound which binds MOLX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with an MOLX protein, wherein determining the ability of the test compound to interact with an MOLX protein comprises determining the ability of the MOLX protein to preferentially bind to or modulate the activity of an MOLX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of MOLX protein. In the case of cell-free assays comprising the membrane-bound form of MOLX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of MOLX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either MOLX protein or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to MOLX protein, or interaction of MOLX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-MOLX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or MOLX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes can be dissociated from the matrix, and the level of MOLX protein binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either the MOLX protein or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated MOLX protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well-known within the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with MOLX protein or target molecules, but which do not interfere with binding of the MOLX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or MOLX protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the MOLX protein or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the MOLX protein or target molecule.

In another embodiment, modulators of MOLX protein expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of MOLX mRNA or protein in the cell is determined. The level of expression of MOLX mRNA or protein in the presence of the candidate compound is compared to the level of expression of MOLX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of MOLX mRNA or protein expression based upon this comparison. For example, when expression of MOLX mRNA or protein is greater (*i.e.,* statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of MOLX mRNA or protein expression. Alternatively, when expression of MOLX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of MOLX mRNA or protein expression. The level of MOLX mRNA or protein expression in the cells can be determined by methods described herein for detecting MOLX mRNA or protein.

In yet another aspect of the invention, the MOLX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos, *et al.*, 1993. *Cell* 72: 223-232; Madura, *et al.*, 1993. *J. Biol. Chem.* 268: 12046-12054; Bartel, *et al.*, 1993. *Biotechniques* 14: 920-924; Iwabuchi, *et al.*, 1993. *Oncogene* 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with MOLX ("MOLX-binding proteins" or "MOLX-bp") and modulate MOLX activity. Such MOLX-binding proteins are also likely to be involved in the propagation of signals by the MOLX proteins as, for example, upstream or downstream elements of the MOLX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for MOLX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming an MOLX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with MOLX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (*i*) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (*ii*) identify an individual from a minute biological sample (tissue typing); and (*iii*) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

Chromosome Mapping

Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the MOLX sequences, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, or fragments or derivatives thereof, can be used to map the location of the MOLX genes, respectively, on a chromosome. The mapping of the MOLX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, MOLX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the MOLX sequences. Computer analysis of the MOLX, sequences can be used to rapidly select primers that do not span more than one exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the MOLX sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals (*e.g.*, human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy mapping of individual genes to specific human chromosomes. *See, e.g.*, D'Eustachio, *et al.*, 1983. *Science* 220: 919-924. Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the MOLX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a reasonable amount of time. For a review of this technique, *see,* Verma, *et al.*, HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found, *e.g.*, in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the MOLX gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

The MOLX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

Furthermore, the sequences of the invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the MOLX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The MOLX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining MOLX protein and/or nucleic acid expression as well as MOLX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant MOLX expression or activity. The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with MOLX protein, nucleic acid expression or activity. For example, mutations in an MOLX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with MOLX protein, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining MOLX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of MOLX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of MOLX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting MOLX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes MOLX protein such that the presence of MOLX is detected in the biological sample. An agent for detecting MOLX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to MOLX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length MOLX nucleic acid, such as the nucleic acid of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, and 205, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to MOLX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting MOLX protein is an antibody capable of binding to MOLX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or $F(ab')_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect MOLX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of MOLX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of MOLX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of MOLX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of MOLX protein include introducing into a subject a labeled anti-MOLX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting MOLX protein, mRNA, or genomic DNA, such that the presence of MOLX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of MOLX protein, mRNA or genomic DNA in the control sample with the presence of MOLX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of MOLX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting MOLX protein or mRNA in a biological sample; means for determining the amount of MOLX in the sample; and means for comparing the amount of MOLX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect MOLX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant MOLX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with MOLX protein, nucleic acid expression or activity. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the invention provides a method for identifying a disease or disorder associated with aberrant MOLX expression or activity in which a test sample is obtained from a subject and MOLX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of MOLX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant MOLX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant MOLX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. Thus, the invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant MOLX expression or activity in which a test sample is obtained and MOLX protein or nucleic acid is detected (*e.g.*, wherein the presence of MOLX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant MOLX expression or activity).

The methods of the invention can also be used to detect genetic lesions in an MOLX gene, thereby determining if a subject with the lesioned gene is at risk for a disorder characterized by aberrant cell proliferation and/or differentiation. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding an MOLX-protein, or the misexpression of the MOLX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of: (*i*) a deletion of one or more nucleotides from an MOLX gene; (*ii*) an addition of one or more nucleotides to an MOLX gene; (*iii*) a substitution of one or more nucleotides of an MOLX gene, (*iv*) a chromosomal rearrangement of an MOLX gene; (*v*) an alteration in the level of a messenger RNA transcript of an MOLX gene, (*vi*) aberrant modification of an MOLX gene, such as of the methylation pattern of the genomic DNA, (*vii*) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of an MOLX gene, (*viii*) a non-wild-type level of an MOLX protein, (*ix*) allelic loss of an MOLX gene, and (*x*) inappropriate post-translational modification of an MOLX protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in an MOLX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.*, U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.*, Landegran, *et al.*, 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for detecting point mutations in the MOLX-gene (*see,* Abravaya, *et al.*, 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to an MOLX gene under conditions such that hybridization and amplification of the MOLX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (*see,* Guatelli, *et al.*, 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see,* Kwoh, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177); Qβ Replicase (*see,* Lizardi, *et al*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in an MOLX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in MOLX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes. *See, e.g.,* Cronin, *et al.*, 1996. *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996. *Nat. Med.* 2: 753-759. For example, genetic mutations in MOLX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al., supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the MOLX gene and detect mutations by comparing the sequence of the sample MOLX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (*see, e.g.,* Naeve, *et al.*, 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publication No. WO 94/16101; Cohen, *et al.*, 1996. *Adv. Chromatography* 36: 127-162; and Griffin, *et al.*, 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

Other methods for detecting mutations in the MOLX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. *See, e.g.,* Myers, *et al.*, 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type MOLX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S_1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. *See, e.g.,* Cotton, *et al.*, 1988. *Proc. Natl. Acad. Sci. USA* 85: 4397; Saleeba, *et al.*, 1992. *Methods Enzymol.* 217: 286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in MOLX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. *See, e.g.,* Hsu, *et al.*, 1994. *Carcinogenesis* 15: 1657-1662. According to an exemplary embodiment, a probe based on an MOLX sequence, *e.g.*, a wild-type MOLX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. *See, e.g.*, U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in MOLX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g.*, Orita, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton, 1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79. Single-stranded DNA fragments of sample and control MOLX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g.*, Keen, *et al.*, 1991. *Trends Genet.* 7: 5.

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g.*, Myers, *et al.*, 1985. *Nature* 313: 495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. *See, e.g.*, Rosenbaum and Reissner, 1987. *Biophys. Chem.* 265: 12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g.*, Saiki, *et al.*, 1986. *Nature* 324: 163; Saiki, *et al.*, 1989. *Proc. Natl. Acad. Sci. USA* 86: 6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g.*, Gibbs, *et al.*, 1989. *Nucl. Acids Res.* 17: 2437-2448) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g.*, Prossner, 1993. *Tibtech.* 11: 238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. *See, e.g.*, Gasparini, *et al.*, 1992. *Mol. Cell Probes* 6: 1. It is anticipated that in certain embodiments amplification may also be performed using *Taq* ligase for amplification. *See, e.g.*, Barany, 1991. *Proc. Natl. Acad. Sci. USA* 88: 189. In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an MOLX gene.

Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which MOLX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

Agents, or modulators that have a stimulatory or inhibitory effect on MOLX activity (*e.g.*, MOLX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (The disorders include metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.) In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of MOLX protein, expression of MOLX nucleic acid, or mutation content of MOLX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996. *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of MOLX protein, expression of MOLX nucleic acid, or mutation content of MOLX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an MOLX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of MOLX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase MOLX gene expression, protein levels, or upregulate MOLX activity, can be monitored in clinical trails of subjects exhibiting decreased MOLX gene expression, protein levels, or downregulated MOLX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease MOLX gene expression, protein levels, or downregulate MOLX activity, can be monitored in clinical trails of subjects exhibiting increased MOLX gene expression, protein levels, or upregulated MOLX activity. In such clinical trials, the expression or activity of MOLX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including MOLX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates MOLX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of MOLX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of MOLX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a subject prior to administration of the agent; (*ii*) detecting the level of expression of an MOLX protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more post-administration samples from the subject; (*iv*) detecting the level of expression or activity of the MOLX protein, mRNA, or genomic DNA in the post-administration samples; (*v*) comparing the level of expression or activity of the MOLX protein, mRNA, or genomic DNA in the pre-administration sample with the MOLX protein, mRNA, or genomic DNA in the post administration sample or samples; and (*vi*) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of MOLX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of MOLX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant MOLX expression or activity. The disorders include cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect

(ASD), atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, neoplasm; adenocarcinoma, lymphoma, uterus cancer, fertility, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Ostoeodystrophy, and other diseases, disorders and conditions of the like.

These methods of treatment will be discussed more fully, below.

Disease and Disorders

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (*i*) an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; (*ii*) antibodies to an aforementioned peptide; (*iii*) nucleic acids encoding an aforementioned peptide; (*iv*) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endoggenous function of an aforementioned peptide by homologous recombination (*see*, *e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (*v*) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.,* by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.,* Northern assays, dot blots, *in situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant MOLX expression or activity, by administering to the subject an agent that modulates MOLX expression or at least one MOLX activity. Subjects at risk for a disease that is caused or contributed to by aberrant MOLX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the MOLX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of MOLX aberrancy, for example, an MOLX agonist or MOLX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

Therapeutic Methods

Another aspect of the invention pertains to methods of modulating MOLX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of MOLX protein activity associated with the cell. An agent that modulates MOLX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of an MOLX protein, a peptide, an MOLX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more MOLX protein activity. Examples of such stimulatory agents include active MOLX protein and a nucleic acid molecule encoding MOLX that has been introduced into the cell. In another embodiment, the agent inhibits one or more MOLX protein activity. Examples of such inhibitory agents include antisense MOLX nucleic acid molecules and anti-MOLX antibodies. These modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an MOLX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, up-regulates or down-regulates) MOLX expression or activity. In another embodiment, the method involves administering an MOLX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant MOLX expression or activity.

Stimulation of MOLX activity is desirable in situations in which MOLX is abnormally downregulated and/or in which increased MOLX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (*e.g.*, cancer or immune associated disorders). Another example of such a situation is where the subject has a gestational disease (*e.g.*, preclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The MOLX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

As an example, a cDNA encoding the MOLX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof. By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hematopoietic disorders, and the various dyslipidemias.

Both the novel nucleic acid encoding the MOLX protein, and the MOLX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.,* some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

Examples

Example 1: Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR; TAQMAN®). RTQ PCR was performed on a Perkin-Elmer Biosystems ABI PRISM® 7700 Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing cells and cell lines from normal and cancer sources), Panel 2 (containing samples derived from tissues, in particular from surgical samples, from normal and cancer sources), Panel 3 (containing samples derived from a wide variety of cancer sources) and Panel 4 (containing cells and cell lines from normal cells and cells related to inflammatory conditions).

First, the RNA samples were normalized to constitutively expressed genes such as β -actin and GAPDH. RNA (~50 ng total or ~1 ng polyA+) was converted to cDNA using the TAQMAN® Reverse Transcription Reagents Kit (PE Biosystems, Foster City, CA; Catalog No. N808-0234) and random hexamers according to the manufacturer's protocol. Reactions were performed in 20 ul and incubated for 30 min. at 48^0C. cDNA (5 ul) was then transferred to a separate plate for the TAQMAN® reaction using β-actin and GAPDH TAQMAN® Assay Reagents (PE Biosystems; Catalog Nos. 4310881E and 4310884E, respectively) and TAQMAN® universal PCR Master Mix (PE Biosystems; Catalog No. 4304447) according to the manufacturer's protocol. Reactions were performed in 25 ul using the following parameters: 2 min. at 50^0C; 10 min. at 95^0C; 15 sec. at 95^0C/1 min. at 60^0C (40 cycles). Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100. The average CT values obtained for ß-actin and GAPDH were used to normalize RNA samples. The RNA sample generating the highest CT value required no further diluting, while all other samples were diluted relative to this sample according to their β -actin /GAPDH average CT values.

Normalized RNA (5 ul) was converted to cDNA and analyzed via TAQMAN® using One Step RT-PCR Master Mix Reagents (PE Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions. Probes and primers were designed for each assay according to Perkin Elmer Biosystem's *Primer Express* Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60° C, primer optimal Tm = 59° C, maximum primer difference = 2° C, probe does not have 5' G, probe T_m must be 10° C greater than primer T_m, amplicon size 75 bp to 100 bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900 nM each, and probe, 200nM.

PCR conditions: Normalized RNA from each tissue and each cell line was spotted in each well of a 96 well PCR plate (Perkin Elmer Biosystems). PCR cocktails including two probes (a probe specific for the target clone and another gene-specific probe multiplexed with the target probe) were set up using 1X TaqMan™ PCR Master Mix for the PE Biosystems 7700, with 5 mM MgCl2, dNTPs (dA, G, C, U at 1:1:1:2 ratios), 0.25 U/ml AmpliTaq Gold™ (PE Biosystems), and 0.4 U/μl RNase inhibitor, and 0.25 U/μl reverse transcriptase. Reverse transcription was performed at 48° C for 30 minutes followed by amplification/PCR cycles as follows: 95° C 10 min, then 40 cycles of 95° C for 15 seconds, 60° C for 1 minute.

In the results for Panel 1, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var= small cell variant,
non-s = non-sm =non-small,
squam = squamous,
pl. eff = pl effusion = pleural effusion,
glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

Panel 2

The plates for Panel 2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologists at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissue were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

Panel 4

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4r) or cDNA (Panel 4d) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene ,La Jolla, CA) and thymus and kidney (Clontech) were employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5 ng/ml, TNF alpha at approximately 5-10 ng/ml, IFN gamma at approximately 20-50 ng/ml, IL-4 at approximately 5-10 ng/ml, IL-9 at approximately 5-10 ng/ml, IL-13 at approximately 5-10 ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20 ng/ml PMA and 1-2 μg/ml ionomycin, IL-12 at 5-10 ng/ml, IFN gamma at 20-50 ng/ml and IL-18 at 5-10 ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5 μg/ml. Samples were taken at 24, 48 and 72 hours for RNA preparation. MLR (mixed lymphocyte reaction) samples were obtained by taking blood from two donors, isolating the mononuclear cells using Ficoll and mixing the isolated mononuclear cells 1:1 at a final concentration of approximately $2x10^6$ cells/ml in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol (5.5 x 10^{-5} M) (Gibco), and 10 mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco), 50 ng/ml GMCSF and 5 ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), 10 mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50 ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100 ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 μg/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and +ve selection. Then CD45RO beads were used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 μg/ml anti-CD28 (Pharmingen) and 3 ug/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2. The expanded CD8 cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4 days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resupended at 10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco). To activate the cells, we used PWM at 5 μg/ml or anti-CD40 (Pharmingen) at approximately 10 μg/ml and IL-4 at 5-10 ng/ml. Cells were harvested for RNA preparation at 24,48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μg/ml anti-CD28 (Pharmingen) and 2 μg/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes

(Poietic Systems, German Town, MD) were cultured at 10^5-10^6 cells/ml in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (4 ng/ml). IL-12 (5 ng/ml) and anti-IL4 (1 □g/ml) were used to direct to Th1, while IL-4 (5 ng/ml) and anti-IFN gamma (1 □g/ml) were used to direct to Th2 and IL-10 at 5 ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), 10 mM Hepes (Gibco) and IL-2 (1 ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 □g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third expansion cultures in Interleukin 2.

The following leukocyte cells lines were obtained from the ATCC: Ramos, EOL-1, KU-812. EOL cells were further differentiated by culture in 0.1 mM dbcAMP at 5 x10^5 cells/ml for 8 days, changing the media every 3 days and adjusting the cell concentration to 5 x10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), 10 mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10 ng/ml and ionomycin at 1 µg/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100 µM non essential amino acids (Gibco), 1 mM sodium pyruvate (Gibco), mercaptoethanol 5.5 x 10^{-5} M (Gibco), and 10 mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at –20 degrees C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300 μl of RNAse-free water and 35 μl buffer (Promega) 5 μl DTT, 7 μl RNAsin and 8 μl DNAse were added. The tube was incubated at 37 degrees C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3 M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNAse free water. RNA was stored at –80 degrees C.

MOL1

Expression of gene GM_79960178 was assessed using the primer-probe set Ag1605, described in Table 12. Results of the RTQ-PCR runs are shown in Tables 13 and 14.

Table 12. Probe Name: Ag1605

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-CCTGAGCTACAACAACATCATG-3'	58.3	22	333	76
Probe	FAM-5'-CCTCATATCCCTGTCCCTCAGCCATA-3'-TAMRA	69	26	378	77
Reverse	5'-GCAGAGTCTAGCATCAGGATGT-3'	58.6	22	407	78

Table 13. Panels 1.3D and 2D

PANEL 1.3D			**PANEL 2D**		
Tissue Name	Rel. Expr., % 1.3dtm2653f_ag1605	Rel. Expr., % 1.3dx4tm5402f_ag1605_b1	Tissue Name	Rel. Expr., % 2Dtm2728f_ag1605	Rel. Expr., % 2dx4tm4732f_ag1605_a2

Liver adenocarcinoma	0	1.9	Normal Colon GENPAK 061003	70.2	70.3
Pancreas	0.2	0	83219 CC Well to Mod Diff (ODO3866)	8.5	6.3
Pancreatic ca. CAPAN 2	0	17.6	83220 CC NAT (ODO3866)	8.1	9.4
Adrenal gland	2.2	1.3	83221 CC Gr.2 rectosigmoid (ODO3868)	4.5	12.1
Thyroid	2	5.6	83222 CC NAT (ODO3868)	1.6	6.3
Salivary gland	4	8.9	83235 CC Mod Diff (ODO3920)	17.9	19.7
Pituitary gland	1.2	1.7	83236 CC NAT (ODO3920)	21.5	11.6
Brain (fetal)	4.4	21.2	83237 CC Gr.2 ascend colon (ODO3921)	18	34.4
Brain (whole)	3.1	30.5	83238 CC NAT (ODO3921)	8.9	9.8
Brain (amygdala)	1.8	6.6	83241 CC from Partial Hepatectomy (ODO4309)	7.1	4.9
Brain (cerebellum)	1.9	14.6	83242 Liver NAT (ODO4309)	17.1	6.9
Brain (hippocampus)	5.8	8.7	87472 Colon mets to lung (OD04451-01)	6.7	11.4
Brain (substantia nigra)	0.8	9.3	87473 Lung NAT (OD04451-02)	0.8	2.9
Brain (thalamus)	1.4	4.8	Normal Prostate Clontech A+ 6546-1	17.8	52.9
Cerebral Cortex	3.8	2.6	84140 Prostate Cancer (OD04410)	18.6	23
Spinal cord	2.6	15.7	84141 Prostate NAT (OD04410)	9.1	22
CNS ca. (glio/astro) U87-MG	0	0	87073 Prostate Cancer (OD04720-01)	20	14.5
CNS ca. (glio/astro) U-118-MG	0.2	1.5	87074 Prostate NAT (OD04720-02)	21.3	38.1
CNS ca. (astro) SW1783	0.8	0	Normal Lung GENPAK 061010	69.7	85.9
CNS ca.* (neuro; met) SK-N-AS	2.8	1.6	83239 Lung Met to Muscle (ODO4286)	11.1	6.3

CNS ca. (astro) SF-539	0.6	0	83240 Muscle NAT (ODO4286)	15.1	23.3
CNS ca. (astro) SNB-75	0.2	0	84136 Lung Malignant Cancer (OD03126)	30.6	30.8
CNS ca. (glio) SNB-19	0.3	9.7	84137 Lung NAT (OD03126)	8	16.3
CNS ca. (glio) U251	0.9	4.8	84871 Lung Cancer (OD04404)	41.8	45.2
CNS ca. (glio) SF-295	100	7.7	84872 Lung NAT (OD04404)	15.4	27.5
Heart (fetal)	3.7	0.9	84875 Lung Cancer (OD04565)	7.4	8.5
Heart	0.4	6.1	84876 Lung NAT (OD04565)	5.3	1.2
Fetal Skeletal	45.1	3.5	85950 Lung Cancer (OD04237-01)	77.9	72.9
Skeletal muscle	5.8	100	85970 Lung NAT (OD04237-02)	14.3	12.9
Bone marrow	2.9	22.8	83255 Ocular Mel Met to Liver (ODO4310)	2.7	6
Thymus	6.3	12.2	83256 Liver NAT (ODO4310)	2.3	5.1
Spleen	7.9	14.6	84139 Melanoma Mets to Lung (OD04321)	1.3	6.2
Lymph node	16.7	57.9	84138 Lung NAT (OD04321)	36.9	22.4
Colorectal	4.3	3.4	Normal Kidney GENPAK 061008	9.2	19.2
Stomach	7.5	20.7	83786 Kidney Ca, Nuclear grade 2 (OD04338)	4.2	6.9
Small intestine	3.4	33.5	83787 Kidney NAT (OD04338)	7	8.3
Colon ca. SW480	0.5	0.6	83788 Kidney Ca Nuclear grade 1/2 (OD04339)	18.7	11.3
Colon ca.* (SW480 met)SW620	0	0	83789 Kidney NAT (OD04339)	4.9	8.5
Colon ca. HT29	0	0	83790 Kidney Ca, Clear cell type (OD04340)	6.3	14.8
Colon ca. HCT-116	0	0	83791 Kidney NAT (OD04340)	10.7	14.6
Colon ca. CaCo-2	0.2	2.2	83792 Kidney Ca, Nuclear grade 3 (OD04348)	6	7.5

83219 CC Well to Mod Diff (ODO3866)	2	0	83793 Kidney NAT (OD04348)	14.5	16.5
Colon ca. HCC-2998	0.4	0	87474 Kidney Cancer (OD04622-01)	15.4	25
Gastric ca.* (liver met) NCI-N87	2.3	7.2	87475 Kidney NAT (OD04622-03)	2.3	2.8
Bladder	0.4	2.5	85973 Kidney Cancer (OD04450-01)	3.6	7.3
Trachea	2.8	4.9	85974 Kidney NAT (OD04450-03)	1.3	13.3
Kidney	0	0	Kidney Cancer Clontech 8120607	7.3	5.2
Kidney (fetal)	1.4	7	Kidney NAT Clontech 8120608	1.1	3.6
Renal ca. 786-0	0	0	Kidney Cancer Clontech 8120613	2.8	7.5
Renal ca. A498	0.2	1.5	Kidney NAT Clontech 8120614	3.7	8
Renal ca. RXF 393	0	3	Kidney Cancer Clontech 9010320	17.4	14.1
Renal ca. ACHN	0.6	1.1	Kidney NAT Clontech 9010321	16.4	11.3
Renal ca. UO-31	0	0	Normal Uterus GENPAK 061018	4.6	5.2
Renal ca. TK-10	0.2	1.2	Uterus Cancer GENPAK 064011	17.2	32.4
Liver	0	0.6	Normal Thyroid Clontech A+ 6570-1	17.3	18.1
Liver (fetal)	1.4	8.8	Thyroid Cancer GENPAK 064010	6.5	1.1
Liver ca. (hepatoblast) HepG2	0.7	24.6	Thyroid Cancer INVITROGEN A302152	1.7	1.6
Lung	2.2	1.3	Thyroid NAT INVITROGEN A302153	9.2	17.7
Lung (fetal)	5.1	15.8	Normal Breast GENPAK 061019	21.3	30.1
Lung ca. (small cell) LX-1	1.3	1.5	84877 Breast Cancer (OD04566)	1.4	1.5
Lung ca. (small cell) NCI-H69	3.3	4.2	85975 Breast Cancer (OD04590-01)	12.9	10.1
Lung ca. (s.cell var.) SHP-77	0.2	1.4	85976 Breast Cancer Mets (OD04590-03)	100	88

Lung ca. (large cell)NCI-H460	0	0	87070 Breast Cancer Metastasis (OD04655-05)	32.8	0
Lung ca. (non-sm. cell) A549	0.8	2.9	GENPAK Breast Cancer 064006	25	28.5
Lung ca. (non-s.cell) NCI-H23	4	9.5	Breast Cancer Res. Gen. 1024	51.8	66.3
Lung ca (non-s.cell) HOP-62	1.8	3.4	Breast Cancer Clontech 9100266	25	25.1
Lung ca. (non-s.cl) NCI-H522	0.3	0	Breast NAT Clontech 9100265	18.2	31.7
Lung ca. (squam.) SW 900	0.5	4.7	Breast Cancer INVITROGEN A209073	15	21
Lung ca. (squam.) NCI-H596	0	0	Breast NAT INVITROGEN A2090734	16.2	12.3
Mammary gland	4.8	0	Normal Liver GENPAK 061009	5.6	4.9
Breast ca.* (pl. effusion) MCF-7	0.4	0.7	Liver Cancer GENPAK 064003	5.4	11.8
Breast ca.* (pl.ef) MDA-MB-231	0.7	6.1	Liver Cancer Research Genetics RNA 1025	3.7	3.6
Breast ca.* (pl. effusion) T47D	0	5.1	Liver Cancer Research Genetics RNA 1026	4.8	5.5
Breast ca. BT-549	0.4	2.8	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	10.6	7
Breast ca. MDA-N	0	0	Paired Liver Tissue Research Genetics RNA 6004-N	19.3	28.4
Ovary	5.9	2.7	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	4.6	6
Ovarian ca. OVCAR-3	0	3.2	Paired Liver Tissue Research Genetics RNA 6005-N	5	0
Ovarian ca. OVCAR-4	1.4	3.7	Normal Bladder GENPAK 061001	18.3	11.5
Ovarian ca. OVCAR-5	0.5	2.5	Bladder Cancer Research Genetics RNA 1023	7.9	21.4

Ovarian ca. OVCAR-8	6.2	1.7	Bladder Cancer INVITROGEN A302173	33	18.9
Ovarian ca. IGROV-1	0	0	87071 Bladder Cancer (OD04718-01)	11	18.5
Ovarian ca.* (ascites) SK-OV-3	0	1.8	87072 Bladder Normal Adjacent (OD04718-03)	9.4	9.7
Uterus	1.8	24.6	Normal Ovary Res. Gen.	11.6	11.3
Placenta	3.3	2.8	Ovarian Cancer GENPAK 064008	23.3	22.9
Prostate	1.6	2.5	87492 Ovary Cancer (OD04768-07)	80.1	100
Prostate ca.* (bone met)PC-3	10.4	26.5	87493 Ovary NAT (OD04768-08)	3.8	6.4
Testis	1.1	0	Normal Stomach GENPAK 061017	15.9	17.1
Melanoma Hs688(A).T	0.2	0	Gastric Cancer Clontech 9060358	36.3	45.8
Melanoma* (met) Hs688(B).T	1.6	0	NAT Stomach Clontech 9060359	44.4	60.8
Melanoma UACC-62	0.3	1.2	Gastric Cancer Clontech 9060395	13.8	20.4
Melanoma M14	0	0	NAT Stomach Clontech 9060394	78.5	93
Melanoma LOX IMVI	0	0.6	Gastric Cancer Clontech 9060397	5.8	11.5
Melanoma* (met) SK-MEL-5	0.5	4.1	NAT Stomach Clontech 9060396	25.5	30.1
Adipose	0.8	2	Gastric Cancer GENPAK 064005	35.1	27.6

Table 14. Panel 3D

Tissue Name	Rel. Expr., % 3dtm5227f_ag1605
94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	0.0
94906_TE671_Medulloblastom/Cerebellum_sscDNA	0.4
94907_D283 Med_Medulloblastoma/Cerebellum_sscDNA	0.0
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	0.0
94909_XF-498_CNS_sscDNA	0.0
94910_SNB-78_CNS/glioma_sscDNA	0.0
94911_SF-268_CNS/glioblastoma_sscDNA	0.0

94912_T98G_Glioblastoma_sscDNA	0.0
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	0.0
94913_SF-295_CNS/glioblastoma_sscDNA	0.2
94914_Cerebellum_sscDNA	1.9
96777_Cerebellum_sscDNA	3.4
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	0.4
94917_DMS-114_Small cell lung cancer_sscDNA	0.0
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	3.8
94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	0.0
94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	14.6
94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	0.0
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	0.2
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	0.0
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	0.0
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	0.0
94927_NCI-H727_Lung carcinoid_sscDNA	0.5
94928_NCI-UMC-11_Lung carcinoid_sscDNA	0.6
94929_LX-1_Small cell lung cancer_sscDNA	0.2
94930_Colo-205_Colon cancer_sscDNA	0.0
94931_KM12_Colon cancer_sscDNA	0.0
94932_KM20L2_Colon cancer_sscDNA	0.0
94933_NCI-H716_Colon cancer_sscDNA	0.0
94935_SW-48_Colon adenocarcinoma_sscDNA	0.1
94936_SW1116_Colon adenocarcinoma_sscDNA	0.0
94937_LS 174T_Colon adenocarcinoma_sscDNA	0.0
94938_SW-948_Colon adenocarcinoma_sscDNA	0.0
94939_SW-480_Colon adenocarcinoma_sscDNA	0.0
94940_NCI-SNU-5_Gastric carcinoma_sscDNA	0.2
94941_KATO III_Gastric carcinoma_sscDNA	0.4
94943_NCI-SNU-16_Gastric carcinoma_sscDNA	0.0
94944_NCI-SNU-1_Gastric carcinoma_sscDNA	0.0
94946_RF-1_Gastric adenocarcinoma_sscDNA	15.9
94947_RF-48_Gastric adenocarcinoma_sscDNA	18.7
96778_MKN-45_Gastric carcinoma_sscDNA	0.0
94949_NCI-N87_Gastric carcinoma_sscDNA	0.0
94951_OVCAR-5_Ovarian carcinoma_sscDNA	0.0

94952_RL95-2_Uterine carcinoma_sscDNA	0.0
94953_HelaS3_Cervical adenocarcinoma_sscDNA	0.0
94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	0.2
94955_ES-2_Ovarian clear cell carcinoma_sscDNA	0.0
94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	14.7
94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	22.7
94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	0.5
94963_Raji_Burkitt's lymphoma_sscDNA	32.3
94964_Daudi_Burkitt's lymphoma_sscDNA	100.0
94965_U266_B-cell plasmacytoma/myeloma_sscDNA	0.3
94968_CA46_Burkitt's lymphoma_sscDNA	22.5
94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	29.5
94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	23.5
94973_Jurkat_T cell leukemia_sscDNA	2.2
94974_TF-1_Erythroleukemia_sscDNA	0.3
94975_HUT 78_T-cell lymphoma_sscDNA	1.6
94977_U937_Histiocytic lymphoma_sscDNA	7.3
94980_KU-812_Myelogenous leukemia_sscDNA	0.1
94981_769-P_Clear cell renal carcinoma_sscDNA	0.2
94983_Caki-2_Clear cell renal carcinoma_sscDNA	0.1
94984_SW 839_Clear cell renal carcinoma_sscDNA	1.0
94986_G401_Wilms' tumor_sscDNA	0.0
94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	0.1
94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	0.0
94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	0.0
94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	0.1
94991_HPAC_Pancreatic adenocarcinoma_sscDNA	0.1
94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	0.0
94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	0.2
94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	0.0
94996_T24_Bladder carcinma (transitional cell)_sscDNA	0.0
94997_5637_Bladder carcinoma_sscDNA	0.0
94998_HT-1197_Bladder carcinoma_sscDNA	0.0
94999_UM-UC-3_Bladder carcinma (transitional cell)_sscDNA	0.0
95000_A204_Rhabdomyosarcoma_sscDNA	0.0
95001_HT-1080_Fibrosarcoma_sscDNA	0.0
95002_MG-63_Osteosarcoma (bone)_sscDNA	0.1

95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	0.2
95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	0.0
95005_A431_Epidermoid carcinoma_sscDNA	0.0
95007_WM266-4_Melanoma_sscDNA	0.0
95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	0.0
95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	0.0
95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	0.0
95014_SCC-9_Squamous cell carcinoma of tongue_sscDNA	0.3
95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0.0
95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	0.0

Table 14A. Panel 2D

Tissue Name	Rel. Expr., % 2Dtm2728f_ag1605	Rel. Expr., % 2dx4tm4732f_ag1605_a2
Normal Colon GENPAK 061003	70.2	70.3
83219 CC Well to Mod Diff (ODO3866)	8.5	6.3
83220 CC NAT (ODO3866)	8.1	9.4
83221 CC Gr.2 rectosigmoid (ODO3868)	4.5	12.1
83222 CC NAT (ODO3868)	1.6	6.3
83235 CC Mod Diff (ODO3920)	17.9	19.7
83236 CC NAT (ODO3920)	21.5	11.6
83237 CC Gr.2 ascend colon (ODO3921)	18	34.4
83238 CC NAT (ODO3921)	8.9	9.8
83241 CC from Partial Hepatectomy (ODO4309)	7.1	4.9
83242 Liver NAT (ODO4309)	17.1	6.9
87472 Colon mets to lung (OD04451-01)	6.7	11.4
87473 Lung NAT (OD04451-02)	0.8	2.9
Normal Prostate Clontech A+ 6546-1	17.8	52.9
84140 Prostate Cancer (OD04410)	18.6	23
84141 Prostate NAT (OD04410)	9.1	22
87073 Prostate Cancer (OD04720-01)	20	14.5
87074 Prostate NAT (OD04720-02)	21.3	38.1
Normal Lung GENPAK 061010	69.7	85.9
83239 Lung Met to Muscle (ODO4286)	11.1	6.3
83240 Muscle NAT (ODO4286)	15.1	23.3
84136 Lung Malignant Cancer (OD03126)	30.6	30.8
84137 Lung NAT (OD03126)	8	16.3
84871 Lung Cancer (OD04404)	41.8	45.2
84872 Lung NAT (OD04404)	15.4	27.5
84875 Lung Cancer (OD04565)	7.4	8.5
84876 Lung NAT (OD04565)	5.3	1.2
85950 Lung Cancer (OD04237-01)	77.9	72.9
85970 Lung NAT (OD04237-02)	14.3	12.9

83255 Ocular Mel Met to Liver (ODO4310)	2.7	6
83256 Liver NAT (ODO4310)	2.3	5.1
84139 Melanoma Mets to Lung (OD04321)	1.3	6.2
84138 Lung NAT (OD04321)	36.9	22.4
Normal Kidney GENPAK 061008	9.2	19.2
83786 Kidney Ca, Nuclear grade 2 (OD04338)	4.2	6.9
83787 Kidney NAT (OD04338)	7	8.3
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	18.7	11.3
83789 Kidney NAT (OD04339)	4.9	8.5
83790 Kidney Ca, Clear cell type (OD04340)	6.3	14.8
83791 Kidney NAT (OD04340)	10.7	14.6
83792 Kidney Ca, Nuclear grade 3 (OD04348)	6	7.5
83793 Kidney NAT (OD04348)	14.5	16.5
87474 Kidney Cancer (OD04622-01)	15.4	25
87475 Kidney NAT (OD04622-03)	2.3	2.8
85973 Kidney Cancer (OD04450-01)	3.6	7.3
85974 Kidney NAT (OD04450-03)	1.3	13.3
Kidney Cancer Clontech 8120607	7.3	5.2
Kidney NAT Clontech 8120608	1.1	3.6
Kidney Cancer Clontech 8120613	2.8	7.5
Kidney NAT Clontech 8120614	3.7	8
Kidney Cancer Clontech 9010320	17.4	14.1
Kidney NAT Clontech 9010321	16.4	11.3
Normal Uterus GENPAK 061018	4.6	5.2
Uterus Cancer GENPAK 064011	17.2	32.4
Normal Thyroid Clontech A+ 6570-1	17.3	18.1
Thyroid Cancer GENPAK 064010	6.5	1.1
Thyroid Cancer INVITROGEN A302152	1.7	1.6
Thyroid NAT INVITROGEN A302153	9.2	17.7
Normal Breast GENPAK 061019	21.3	30.1
84877 Breast Cancer (OD04566)	1.4	1.5
85975 Breast Cancer (OD04590-01)	12.9	10.1
85976 Breast Cancer Mets (OD04590-03)	100	88
87070 Breast Cancer Metastasis (OD04655-05)	32.8	0
GENPAK Breast Cancer 064006	25	28.5
Breast Cancer Res. Gen. 1024	51.8	66.3
Breast Cancer Clontech 9100266	25	25.1
Breast NAT Clontech 9100265	18.2	31.7
Breast Cancer INVITROGEN A209073	15	21
Breast NAT INVITROGEN A2090734	16.2	12.3
Normal Liver GENPAK 061009	5.6	4.9
Liver Cancer GENPAK 064003	5.4	11.8
Liver Cancer Research Genetics RNA 1025	3.7	3.6
Liver Cancer Research Genetics RNA 1026	4.8	5.5
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	10.6	7

Paired Liver Tissue Research Genetics RNA 6004-N	19.3	28.4
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	4.6	6
Paired Liver Tissue Research Genetics RNA 6005-N	5	0
Normal Bladder GENPAK 061001	18.3	11.5
Bladder Cancer Research Genetics RNA 1023	7.9	21.4
Bladder Cancer INVITROGEN A302173	33	18.9
87071 Bladder Cancer (OD04718-01)	11	18.5
87072 Bladder Normal Adjacent (OD04718-03)	9.4	9.7
Normal Ovary Res. Gen.	11.6	11.3
Ovarian Cancer GENPAK 064008	23.3	22.9
87492 Ovary Cancer (OD04768-07)	80.1	100
87493 Ovary NAT (OD04768-08)	3.8	6.4
Normal Stomach GENPAK 061017	15.9	17.1
Gastric Cancer Clontech 9060358	36.3	45.8
NAT Stomach Clontech 9060359	44.4	60.8
Gastric Cancer Clontech 9060395	13.8	20.4
NAT Stomach Clontech 9060394	78.5	93
Gastric Cancer Clontech 9060397	5.8	11.5
NAT Stomach Clontech 9060396	25.5	30.1
Gastric Cancer GENPAK 064005	35.1	27.6

Table 14B. Panel 4.1D

Tissue Name	Rel. Expr., % 4.1dx4tm5937f_ag1605_a2
93768_Secondary Th1_anti-CD28/anti-CD3	1.3
93769_Secondary Th2_anti-CD28/anti-CD3	2
93770_Secondary Tr1_anti-CD28/anti-CD3	1
93573_Secondary Th1_resting day 4-6 in IL-2	1.3
93572_Secondary Th2_resting day 4-6 in IL-2	2.9
93571_Secondary Tr1_resting day 4-6 in IL-2	3
93568_primary Th1_anti-CD28/anti-CD3	1
93569_primary Th2_anti-CD28/anti-CD3	0.6
93570_primary Tr1_anti-CD28/anti-CD3	0.5
93565_primary Th1_resting dy 4-6 in IL-2	2
93566_primary Th2_resting dy 4-6 in IL-2	1.4
93567_primary Tr1_resting dy 4-6 in IL-2	2.6
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	3.6
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	3.6
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	3.2
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in	2

IL-2	
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.9
93354_CD4_none	2
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	2.9
93103_LAK cells_resting	7.8
93788_LAK cells_IL-2	5.5
93787_LAK cells_IL-2+IL-12	3.7
93789_LAK cells_IL-2+IFN gamma	5.1
93790_LAK cells_IL-2+ IL-18	4.8
93104_LAK cells_PMA/ionomycin and IL-18	1.7
93578_NK Cells IL-2_resting	4.5
93109_Mixed Lymphocyte Reaction_Two Way MLR	10.5
93110_Mixed Lymphocyte Reaction_Two Way MLR	4.5
93111_Mixed Lymphocyte Reaction_Two Way MLR	2.4
93112_Mononuclear Cells (PBMCs)_resting	2.9
93113_Mononuclear Cells (PBMCs)_PWM	4.4
93114_Mononuclear Cells (PBMCs)_PHA-L	10
93249_Ramos (B cell)_none	94.1
93250_Ramos (B cell)_ionomycin	100
93349_B lymphocytes_PWM	16.9
93350_B lymphoytes_CD40L and IL-4	61.3
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	33.7
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	11.9
93356_Dendritic Cells_none	2
93355_Dendritic Cells_LPS 100 ng/ml	1.5
93775_Dendritic Cells_anti-CD40	1.6
93774_Monocytes_resting	3.3
93776_Monocytes_LPS 50 ng/ml	5.3
93581_Macrophages_resting	2.4
93582_Macrophages_LPS 100 ng/ml	1
93098_HUVEC (Endothelial)_none	0.1
93099_HUVEC (Endothelial)_starved	0.2
93100_HUVEC (Endothelial)_IL-1b	0
93779_HUVEC (Endothelial)_IFN gamma	0.2
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.2
93101_HUVEC (Endothelial)_TNF alpha + IL4	0.2
93781_HUVEC (Endothelial)_IL-11	0.4
93583_Lung Microvascular Endothelial Cells_none	0.7
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
92662_Microvascular Dermal endothelium_none	0
92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.9
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	1.2

93347_Small Airway Epithelium_none	0
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.2
92668_Coronery Artery SMC_resting	0.4
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
93107_astrocytes_resting	0.3
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.2
92666_KU-812 (Basophil)_resting	0
92667_KU-812 (Basophil)_PMA/ionoycin	0.3
93579_CCD1106 (Keratinocytes)_none	0.2
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.4
93791_Liver Cirrhosis	0.4
93577_NCI-H292	0
93358_NCI-H292_IL-4	0
93360_NCI-H292_IL-9	0
93359_NCI-H292_IL-13	0.6
93357_NCI-H292_IFN gamma	0.2
93777_HPAEC_-	0
93778_HPAEC_IL-1 beta/TNA alpha	0
93254_Normal Human Lung Fibroblast_none	1.9
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.3
93257_Normal Human Lung Fibroblast_IL-4	0.3
93256_Normal Human Lung Fibroblast_IL-9	0.5
93255_Normal Human Lung Fibroblast_IL-13	0
93258_Normal Human Lung Fibroblast_IFN gamma	1.1
93106_Dermal Fibroblasts CCD1070_resting	0
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.6
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0
93772_dermal fibroblast_IFN gamma	0
93771_dermal fibroblast_IL-4	0.2
93892_Dermal fibroblasts_none	0
99202_Neutrophils_TNFa+LPS	3.6
99203_Neutrophils_none	15.8
735010_Colon_normal	5.1
735019_Lung_none	1.6
64028-1_Thymus_none	12.2
64030-1_Kidney_none	0.3

The RTQ-PCR analysis (Table 13 and 14) reveals that MOL1 is predominantly expressed in cell lines derived from lymphoma and leukemia, specifically Burkitt's lymphoma in panel 3D. This result is supported by the presence of GenBank ESTs coming from T cells from T cell leukemia (see Unigene http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=87968). Recent report indicates that this receptor nomally aids the immune cells to sense the presence of unmethylated CpG dinucleotides (Hemmi H, Takeuchi O, Kawai T, Kaisho T, Sato S, Sanjo H, Matsumoto M, Hoshino K, Wagner H, Takeda K, Akira S. A Toll-like receptor recognizes bacterial DNA. Nature 2000 Dec 7;408(6813):740-5) and to induce proliferation of splenocytes, inflammatory cytokine production from macrophages and maturation of dendritic cells. The signaling pathway mediated by toll-like receptor 9 is through the activation of NF-kB. There is evidence that NF-kappaB activity is necessary for survival of lymphoma and leukemia cells (Constitutive activation of NF-kappaB in primary adult T-cell leukemia cells. Mori N, Fujii M, Ikeda S, Yamada Y, Tomonaga M, Ballard DW, Yamamoto N. Blood 1999 Apr 1;93(7):2360-8; Inhibition of NF-kappaB induces apoptosis of KSHV-infected primary effusion lymphoma cells. Keller SA, Schattner EJ, Cesarman E. Blood, 1 October 2000, 96, No. 7, pp. 2537-2542). Overexpression of toll-like receptor 9 by lymphoma and leukemia cells is likely to mediate ligand-independent signaling, affecting the normal processes of activation, proliferation and tumorogenesis. Therefore the protein encoded (GM_79960178) may serve as a potential marker for lymphoma and leukemia cells. In addition, human monoclonal antibodies directed against this protein could be therapeutics for the treatment of lymphoma and leukemia.

MOL2

Expression of gene MOL2 was assessed using the primer-probe set Ag743, described in Table 15. Results of the RTQ-PCR runs are shown in Table 16.

Table 15. Probe Name: Ag743

Primers	Sequences	Tm	Length	Start Position	SEQID NO:
Forward	5'-ATGTCTTGGTGGATGCAGAA-3'	59.1	20	1304	79
Probe	TET-5'-CGGACTATAGCATTTCTAAGCGCCTCG-3'-TAMRA	69.2	27	1340	80
Reverse	5'-CACATCCTCCTTGCAAATGT-3'	58.6	20	1370	81

Table 16. Panels 1.3D and 4D

PANEL 1.3 D		PANEL 4D	
Tissue Name	Rel. Expr., % 1.3dx4tm5604t_ag743_a1	Tissue Name	Rel. Expr., % 4Dtm2477t_ag743
Liver adenocarcinoma	36.4	93768_Secondary Th1_anti-CD28/anti-CD3	27.2
Pancreas	4.6	93769_Secondary Th2_anti-CD28/anti-CD3	19.6
Pancreatic ca. CAPAN 2	16.6	93770_Secondary Tr1_anti-CD28/anti-CD3	23.2
Adrenal gland	6.5	93573_Secondary Th1_resting day 4-6 in IL-2	7.2
Thyroid	5.2	93572_Secondary Th2_resting day 4-6 in IL-2	7.1
Salivary gland	12.0	93571_Secondary Tr1_resting day 4-6 in IL-2	11.9
Pituitary gland	22.7	93568_primary Th1_anti-CD28/anti-CD3	43.2
Brain (fetal)	8.4	93569_primary Th2_anti-CD28/anti-CD3	32.1
Brain (whole)	38.6	93570_primary Tr1_anti-CD28/anti-CD3	50.0
Brain (amygdala)	24.8	93565_primary Th1_resting dy 4-6 in IL-2	43.8
Brain (cerebellum)	31.4	93566_primary Th2_resting dy 4-6 in IL-2	16.4
Brain (hippocampus)	22.0	93567_primary Tr1_resting dy 4-6 in IL-2	22.4
Brain (substantia nigra)	11.8	93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	23.0
Brain (thalamus)	30.3	93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	25.5
Cerebral Cortex	22.0	93251_CD8 Lymphocytes_anti-CD28/anti-CD3	16.0
Spinal cord	20.6	93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	15.0
CNS ca. (glio/astro) U87-MG	28.1	93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	10.2
CNS ca. (glio/astro) U-118-MG	27.9	93354_CD4_none	4.0

CNS ca. (astro) SW1783	31.1	93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	9.6
CNS ca.* (neuro; met) SK-N-AS	19.3	93103_LAK cells_resting	12.9
CNS ca. (astro) SF-539	47.2	93788_LAK cells_IL-2	14.9
CNS ca. (astro) SNB-75	10.2	93787_LAK cells_IL-2+IL-12	12.5
CNS ca. (glio) SNB-19	24.3	93789_LAK cells_IL-2+IFN gamma	22.2
CNS ca. (glio) U251	20.9	93790_LAK cells_IL-2+ IL-18	15.7
CNS ca. (glio) SF-295	10.7	93104_LAK cells_PMA/ionomycin and IL-18	4.0
Heart (fetal)	2.0	93578_NK Cells IL-2_resting	12.0
Heart	6.5	93109_Mixed Lymphocyte Reaction_Two Way MLR	9.8
Fetal Skeletal	0.7	93110_Mixed Lymphocyte Reaction_Two Way MLR	14.3
Skeletal muscle	18.3	93111_Mixed Lymphocyte Reaction_Two Way MLR	11.7
Bone marrow	11.2	93112_Mononuclear Cells (PBMCs)_resting	5.8
Thymus	7.8	93113_Mononuclear Cells (PBMCs)_PWM	51.8
Spleen	7.2	93114_Mononuclear Cells (PBMCs)_PHA-L	27.5
Lymph node	7.5	93249_Ramos (B cell)_none	0.2
Colorectal	28.4	93250_Ramos (B cell)_ionomycin	6.7
Stomach	6.5	93349_B lymphocytes_PWM	100.0
Small intestine	10.0	93350_B lymphoytes_CD40L and IL-4	23.7
Colon ca. SW480	23.2	92665_EOL-1 (Eosinophil)_dbcAMP differentiated	15.5
Colon ca.* (SW480 met)SW620	12.3	93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	10.4
Colon ca. HT29	1.7	93356_Dendritic Cells_none	15.3
Colon ca.	13.1	93355_Dendritic Cells_LPS 100	6.7

HCT-116		ng/ml	
Colon ca. CaCo-2	12.5	93775_Dendritic Cells_anti-CD40	16.7
83219 CC Well to Mod Diff (ODO3866)	10.4	93774_Monocytes_resting	14.9
Colon ca. HCC-2998	11.3	93776_Monocytes_LPS 50 ng/ml	4.0
Gastric ca.* (liver met) NCI-N87	17.6	93581_Macrophages_resting	19.5
Bladder	17.6	93582_Macrophages_LPS 100 ng/ml	7.5
Trachea	7.6	93098_HUVEC (Endothelial)_none	33.0
Kidney	5.7	93099_HUVEC (Endothelial)_starved	66.0
Kidney (fetal)	6.4	93100_HUVEC (Endothelial)_IL-1b	29.3
Renal ca. 786-0	10.0	93779_HUVEC (Endothelial)_IFN gamma	33.0
Renal ca. A498	23.6	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	23.0
Renal ca. RXF 393	37.8	93101_HUVEC (Endothelial)_TNF alpha + IL4	'19.9
Renal ca. ACHN	18.1	93781_HUVEC (Endothelial)_IL-11	22.4
Renal ca. UO-31	26.1	93583_Lung Microvascular Endothelial Cells_none	27.5
Renal ca. TK-10	10.9	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	25.2
Liver	2.2	92662_Microvascular Dermal endothelium_none	51.4
Liver (fetal)	4.4	92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	22.5
Liver ca. (hepatoblast) HepG2	28.1	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	17.0
Lung	12.4	93347_Small Airway Epithelium_none	20.9
Lung (fetal)	5.2	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	84.7

Lung ca. (small cell) LX-1	10.8	92668_Coronery Artery SMC_resting	37.9
Lung ca. (small cell) NCI-H69	20.2	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	26.8
Lung ca. (s.cell var.) SHP-77	20.1	93107_astrocytes_resting	47.6
Lung ca. (large cell)NCI-H460	10.7	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	20.0
Lung ca. (non-sm. cell) A549	5.5	92666_KU-812 (Basophil)_resting	25.0
Lung ca. (non-s.cell) NCI-H23	13.2	92667_KU-812 (Basophil)_PMA/ionoycin	31.9
Lung ca (non-s.cell) HOP-62	18.3	93579_CCD1106 (Keratinocytes)_none	47.0
Lung ca. (non-s.cl) NCI-H522	13.8	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	7.2
Lung ca. (squam.) SW 900	17.2	93791_Liver Cirrhosis	4.2
Lung ca. (squam.) NCI-H596	20.9	93792_Lupus Kidney	3.8
Mammary gland	17.8	93577_NCI-H292	55.1
Breast ca.* (pl. effusion) MCF-7	20.4	93358_NCI-H292_IL-4	68.8
Breast ca.* (pl.ef) MDA-MB-231	22.5	93360_NCI-H292_IL-9	59.5
Breast ca.* (pl. effusion) T47D	15.5	93359_NCI-H292_IL-13	35.1
Breast ca. BT-549	13.9	93357_NCI-H292_IFN gamma	37.9
Breast ca. MDA-N	9.9	93777_HPAEC_-	32.3
Ovary	5.6	93778_HPAEC_IL-1 beta/TNA alpha	23.2
Ovarian ca.	15.4	93254_Normal Human Lung	29.7

OVCAR-3		Fibroblast_none	
Ovarian ca. OVCAR-4	12.4	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	16.8
Ovarian ca. OVCAR-5	27.2	93257_Normal Human Lung Fibroblast_IL-4	55.5
Ovarian ca. OVCAR-8	9.0	93256_Normal Human Lung Fibroblast_IL-9	34.9
Ovarian ca. IGROV-1	22.6	93255_Normal Human Lung Fibroblast_IL-13	36.9
Ovarian ca.* (ascites) SK-OV-3	100.0	93258_Normal Human Lung Fibroblast_IFN gamma	58.6
Uterus	6.1	93106_Dermal Fibroblasts CCD1070_resting	74.2
Plancenta	15.8	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	64.2
Prostate	5.6	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	27.7
Prostate ca.* (bone met)PC-3	50.1	93772_dermal fibroblast_IFN gamma	24.0
Testis	8.3	93771_dermal fibroblast_IL-4	58.2
Melanoma Hs688(A).T	12.6	93259_IBD Colitis 1**	2.8
Melanoma* (met) Hs688(B).T	14.5	93260_IBD Colitis 2	1.1
Melanoma UACC-62	18.8	93261_IBD Crohns	2.1
Melanoma M14	19.7	735010_Colon_normal	14.3
Melanoma LOX IMVI	8.8	735019_Lung_none	21.5
Melanoma* (met) SK-MEL-5	11.0	64028-1_Thymus_none	27.0
Adipose	14.5	64030-1_Kidney_none	31.2

MOL2 is widely expressed in tissues and cell lines represented in both panels 1.3D and 4D, with highest expression being in one ovarian cancer cell line (SK-OV-3). Thus, it could serve as a diagnostic marker for ovarian cancer.

MOL3

Expression of MOL3 was assessed using the primer-probe sets Ag474 and Ag770, described in Tables 17 and 18. Results of the RTQ-PCR runs are shown in Tables 19 and 20.

Table 17. Probe name: Ag474

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-GGCACTGTCCCTCTGCACAT-3'	20	493	82
Probe	FAM-5'-CCCTGAGAAAGATCTGCCACAAAGACATCTG-3'-TAMRA	31	516	83
Reverse	5'-AACCTGCCCACAGAGCAATC-3'	20	549	84

Table 18. Probe name: Ag770

Primers	Sequences	Tm	Length	Start Position
Forward	5'-ACAGTGCTGTCGCTGGTACTT-3'	60	21	717
Probe	FAM-5'-TTCGTACTGAAAGGCGTACCTCTCCA-3'-TAMRA	67.9	26	746
Reverse	5'-CTCAAACAGCTCACGAGTGAT-3'	58.1	21	773

Table 19. Ag474

PANEL 1.3D		PANEL 2D	
Tissue Name	Rel. Expr., % 1.3Dtm3254f_ag474	Tissue Name	Rel. Expr., % 2Dtm3255f_ag474
Liver adenocarcinoma	0.0	Normal Colon GENPAK 061003	0.3
Pancreas	0.0	83219 CC Well to Mod Diff (ODO3866)	0.0
Pancreatic ca. CAPAN 2	0.0	83220 CC NAT (ODO3866)	0.0
Adrenal gland	0.3	83221 CC Gr.2 rectosigmoid (ODO3868)	0.0

Thyroid	0.0	83222 CC NAT (ODO3868)	0.0
Salivary gland	0.0	83235 CC Mod Diff (ODO3920)	0.0
Pituitary gland	0.0	83236 CC NAT (ODO3920)	0.0
Brain (fetal)	0.2	83237 CC Gr.2 ascend colon (ODO3921)	0.0
Brain (whole)	0.0	83238 CC NAT (ODO3921)	0.0
Brain (amygdala)	0.1	83241 CC from Partial Hepatectomy (ODO4309)	3.8
Brain (cerebellum)	0.0	83242 Liver NAT (ODO4309)	100.0
Brain (hippocampus)	0.0	87472 Colon mets to lung (OD04451-01)	0.0
Brain (substantia nigra)	0.0	87473 Lung NAT (OD04451-02)	0.0
Brain (thalamus)	0.0	Normal Prostate Clontech A+ 6546-1	0.0
Cerebral Cortex	0.1	84140 Prostate Cancer (OD04410)	0.0
Spinal cord	0.0	84141 Prostate NAT (OD04410)	0.0
CNS ca. (glio/astro) U87-MG	0.3	87073 Prostate Cancer (OD04720-01)	0.0
CNS ca. (glio/astro) U-118-MG	0.0	87074 Prostate NAT (OD04720-02)	0.0
CNS ca. (astro) SW1783	0.0	Normal Lung GENPAK 061010	0.0
CNS ca.* (neuro; met) SK-N-AS	0.0	83239 Lung Met to Muscle (ODO4286)	0.0
CNS ca. (astro) SF-539	0.0	83240 Muscle NAT (ODO4286)	0.0
CNS ca. (astro) SNB-75	0.0	84136 Lung Malignant Cancer (OD03126)	0.0
CNS ca. (glio) SNB-19	0.0	84137 Lung NAT (OD03126)	0.0
CNS ca. (glio) U251	0.0	84871 Lung Cancer (OD04404)	0.0
CNS ca. (glio) SF-295	0.0	84872 Lung NAT (OD04404)	0.0
Heart (fetal)	0.0	84875 Lung Cancer (OD04565)	0.0
Heart	0.0	84876 Lung NAT (OD04565)	0.0
Fetal Skeletal	0.2	85950 Lung Cancer	0.0

		(OD04237-01)	
Skeletal muscle	0.0	85970 Lung NAT (OD04237-02)	0.0
Bone marrow	0.0	83255 Ocular Mel Met to Liver (ODO4310)	0.0
Thymus	0.0	83256 Liver NAT (ODO4310)	64.2
Spleen	0.2	84139 Melanoma Mets to Lung (OD04321)	0.0
Lymph node	0.0	84138 Lung NAT (OD04321)	0.0
Colorectal	0.0	Normal Kidney GENPAK 061008	0.0
Stomach	0.1	83786 Kidney Ca, Nuclear grade 2 (OD04338)	0.0
Small intestine	0.0	83787 Kidney NAT (OD04338)	0.0
Colon ca. SW480	0.3	83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.0
Colon ca.* (SW480 met)SW620	0.0	83789 Kidney NAT (OD04339)	0.0
Colon ca. HT29	0.0	83790 Kidney Ca, Clear cell type (OD04340)	0.1
Colon ca. HCT-116	0.0	83791 Kidney NAT (OD04340)	0.0
Colon ca. CaCo-2	0.3	83792 Kidney Ca, Nuclear grade 3 (OD04348)	0.0
83219 CC Well to Mod Diff (ODO3866)	0.3	83793 Kidney NAT (OD04348)	0.0
Colon ca. HCC-2998	0.5	87474 Kidney Cancer (OD04622-01)	0.0
Gastric ca.* (liver met) NCI-N87	0.0	87475 Kidney NAT (OD04622-03)	0.0
Bladder	0.0	85973 Kidney Cancer (OD04450-01)	0.0
Trachea	0.0	85974 Kidney NAT (OD04450-03)	0.1
Kidney	0.0	Kidney Cancer Clontech 8120607	0.0
Kidney (fetal)	0.0	Kidney NAT Clontech 8120608	0.0
Renal ca. 786-0	0.0	Kidney Cancer Clontech 8120613	0.0
Renal ca. A498	0.0	Kidney NAT Clontech 8120614	0.0
Renal ca.	0.0	Kidney Cancer Clontech	0.0

RXF 393		9010320	
Renal ca. ACHN	0.0	Kidney NAT Clontech 9010321	0.0
Renal ca. UO-31	0.3	Normal Uterus GENPAK 061018	0.0
Renal ca. TK-10	0.1	Uterus Cancer GENPAK 064011	0.0
Liver	100.0	Normal Thyroid Clontech A+ 6570-1	0.0
Liver (fetal)	1.8	Thyroid Cancer GENPAK 064010	0.0
Liver ca. (hepatoblast) HepG2	0.0	Thyroid Cancer INVITROGEN A302152	0.0
Lung	0.0	Thyroid NAT INVITROGEN A302153	0.0
Lung (fetal)	0.0	Normal Breast GENPAK 061019	0.0
Lung ca. (small cell) LX-1	0.0	84877 Breast Cancer (OD04566)	0.0
Lung ca. (small cell) NCI-H69	0.0	85975 Breast Cancer (OD04590-01)	0.0
Lung ca. (s.cell var.) SHP-77	0.0	85976 Breast Cancer Mets (OD04590-03)	0.0
Lung ca. (large cell)NCI-H460	0.0	87070 Breast Cancer Metastasis (OD04655-05)	0.0
Lung ca. (non-sm. cell) A549	0.1	GENPAK Breast Cancer 064006	0.2
Lung ca. (non-s.cell) NCI-H23	0.2	Breast Cancer Res. Gen. 1024	0.2
Lung ca (non-s.cell) HOP-62	0.0	Breast Cancer Clontech 9100266	0.0
Lung ca. (non-s.cl) NCI-H522	0.0	Breast NAT Clontech 9100265	0.0
Lung ca. (squam.) SW 900	0.0	Breast Cancer INVITROGEN A209073	0.0
Lung ca. (squam.) NCI-H596	0.0	Breast NAT INVITROGEN A2090734	0.0
Mammary gland	0.0	Normal Liver GENPAK 061009	38.4
Breast ca.* (pl. effusion) MCF-7	0.0	Liver Cancer GENPAK 064003	49.0
Breast ca.* (pl.ef) MDA-MB-231	0.0	Liver Cancer Research Genetics RNA 1025	62.4
Breast ca.* (pl. effusion) T47D	0.0	Liver Cancer Research Genetics RNA 1026	12.9
Breast ca. BT-549	0.0	Paired Liver Cancer Tissue Research Genetics RNA	74.2

		6004-T	
Breast ca. MDA-N	0.1	Paired Liver Tissue Research Genetics RNA 6004-N	8.5
Ovary	0.0	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	5.0
Ovarian ca. OVCAR-3	0.5	Paired Liver Tissue Research Genetics RNA 6005-N	18.6
Ovarian ca. OVCAR-4	0.0	Normal Bladder GENPAK 061001	0.0
Ovarian ca. OVCAR-5	0.0	Bladder Cancer Research Genetics RNA 1023	0.0
Ovarian ca. OVCAR-8	0.0	Bladder Cancer INVITROGEN A302173	0.0
Ovarian ca. IGROV-1	0.0	87071 Bladder Cancer (OD04718-01)	0.0
Ovarian ca.* (ascites) SK-OV-3	0.0	87072 Bladder Normal Adjacent (OD04718-03)	0.0
Uterus	0.0	Normal Ovary Res. Gen.	0.0
Placenta	0.0	Ovarian Cancer GENPAK 064008	0.0
Prostate	0.1	87492 Ovary Cancer (OD04768-07)	0.1
Prostate ca.* (bone met)PC-3	0.0	87493 Ovary NAT (OD04768-08)	0.0
Testis	0.3	Normal Stomach GENPAK 061017	0.0
Melanoma Hs688(A).T	0.0	Gastric Cancer Clontech 9060358	0.0
Melanoma* (met) Hs688(B).T	0.0	NAT Stomach Clontech 9060359	0.0
Melanoma UACC-62	0.0	Gastric Cancer Clontech 9060395	0.4
Melanoma M14	0.0	NAT Stomach Clontech 9060394	0.0
Melanoma LOX IMVI	0.0	Gastric Cancer Clontech 9060397	0.3
Melanoma* (met) SK-MEL-5	0.0	NAT Stomach Clontech 9060396	0.0
Adipose	0.0	Gastric Cancer GENPAK 064005	0.0

Table 20. Ag770

PANEL 1.3D		**PANEL 4D**		

Tissue Name	Rel. Expr., % 1.3dx4tm5495f_ag770_b2	Tissue Name	Rel. Expr., % 4dtm1843f_ag770	Rel. Expr., % 4Dtm1910f_ag770
Liver adenocarcinoma	0.0	93768_Secondary Th1_anti-CD28/anti-CD3	0.0	0.0
Pancreas	0.0	93769_Secondary Th2_anti-CD28/anti-CD3	6.4	0.0
Pancreatic ca. CAPAN 2	0.0	93770_Secondary Tr1_anti-CD28/anti-CD3	3.1	0.0
Adrenal gland	0.0	93573_Secondary Th1_resting day 4-6 in IL-2	0.0	0.0
Thyroid	0.0	93572_Secondary Th2_resting day 4-6 in IL-2	0.0	0.0
Salivary gland	0.0	93571_Secondary Tr1_resting day 4-6 in IL-2	0.0	0.0
Pituitary gland	0.0	93568_primary Th1_anti-CD28/anti-CD3	3.7	0.0
Brain (fetal)	0.0	93569_primary Th2_anti-CD28/anti-CD3	0.0	0.0
Brain (whole)	0.0	93570_primary Tr1_anti-CD28/anti-CD3	0.0	0.0
Brain (amygdala)	0.0	93565_primary Th1_resting dy 4-6 in IL-2	0.0	4.8
Brain (cerebellum)	0.2	93566_primary Th2_resting dy 4-6 in IL-2	0.0	2.2
Brain (hippocampus)	0.1	93567_primary Tr1_resting dy 4-6 in IL-2	0.0	7.0
Brain (substantia nigra)	0.0	93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	3.1	0.0
Brain (thalamus)	0.0	93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	0.0
Cerebral Cortex	0.0	93251_CD8 Lymphocytes_anti-CD28/anti-CD3	1.4	0.0
Spinal cord	0.0	93353_chronic CD8 Lymphocytes 2ry_resting day 4-6 in IL-2	0.0	0.0
CNS ca. (glio/astro) U87-MG	0.0	93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	0.0

CNS ca. (glio/astro) U-118-MG	0.0	93354_CD4_none	0.0	0.0
CNS ca. (astro) SW1783	0.0	93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.0	41.2
CNS ca.* (neuro; met) SK-N-AS	0.0	93103_LAK cells_resting	0.0	0.0
CNS ca. (astro) SF-539	0.0	93788_LAK cells_IL-2	0.0	0.0
CNS ca. (astro) SNB-75	0.0	93787_LAK cells_IL-2+IL-12	0.0	0.0
CNS ca. (glio) SNB-19	0.0	93789_LAK cells_IL-2+IFN gamma	0.0	0.0
CNS ca. (glio) U251	0.0	93790_LAK cells_IL-2+ IL-18	0.0	0.0
CNS ca. (glio) SF-295	0.0	93104_LAK cells_PMA/ionomycin and IL-18	0.0	5.9
Heart (fetal)	0.0	93578_NK Cells IL-2_resting	0.0	0.0
Heart	0.3	93109_Mixed Lymphocyte Reaction_Two Way MLR	6.0	0.0
Fetal Skeletal	0.0	93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	0.0
Skeletal muscle	0.0	93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	1.3
Bone marrow	0.0	93112_Mononuclear Cells (PBMCs)_resting	0.0	18.4
Thymus	0.0	93113_Mononuclear Cells (PBMCs)_PWM	0.0	0.0
Spleen	0.0	93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	6.6
Lymph node	0.0	93249_Ramos (B cell)_none	5.7	0.0
Colorectal	0.1	93250_Ramos (B cell)_ionomycin	0.0	0.0
Stomach	0.0	93349_B lymphocytes_PWM	0.0	0.0
Small intestine	0.0	93350_B lymphoytes_CD40L and IL-4	0.0	0.0
Colon ca. SW480	0.0	92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	3.2

Colon ca.* (SW480 met)SW620	0.2	93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0	0.0
Colon ca. HT29	0.0	93356_Dendritic Cells_none	0.0	0.0
Colon ca. HCT-116	0.0	93355_Dendritic Cells_LPS 100 ng/ml	0.0	0.0
Colon ca. CaCo-2	0.0	93775_Dendritic Cells_anti-CD40	0.0	0.0
83219 CC Well to Mod Diff (ODO3866)	0.0	93774_Monocytes_resting	0.0	0.0
Colon ca. HCC-2998	1.3	93776_Monocytes_LPS 50 ng/ml	0.0	0.0
Gastric ca.* (liver met) NCI-N87	0.2	93581_Macrophages_resting	1.1	0.0
Bladder	0.0	93582_Macrophages_LPS 100 ng/ml	0.0	5.9
Trachea	0.0	93098_HUVEC (Endothelial)_none	0.0	0.0
Kidney	0.0	93099_HUVEC (Endothelial)_starved	0.0	0.0
Kidney (fetal)	0.0	93100_HUVEC (Endothelial)_IL-1b	0.0	0.0
Renal ca. 786-0	0.0	93779_HUVEC (Endothelial)_IFN gamma	0.0	0.0
Renal ca. A498	0.5	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0	0.0
Renal ca. RXF 393	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0	0.0
Renal ca. ACHN	0.0	93781_HUVEC (Endothelial)_IL-11	0.0	0.0
Renal ca. UO-31	0.0	93583_Lung Microvascular Endothelial Cells_none	0.0	0.0
Renal ca. TK-10	0.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
Liver	100.0	92662_Microvascular Dermal endothelium_none	0.0	0.0
Liver (fetal)	0.3	92663_Microsvasular Dermal endothelium_TNFa	0.0	0.0

		(4 ng/ml) and IL1b (1 ng/ml)		
Liver ca. (hepatoblast) HepG2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0.0	2.2
Lung	0.0	93347_Small Airway Epithelium_none	0.0	0.0
Lung (fetal)	0.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	3.7
Lung ca. (small cell) LX-1	0.0	92668_Coronery Artery SMC_resting	0.0	0.0
Lung ca. (small cell) NCI-H69	0.0	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
Lung ca. (s.cell var.) SHP-77	0.0	93107_astrocytes_resting	0.0	3.4
Lung ca. (large cell)NCI-H460	0.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0	0.0
Lung ca. (non-sm. cell) A549	0.0	92666_KU-812 (Basophil)_resting	0.0	1.6
Lung ca. (non-s.cell) NCI-H23	0.0	92667_KU-812 (Basophil)_PMA/ionoycin	0.0	0.0
Lung ca (non-s.cell) HOP-62	0.0	93579_CCD1106 (Keratinocytes)_none	0.0	0.0
Lung ca. (non-s.cl) NCI-H522	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0	0.0
Lung ca. (squam.) SW 900	0.5	93791_Liver Cirrhosis	100.0	100.0
Lung ca. (squam.) NCI-H596	0.0	93792_Lupus Kidney	0.0	0.0
Mammary gland	0.0	93577_NCI-H292	0.0	0.0
Breast ca.* (pl. effusion) MCF-7	0.0	93358_NCI-H292_IL-4	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	0.0	93360_NCI-H292_IL-9	0.0	0.0
Breast ca.* (pl. effusion) T47D	0.0	93359_NCI-H292_IL-13	0.0	0.0
Breast ca. BT-549	0.0	93357_NCI-H292_IFN gamma	0.0	0.0

Breast ca. MDA-N	0.0	93777_HPAEC_-	2.3	3.4
Ovary	0.0	93778_HPAEC_IL-1 beta/TNA alpha	0.0	0.0
Ovarian ca. OVCAR-3	0.0	93254_Normal Human Lung Fibroblast_none	3.4	0.0
Ovarian ca. OVCAR-4	0.0	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0	0.0
Ovarian ca. OVCAR-5	0.0	93257_Normal Human Lung Fibroblast_IL-4	0.0	0.0
Ovarian ca. OVCAR-8	0.0	93256_Normal Human Lung Fibroblast_IL-9	0.0	0.0
Ovarian ca. IGROV-1	0.0	93255_Normal Human Lung Fibroblast_IL-13	0.0	0.0
Ovarian ca.* (ascites) SK-OV-3	0.0	93258_Normal Human Lung Fibroblast_IFN gamma	0.0	0.0
Uterus	0.5	93106_Dermal Fibroblasts CCD1070_resting	0.0	0.0
Plancenta	0.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0.0	0.0
Prostate	0.0	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0	4.3
Prostate ca.* (bone met)PC-3	0.0	93772_dermal fibroblast_IFN gamma	0.0	7.9
Testis	0.4	93771_dermal fibroblast_IL-4	0.0	0.0
Melanoma Hs688(A).T	0.0	93259_IBD Colitis 1**	6.0	13.1
Melanoma* (met) Hs688(B).T	0.0	93260_IBD Colitis 2	2.8	5.2
Melanoma UACC-62	0.3	93261_IBD Crohns	0.0	1.9
Melanoma M14	0.1	735010_Colon_normal	1.3	3.2
Melanoma LOX IMVI	0.0	735019_Lung_none	14.9	0.0
Melanoma* (met) SK-MEL-5	0.4	64028-1_Thymus_none	2.3	7.3
Adipose	0.0	64030-1_Kidney_none	0.0	0.0

Both probe/primer sets are specific for the sequence of gene Acc. No. MOL3. Unigene data at http://www.ncbi.nlm.nih.gov/UniGene/clust.cgi?ORG=Hs&CID=8509 and our RTQ-PCR panels 1.3D,2D and 4D indicate that this gene is specifically expressed by the liver and upregulated in some hepatocellular carcinomas (HCCs).There is evidence suggesting that the examination of the serum complements may be a useful tool for the detection of HCCs in liver cirrosis (LC) patients. (Takezaki E, Murakami S, Nishibayashi H, Kagawa K, Ohmori H. Gan No Rinsho 1990 Oct;36(12):2119-22). Therefore the serum level of this protein can be used as a diagnostic marker to detect LC and HCC and antibodies directed against this protein can be a potential therapeutic agent against LC and HCC. In addition, this molecule can also serve as a specific marker for differentiating liver from other tissues.

MOL4

Expression of gene MOL4 was assessed using the primer-probe set Ag1611, described in Table 21

Table 21. Probe Name: Ag1611

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-ATATGCTGTGCTGCATTCAGT-3'	58.4	21	40	85
Probe	TET-5'-CTGCCTGGTCAGTGAACAATTTCCTG-3'-TAMRA	68.9	26	65	86
Reverse	5'-CAAGGCCACACTAGTCGTGTAG-3'	59.9	22	117	87

Expression of this gene in panels 1.3D, 4D and 2 is at very low to undetectable levels (Ct values>35) in a number of tissues.

MOL6

Expression of gene MOL6a was assessed using the primer-probe set Ag1167, described in Table 22. Results of the RTQ-PCR runs are shown in Tables 23 and 24.

Table 22. Probe Name: Ag1167

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-TCTTTGCTGACTCATCTGTTCA-3'	58.7	22	51	88
Probe	TET-5'-AAGAAGACCCTGCTCCCTATTTGGTG-3'-TAMRA	67.5	26	75	89
Reverse	5'-AGGGGTTGAAGTGAGACTTGAG-3'	59.8	22	104	90

Table 23. Panels 1.3D and 4D

PANEL 1.3D		PANEL 4D	
Tissue Name	Rel. Expr., % 1.3dx4tm5586t_ag1167_a1	Tissue Name	Rel. Expr., % 4Dtm1937t_ag1167
Liver adenocarcinoma	1.1	93768_Secondary Th1_anti-CD28/anti-CD3	1.7
Pancreas	0.0	93769_Secondary Th2_anti-CD28/anti-CD3	0.0
Pancreatic ca. CAPAN 2	1.0	93770_Secondary Tr1_anti-CD28/anti-CD3	0.9
Adrenal gland	0.0	93573_Secondary Th1_resting day 4-6 in IL-2	2.7
Thyroid	0.0	93572_Secondary Th2_resting day 4-6 in IL-2	0.0
Salivary gland	0.0	93571_Secondary Tr1_resting day 4-6 in IL-2	0.0
Pituitary gland	2.1	93568_primary Th1_anti-CD28/anti-CD3	0.0
Brain (fetal)	4.1	93569_primary Th2_anti-CD28/anti-CD3	3.0
Brain (whole)	1.1	93570_primary Tr1_anti-CD28/anti-CD3	2.4
Brain (amygdala)	4.1	93565_primary Th1_resting dy 4-6 in IL-2	5.3
Brain (cerebellum)	6.7	93566_primary Th2_resting dy 4-6 in IL-2	3.7
Brain (hippocampus)	4.3	93567_primary Tr1_resting dy 4-6 in IL-2	3.7

		IL-2	
Brain (substantia nigra)	5.4	93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	1.6
Brain (thalamus)	4.7	93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	2.6
Cerebral Cortex	1.3	93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.9
Spinal cord	1.6	93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.4
CNS ca. (glio/astro) U87-MG	0.0	93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.9
CNS ca. (glio/astro) U-118-MG	0.0	93354_CD4_none	1.0
CNS ca. (astro) SW1783	0.0	93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	2.5
CNS ca.* (neuro; met) SK-N-AS	0.0	93103_LAK cells_resting	7.0
CNS ca. (astro) SF-539	0.0	93788_LAK cells_IL-2	0.9
CNS ca. (astro) SNB-75	2.4	93787_LAK cells_IL-2+IL-12	1.6
CNS ca. (glio) SNB-19	4.3	93789_LAK cells_IL-2+IFN gamma	5.8
CNS ca. (glio) U251	1.3	93790_LAK cells_IL-2+ IL-18	1.7
CNS ca. (glio) SF-295	0.0	93104_LAK cells_PMA/ionomycin and IL-18	0.0
Heart (fetal)	0.0	93578_NK Cells IL-2_resting	2.2
Heart	0.0	93109_Mixed Lymphocyte Reaction_Two Way MLR	2.4
Fetal Skeletal	0.0	93110_Mixed Lymphocyte Reaction_Two Way MLR	1.6
Skeletal muscle	1.0	93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0
Bone marrow	0.0	93112_Mononuclear Cells (PBMCs)_resting	0.0
Thymus	0.0	93113_Mononuclear Cells (PBMCs)_PWM	6.0
Spleen	16.0	93114_Mononuclear Cells (PBMCs)_PHA-L	0.9
Lymph node	1.4	93249_Ramos (B cell)_none	6.8
Colorectal	0.0	93250_Ramos (B cell)_ionomycin	5.9
Stomach	0.0	93349_B lymphocytes_PWM	3.8

Small intestine	2.9	93350_B lymphoytes_CD40L and IL-4	2.4
Colon ca. SW480	0.0	92665_EOL-1 (Eosinophil)_dbcAMP differentiated	82.9
Colon ca.* (SW480 met)SW620	1.7	93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	100.0
Colon ca. HT29	0.0	93356_Dendritic Cells_none	2.5
Colon ca. HCT-116	3.9	93355_Dendritic Cells_LPS 100 ng/ml	0.9
Colon ca. CaCo-2	1.0	93775_Dendritic Cells_anti-CD40	2.5
83219 CC Well to Mod Diff (ODO3866)	0.0	93774_Monocytes_resting	0.0
Colon ca. HCC-2998	1.9	93776_Monocytes_LPS 50 ng/ml	0.8
Gastric ca.* (liver met) NCI-N87	2.3	93581_Macrophages_resting	0.8
Bladder	4.9	93582_Macrophages_LPS 100 ng/ml	0.4
Trachea	0.0	93098_HUVEC (Endothelial)_none	0.9
Kidney	1.8	93099_HUVEC (Endothelial)_starved	1.5
Kidney (fetal)	2.3	93100_HUVEC (Endothelial)_IL-1b	0.0
Renal ca. 786-0	0.0	93779_HUVEC (Endothelial)_IFN gamma	2.4
Renal ca. A498	0.9	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
Renal ca. RXF 393	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	0.0
Renal ca. ACHN	1.5	93781_HUVEC (Endothelial)_IL-11	0.9
Renal ca. UO-31	0.0	93583_Lung Microvascular Endothelial Cells_none	2.1
Renal ca. TK-10	4.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.3
Liver	0.0	92662_Microvascular Dermal endothelium_none	1.2
Liver (fetal)	0.0	92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.5
Liver ca. (hepatoblast) HepG2	0.5	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	44.1

Lung	0.0	93347_Small Airway Epithelium_none	5.6
Lung (fetal)	2.2	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	25.7
Lung ca. (small cell) LX-1	5.2	92668_Coronery Artery SMC_resting	0.7
Lung ca. (small cell) NCI-H69	2.8	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
Lung ca. (s.cell var.) SHP-77	0.8	93107_astrocytes_resting	3.5
Lung ca. (large cell)NCI-H460	2.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.4
Lung ca. (non-sm. cell) A549	1.8	92666_KU-812 (Basophil)_resting	20.4
Lung ca. (non-s.cell) NCI-H23	4.7	92667_KU-812 (Basophil)_PMA/ionoycin	34.2
Lung ca (non-s.cell) HOP-62	1.3	93579_CCD1106 (Keratinocytes)_none	0.7
Lung ca. (non-s.cl) NCI-H522	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	19.1
Lung ca. (squam.) SW 900	0.0	93791_Liver Cirrhosis	3.2
Lung ca. (squam.) NCI-H596	2.2	93792_Lupus Kidney	5.2
Mammary gland	0.8	93577_NCI-H292	6.3
Breast ca.* (pl. effusion) MCF-7	3.8	93358_NCI-H292_IL-4	7.4
Breast ca.* (pl.ef) MDA-MB-231	0.0	93360_NCI-H292_IL-9	6.5
Breast ca.* (pl. effusion) T47D	0.0	93359_NCI-H292_IL-13	8.8
Breast ca. BT-549	0.0	93357_NCI-H292_IFN gamma	4.2
Breast ca. MDA-N	0.0	93777_HPAEC_-	0.9
Ovary	0.0	93778_HPAEC_IL-1 beta/TNA alpha	1.4
Ovarian ca. OVCAR-3	0.0	93254_Normal Human Lung Fibroblast_none	0.0
Ovarian ca. OVCAR-4	1.6	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0.0
Ovarian ca. OVCAR-5	1.9	93257_Normal Human Lung Fibroblast_IL-4	1.5

Ovarian ca. OVCAR-8	2.8	93256_Normal Human Lung Fibroblast_IL-9	0.0
Ovarian ca. IGROV-1	2.7	93255_Normal Human Lung Fibroblast_IL-13	1.9
Ovarian ca.* (ascites) SK-OV-3	5.6	93258_Normal Human Lung Fibroblast_IFN gamma	2.2
Uterus	0.6	93106_Dermal Fibroblasts CCD1070_resting	0.8
Plancenta	1.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	1.6
Prostate	0.0	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0
Prostate ca.* (bone met)PC-3	0.0	93772_dermal fibroblast_IFN gamma	2.0
Testis	100.0	93771_dermal fibroblast_IL-4	0.9
Melanoma Hs688(A).T	0.0	93259_IBD Colitis 1**	21.0
Melanoma* (met) Hs688(B).T	0.0	93260_IBD Colitis 2	1.3
Melanoma UACC-62	0.0	93261_IBD Crohns	0.7
Melanoma M14	0.9	735010_Colon_normal	0.7
Melanoma LOX IMVI	0.0	735019_Lung_none	2.2
Melanoma* (met) SK-MEL-5	0.0	64028-1_Thymus_none	41.8
Adipose	1.9	64030-1_Kidney_none	6.0

Table 24. Panels 2D and 3D

PANEL 2D		PANEL 3D	
Tissue Name	Rel. Expr., % 2Dtm2324t_ag1167	Tissue Name	Rel. Expr., % 3dtm5309t_ag1167
Normal Colon GENPAK 061003	2.9	94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	4.0
83219 CC Well to Mod Diff (ODO3866)	2.5	94906_TE671_Medulloblastom/Cerebellum_sscDNA	0.0
83220 CC NAT (ODO3866)	18.9	94907_D283 Med_Medulloblastoma/Cerebellum_sscDNA	8.4
83221 CC Gr.2	2.2	94908_PFSK-1_Primitive	7.0

rectosigmoid (ODO3868)		Neuroectodermal/Cerebellum_sscDNA	
83222 CC NAT (ODO3868)	0.0	94909_XF-498_CNS_sscDNA	0.0
83235 CC Mod Diff (ODO3920)	6.3	94910_SNB-78_CNS/glioma_sscDNA	10.2
83236 CC NAT (ODO3920)	12.6	94911_SF-268_CNS/glioblastoma_sscDNA	0.0
83237 CC Gr.2 ascend colon (ODO3921)	0.0	94912_T98G_Glioblastoma_sscDNA	0.0
83238 CC NAT (ODO3921)	7.7	96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	0.0
83241 CC from Partial Hepatectomy (ODO4309)	2.9	94913_SF-295_CNS/glioblastoma_sscDNA	0.0
83242 Liver NAT (ODO4309)	0.0	94914_Cerebellum_sscDNA	66.0
87472 Colon mets to lung (OD04451-01)	5.0	96777_Cerebellum_sscDNA	4.4
87473 Lung NAT (OD04451-02)	9.9	94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	7.3
Normal Prostate Clontech A+ 6546-1	17.4	94917_DMS-114_Small cell lung cancer_sscDNA	0.0
84140 Prostate Cancer (OD04410)	2.7	94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	100.0
84141 Prostate NAT (OD04410)	26.2	94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	16.4
87073 Prostate Cancer (OD04720-01)	20.6	94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	2.1
87074 Prostate NAT (OD04720-02)	13.9	94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	0.0
Normal Lung GENPAK 061010	17.7	94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	3.5
83239 Lung Met to Muscle (ODO4286)	5.0	94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	0.0
83240 Muscle NAT (ODO4286)	2.6	94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	0.0
84136 Lung Malignant Cancer (OD03126)	4.9	94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	11.3
84137 Lung NAT (OD03126)	0.0	94927_NCI-H727_Lung carcinoid_sscDNA	3.0
84871 Lung Cancer (OD04404)	5.5	94928_NCI-UMC-11_Lung carcinoid_sscDNA	10.1

84872 Lung NAT (OD04404)	2.4	94929_LX-1_Small cell lung cancer_sscDNA	0.0
84875 Lung Cancer (OD04565)	2.5	94930_Colo-205_Colon cancer_sscDNA	0.0
84876 Lung NAT (OD04565)	7.7	94931_KM12_Colon cancer_sscDNA	4.9
85950 Lung Cancer (OD04237-01)	18.4	94932_KM20L2_Colon cancer_sscDNA	0.0
85970 Lung NAT (OD04237-02)	7.8	94933_NCI-H716_Colon cancer_sscDNA	0.0
83255 Ocular Mel Met to Liver (ODO4310)	0.0	94935_SW-48_Colon adenocarcinoma_sscDNA	0.0
83256 Liver NAT (ODO4310)	0.0	94936_SW1116_Colon adenocarcinoma_sscDNA	1.6
84139 Melanoma Mets to Lung (OD04321)	3.0	94937_LS 174T_Colon adenocarcinoma_sscDNA	0.0
84138 Lung NAT (OD04321)	2.6	94938_SW-948_Colon adenocarcinoma_sscDNA	4.4
Normal Kidney GENPAK 061008	100.0	94939_SW-480_Colon adenocarcinoma_sscDNA	0.0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	56.6	94940_NCI-SNU-5_Gastric carcinoma_sscDNA	0.0
83787 Kidney NAT (OD04338)	23.2	94941_KATO III_Gastric carcinoma_sscDNA	2.6
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.0	94943_NCI-SNU-16_Gastric carcinoma_sscDNA	3.6
83789 Kidney NAT (OD04339)	46.0	94944_NCI-SNU-1_Gastric carcinoma_sscDNA	0.0
83790 Kidney Ca, Clear cell type (OD04340)	12.9	94946_RF-1_Gastric adenocarcinoma_sscDNA	0.0
83791 Kidney NAT (OD04340)	24.5	94947_RF-48_Gastric adenocarcinoma_sscDNA	0.0
83792 Kidney Ca, Nuclear grade 3 (OD04348)	4.5	96778_MKN-45_Gastric carcinoma_sscDNA	0.0
83793 Kidney NAT (OD04348)	44.4	94949_NCI-N87_Gastric carcinoma_sscDNA	0.0
87474 Kidney Cancer (OD04622-01)	2.8	94951_OVCAR-5_Ovarian carcinoma_sscDNA	0.0
87475 Kidney NAT (OD04622-03)	0.0	94952_RL95-2_Uterine carcinoma_sscDNA	0.0
85973 Kidney Cancer (OD04450-01)	4.4	94953_HelaS3_Cervical adenocarcinoma_sscDNA	0.0

85974 Kidney NAT (OD04450-03)	24.8	94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	5.8
Kidney Cancer Clontech 8120607	0.0	94955_ES-2_Ovarian clear cell carcinoma_sscDNA	0.0
Kidney NAT Clontech 8120608	0.0	94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	0.0
Kidney Cancer Clontech 8120613	0.0	94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	0.0
Kidney NAT Clontech 8120614	0.0	94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	28.3
Kidney Cancer Clontech 9010320	2.6	94963_Raji_Burkitt's lymphoma_sscDNA	0.0
Kidney NAT Clontech 9010321	8.4	94964_Daudi_Burkitt's lymphoma_sscDNA	2.9
Normal Uterus GENPAK 061018	0.0	94965_U266_B-cell plasmacytoma/myeloma_sscDNA	6.4
Uterus Cancer GENPAK 064011	16.2	94968_CA46_Burkitt's lymphoma_sscDNA	0.0
Normal Thyroid Clontech A+ 6570-1	1.8	94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	0.0
Thyroid Cancer GENPAK 064010	27.2	94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	6.7
Thyroid Cancer INVITROGEN A302152	5.2	94973_Jurkat_T cell leukemia_sscDNA	4.2
Thyroid NAT INVITROGEN A302153	19.9	94974_TF-1_Erythroleukemia_sscDNA	2.4
Normal Breast GENPAK 061019	47.3	94975_HUT 78_T-cell lymphoma_sscDNA	2.8
84877 Breast Cancer (OD04566)	7.0	94977_U937_Histiocytic lymphoma_sscDNA	6.6
85975 Breast Cancer (OD04590-01)	15.7	94980_KU-812_Myelogenous leukemia_sscDNA	18.2
85976 Breast Cancer Mets (OD04590-03)	17.7	94981_769-P_Clear cell renal carcinoma_sscDNA	2.6
87070 Breast Cancer Metastasis (OD04655-05)	76.8	94983_Caki-2_Clear cell renal carcinoma_sscDNA	0.0
GENPAK Breast Cancer 064006	42.6	94984_SW 839_Clear cell renal carcinoma_sscDNA	1.9
Breast Cancer Res. Gen. 1024	47.6	94986_G401_Wilms' tumor_sscDNA	0.0
Breast Cancer Clontech 9100266	2.6	94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	0.0
Breast NAT Clontech 9100265	5.1	94988_CAPAN-1_Pancreatic adenocarcinoma (liver	0.0

		metastasis)_sscDNA	
Breast Cancer INVITROGEN A209073	10.7	94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	3.2
Breast NAT INVITROGEN A2090734	12.9	94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	0.0
Normal Liver GENPAK 061009	13.1	94991_HPAC_Pancreatic adenocarcinoma_sscDNA	3.6
Liver Cancer GENPAK 064003	4.8	94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	0.0
Liver Cancer Research Genetics RNA 1025	2.5	94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	13.6
Liver Cancer Research Genetics RNA 1026	0.0	94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	0.0
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	5.4	94996_T24_Bladder carcinma (transitional cell)_sscDNA	3.1
Paired Liver Tissue Research Genetics RNA 6004-N	2.5	94997_5637_Bladder carcinoma_sscDNA	0.0
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0.0	94998_HT-1197_Bladder carcinoma_sscDNA	20.2
Paired Liver Tissue Research Genetics RNA 6005-N	0.0	94999_UM-UC-3_Bladder carcinoma (transitional cell)_sscDNA	0.0
Normal Bladder GENPAK 061001	3.1	95000_A204_Rhabdomyosarcoma_sscDNA	3.3
Bladder Cancer Research Genetics RNA 1023	0.0	95001_HT-1080_Fibrosarcoma_sscDNA	5.2
Bladder Cancer INVITROGEN A302173	16.7	95002_MG-63_Osteosarcoma (bone)_sscDNA	0.0
87071 Bladder Cancer (OD04718-01)	0.0	95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	7.9
87072 Bladder Normal Adjacent (OD04718-03)	2.9	95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	0.0
Normal Ovary Res. Gen.	0.0	95005_A431_Epidermoid carcinoma_sscDNA	0.0

Ovarian Cancer GENPAK 064008	12.6	95007_WM266-4_Melanoma_sscDNA	0.0
87492 Ovary Cancer (OD04768-07)	2.9	95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	0.0
87493 Ovary NAT (OD04768-08)	0.0	95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	0.0
Normal Stomach GENPAK 061017	5.9	95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	0.0
Gastric Cancer Clontech 9060358	0.0	95014_SCC-9_Squamous cell carcinoma of tongue_sscDNA	0.0
NAT Stomach Clontech 9060359	0.0	95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0.0
Gastric Cancer Clontech 9060395	2.9	95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	0.0
NAT Stomach Clontech 9060394	0.0		
Gastric Cancer Clontech 9060397	0.0		
NAT Stomach Clontech 9060396	0.0		
Gastric Cancer GENPAK 064005	10.5		

Expression of gene MOL6 in panel 1.3D is detected in the testes and at very low levels in the spleen, but not in any other tissues. Expression in panel 2D indicates higher expression in normal kidney and markedly lower expression in kidney cancer. This indicates a potential role for this gene as a protein therapeutic in cases of kidney cancer. In panel 3D, expression is seen to be highest in a specimen of small cell lung cancer, chronic myelogenous leukemia and bladder cancer.

Expression of gene MOL6 in Panel 4D is up-regulated in keratinocytes and small airway epithelium after treatment with TNF alpha and IL-1 beta. It is also upregulated in eosinophils regardless of treatment and in normal thymus.

Potential Role(s) of MOL6 in Inflammation: The expression pattern of GM_87760758_A shows that it is induced in keratinocytes and small airway epithelium in response to pro-inflammatory cytokines. Thus the protein in question may contribute to tissue destruction in the airways, recruitment of leukocytes, and tissue remodeling (Reichart et al., 1996 J. Pathol. 178 (2): 215-20).

Impact of Therapeutic Targeting of MOL6: Antibodies or small molecule therapeutics to MOL6 may reduce or inhibit tissue damage due to inflammation in psoriasis, asthma and other mast cell-mediated diseases both in the skin and in the airways. The results are also suggestive of a potential role for MOL6 in the treatment for emphysema (Rice et al., 1998 Curr Pharm Des 4(5): 381-96).

MOL7

Expression of gene MOL7 was assessed using the primer-probe sets Ag1876, described in Table 25. Results of the RTQ-PCR runs are shown in Table 26.

Table 25. Probe name: Ag1876

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-AGCAAGATTGCTCACACAGAGT-3'	59.2	22	668	91
Probe	TET-5'-CCAGTCAATACCATCATCATCCATGAGG-3'-TAMRA	69.1	28	692	92
Reverse	5'-TATGTTGTTGCTCATGGAGTTG-3'	58.7	22	730	93

Table 26. Panel 1.3D

Tissue Name	Rel. Expr., % 1.3dx4tm5422t_ag1876_a1	Tissue Name	Rel. Expr., % 1.3dx4tm5422t_ag1876_a1
Liver adenocarcinoma	0.0	Kidney (fetal)	0.0
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.4	Renal ca. A498	0.5
Adrenal gland	0.7	Renal ca. RXF 393	0.0
Thyroid	0.0	Renal ca. ACHN	0.6
Salivary gland	0.4	Renal ca. UO-31	0.0
Pituitary gland	0.0	Renal ca. TK-10	0.4
Brain (fetal)	0.3	Liver	0.0
Brain (whole)	4.2	Liver (fetal)	0.0
Brain (amygdala)	2.5	Liver ca. (hepatoblast) HepG2	0.0

Brain (cerebellum)	0.8	Lung	0.0
Brain (hippocampus)	2.7	Lung (fetal)	0.0
Brain (substantia nigra)	1.4	Lung ca. (small cell) LX-1	1.3
Brain (thalamus)	1.6	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.6	Lung ca. (s.cell var.) SHP-77	0.0
Spinal cord	0.4	Lung ca. (large cell)NCI-H460	0.4
CNS ca. (glio/astro) U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.5
CNS ca. (glio/astro) U-118-MG	0.2	Lung ca. (non-s.cell) NCI-H23	0.0
CNS ca. (astro) SW1783	0.0	Lung ca (non-s.cell) HOP-62	0.0
CNS ca.* (neuro; met) SK-N-AS	0.7	Lung ca. (non-s.cl) NCI-H522	0.3
CNS ca. (astro) SF-539	0.0	Lung ca. (squam.) SW 900	0.8
CNS ca. (astro) SNB-75	0.0	Lung ca. (squam.) NCI-H596	0.0
CNS ca. (glio) SNB-19	2.2	Mammary gland	0.0
CNS ca. (glio) U251	1.3	Breast ca.* (pl. effusion) MCF-7	2.9
CNS ca. (glio) SF-295	0.4	Breast ca.* (pl.ef) MDA-MB-231	0.0
Heart (fetal)	0.0	Breast ca.* (pl. effusion) T47D	0.0
Heart	0.0	Breast ca. BT-549	0.6
Fetal Skeletal	0.0	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	1.0	Ovarian ca. OVCAR-4	0.0
Spleen	0.0	Ovarian ca. OVCAR-5	0.3
Lymph node	0.5	Ovarian ca. OVCAR-8	0.8
Colorectal	0.0	Ovarian ca. IGROV-1	0.0
Stomach	0.4	Ovarian ca.* (ascites) SK-OV-3	0.6

Small intestine	0.7	Uterus	0.0
Colon ca. SW480	0.0	Plancenta	5.5
Colon ca.* (SW480 met)SW620	0.6	Prostate	0.0
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.3	Testis	100.0
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
83219 CC Well to Mod Diff (ODO3866)	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.2	Melanoma UACC-62	1.4
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma M14	0.0
Bladder	0.0	Melanoma LOX IMVI	0.0
Trachea	32.3	Melanoma* (met) SK-MEL-5	0.0
Kidney	0.0	Adipose	8.2

Expression of MOL7 in panel 1.3D was highest in testis, followed by trachea. Expression in the brain is at much lower levels. This molecule may therefore have a role in male fertility. There was low to undetectable expression in the samples of panel 4D (CT values >35).

MOL8b

Expression of gene MOL8b was assessed using the primer-probe sets Ag3183, described in Table 27. Results of the RTQ-PCR runs are shown in Table 28.

Table 27. Probe name: Ag3183

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-AAGGGGACGAGTGTGGGATT-3'	62	20	211	94
Probe	TET-5'-	74	22	301	95

	TGGCACCGAAGTAGCCGTGGCG-3'-TAMRA				
Reverse	5'-GCGGGCACTTGGTGTCGCA-3'	64	19	325	96

Table 28. Panel 4D

Tissue Name	Rel. Expr., % 4dx4tm4998t_ag3183_a2	Tissue Name	Rel. Expr., % 4dx4tm4998t_ag3183_a2
93768_Secondary Th1_anti-CD28/anti-CD3	0.0	93100_HUVEC (Endothelial)_IL-1b	5.7
93769_Secondary Th2_anti-CD28/anti-CD3	0.0	93779_HUVEC (Endothelial)_IFN gamma	18.4
93770_Secondary Tr1_anti-CD28/anti-CD3	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	9.6
93573_Secondary Th1_resting day 4-6 in IL-2	0.0	93101_HUVEC (Endothelial)_TNF alpha + IL4	11.2
93572_Secondary Th2_resting day 4-6 in IL-2	0.0	93781_HUVEC (Endothelial)_IL-11	19.3
93571_Secondary Tr1_resting day 4-6 in IL-2	2.5	93583_Lung Microvascular Endothelial Cells_none	21.6
93568_primary Th1_anti-CD28/anti-CD3	0.0	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	32.1
93569_primary Th2_anti-CD28/anti-CD3	0.0	92662_Microvascular Dermal endothelium_none	10.7
93570_primary Tr1_anti-CD28/anti-CD3	0.0	92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	5.0
93565_primary Th1_resting dy 4-6 in IL-2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	11.6
93566_primary Th2_resting dy 4-6 in IL-2	2.3	93347_Small Airway Epithelium_none	5.6
93567_primary Tr1_resting dy 4-6 in IL-2	0.7	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	4.8

93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	29.9	92668_Coronery Artery SMC_resting	46.8
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0.0	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	45.1
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.0	93107_astrocytes_resting	82.4
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	74.9
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0	92666_KU-812 (Basophil)_resting	0.0
93354_CD4_none	0.4	92667_KU-812 (Basophil)_PMA/ionoycin	0.0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	2.1	93579_CCD1106 (Keratinocytes)_none	0.0
93103_LAK cells_resting	0.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0.0
93788_LAK cells_IL-2	0.0	93791_Liver Cirrhosis	5.6
93787_LAK cells_IL-2+IL-12	0.0	93792_Lupus Kidney	9.3
93789_LAK cells_IL-2+IFN gamma	0.0	93577_NCI-H292	2.5
93790_LAK cells_IL-2+ IL-18	0.0	93358_NCI-H292_IL-4	0.0
93104_LAK cells_PMA/ionomycin and IL-18	0.0	93360_NCI-H292_IL-9	0.0
93578_NK Cells IL-2_resting	0.0	93359_NCI-H292_IL-13	3.8
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93357_NCI-H292_IFN gamma	0.0
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93777_HPAEC_-	31.9
93111_Mixed Lymphocyte Reaction_Two Way MLR	0.0	93778_HPAEC_IL-1 beta/TNA alpha	22.4
93112_Mononuclear Cells (PBMCs)_resting	0.0	93254_Normal Human Lung Fibroblast_none	44.4
93113_Mononuclear Cells (PBMCs)_PWM	1.8	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	28.3

93114_Mononuclear Cells (PBMCs)_PHA-L	0.0	93257_Normal Human Lung Fibroblast_IL-4	62.6
93249_Ramos (B cell)_none	0.0	93256_Normal Human Lung Fibroblast_IL-9	100.0
93250_Ramos (B cell)_ionomycin	0.0	93255_Normal Human Lung Fibroblast_IL-13	73.3
93349_B lymphocytes_PWM	0.0	93258_Normal Human Lung Fibroblast_IFN gamma	57.1
93350_B lymphoytes_CD40L and IL-4	0.0	93106_Dermal Fibroblasts CCD1070_resting	91.5
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	31.1
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	1.2	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	69.7
93356_Dendritic Cells_none	1.8	93772_dermal fibroblast_IFN gamma	18.3
93355_Dendritic Cells_LPS 100 ng/ml	0.0	93771_dermal fibroblast_IL-4	22.4
93775_Dendritic Cells_anti-CD40	0.4	93259_IBD Colitis 1**	3.2
93774_Monocytes_resting	2.8	93260_IBD Colitis 2	0.0
93776_Monocytes_LPS 50 ng/ml	0.0	93261_IBD Crohns	0.8
93581_Macrophages_resting	0.0	735010_Colon_normal	8.9
93582_Macrophages_LPS 100 ng/ml	0.0	735019_Lung_none	18.5
93098_HUVEC (Endothelial)_none	8.4	64028-1_Thymus_none	9.4
93099_HUVEC (Endothelial)_starved	29.9	64030-1_Kidney_none	3.0

Expression of gene CG50889_02 in two runs of panel 1.3D was not reproducible and is not considered further.

Expression of gene CG50889_02 in Panel 4D: There is 30-fold increase in the expression of CG50889_02 in activated naïve T cells (CD4+ CD45RA cells) as compared to resting CD4 cells. This protein is expressed both in resting and activated fibroblasts, endothelium, and epithelium.

Potential Role(s) of CG50889-02 in Inflammation

MOL8b may be important in the initial activation of naïve T cells. Activated T cells initiate the inflammatory process by secreting cytokines and chemokines, which in turn induce B cell antibody production leading to the extravasation of leukocytes into inflammatory sites.

Impact of Therapeutic Targeting of MOL8b:

Antibody or small molecule therapeutics to MOL8b may block T cell activation in response to tissue transplant and reduce or block rejection. These therapeutic drugs may also reduce or prevent inflammation in asthma/allergy, psoriasis, arthritis and diabetes in which activated T cells play a pivotal role. Antibodies to MOL8b may also serve as a diagnostic or experimental tool to identify and differentiate naïve activated T cells from more differentiated T cell population (memory T cells).

MOL9a

Expression of gene MOL9a was assessed using the primer-probe set Ag673, described in Table 29. Results of the RTQ-PCR runs are shown in Tables 30 and 31.

Table 29. Probe name: Ag673

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-TAGAGTTGGTGGTTCCAGGATT-3'	59.9	22	6	97
Probe	FAM-5'-TGATGTCTCCTCTTCAGGCAATGTCT-3'-TAMRA	66.6	26	56	98
Reverse	5'-TCTGCCAGCCACAGTATAGG-3'	58.9	20	83	99

Table 30. Panels 1.3D and 2D

PANEL 1.3D		PANEL 2D	
Tissue Name	Rel. Expr., % 1.3dx4tm5796f_ag673_b1	Tissue Name	Rel. Expr., % 2Dtm2310f_ag673
Liver adenocarcinoma	23.4	Normal Colon GENPAK 061003	39.2
Pancreas	0.9	83219 CC Well to Mod Diff (ODO3866)	15.0
Pancreatic ca. CAPAN 2	8.4	83220 CC NAT (ODO3866)	15.1

Adrenal gland	0.2	83221 CC Gr.2 rectosigmoid (ODO3868)	13.1
Thyroid	0.9	83222 CC NAT (ODO3868)	3.9
Salivary gland	0.2	83235 CC Mod Diff (ODO3920)	20.3
Pituitary gland	0.4	83236 CC NAT (ODO3920)	7.6
Brain (fetal)	8.2	83237 CC Gr.2 ascend colon (ODO3921)	36.3
Brain (whole)	4.0	83238 CC NAT (ODO3921)	4.8
Brain (amygdala)	1.5	83241 CC from Partial Hepatectomy (ODO4309)	30.6
Brain (cerebellum)	2.2	83242 Liver NAT (ODO4309)	20.3
Brain (hippocampus)	2.9	87472 Colon mets to lung (OD04451-01)	41.5
Brain (substantia nigra)	1.6	87473 Lung NAT (OD04451-02)	12.1
Brain (thalamus)	1.6	Normal Prostate Clontech A+ 6546-1	25.5
Cerebral Cortex	5.3	84140 Prostate Cancer (OD04410)	22.5
Spinal cord	1.7	84141 Prostate NAT (OD04410)	23.2
CNS ca. (glio/astro) U87-MG	6.5	87073 Prostate Cancer (OD04720-01)	10.7
CNS ca. (glio/astro) U-118-MG	8.5	87074 Prostate NAT (OD04720-02)	24.5
CNS ca. (astro) SW1783	21.6	Normal Lung GENPAK 061010	27.0
CNS ca.* (neuro; met) SK-N-AS	12.6	83239 Lung Met to Muscle (ODO4286)	63.3
CNS ca. (astro) SF-539	3.9	83240 Muscle NAT (ODO4286)	50.7
CNS ca. (astro) SNB-75	18.7	84136 Lung Malignant Cancer (OD03126)	42.3
CNS ca. (glio) SNB-19	4.3	84137 Lung NAT (OD03126)	29.1
CNS ca. (glio) U251	17.7	84871 Lung Cancer (OD04404)	69.3
CNS ca. (glio) SF-295	12.6	84872 Lung NAT (OD04404)	26.8
Heart (fetal)	0.2	84875 Lung Cancer (OD04565)	19.1
Heart	0.6	84876 Lung NAT (OD04565)	12.2
Fetal Skeletal	0.8	85950 Lung Cancer (OD04237-01)	94.0

Skeletal muscle	6.5	85970 Lung NAT (OD04237-02)	20.3
Bone marrow	0.7	83255 Ocular Mel Met to Liver (ODO4310)	74.2
Thymus	0.4	83256 Liver NAT (ODO4310)	40.1
Spleen	0.3	84139 Melanoma Mets to Lung (OD04321)	36.3
Lymph node	0.8	84138 Lung NAT (OD04321)	29.7
Colorectal	1.2	Normal Kidney GENPAK 061008	62.4
Stomach	0.2	83786 Kidney Ca, Nuclear grade 2 (OD04338)	66.0
Small intestine	0.4	83787 Kidney NAT (OD04338)	23.3
Colon ca. SW480	10.2	83788 Kidney Ca Nuclear grade 1/2 (OD04339)	34.9
Colon ca.* (SW480 met)SW620	59.0	83789 Kidney NAT (OD04339)	31.0
Colon ca. HT29	8.4	83790 Kidney Ca, Clear cell type (OD04340)	45.7
Colon ca. HCT-116	14.7	83791 Kidney NAT (OD04340)	33.0
Colon ca. CaCo-2	18.6	83792 Kidney Ca, Nuclear grade 3 (OD04348)	18.3
83219 CC Well to Mod Diff (ODO3866)	2.2	83793 Kidney NAT (OD04348)	42.9
Colon ca. HCC-2998	16.6	87474 Kidney Cancer (OD04622-01)	14.5
Gastric ca.* (liver met) NCI-N87	12.3	87475 Kidney NAT (OD04622-03)	3.9
Bladder	5.9	85973 Kidney Cancer (OD04450-01)	70.2
Trachea	0.3	85974 Kidney NAT (OD04450-03)	31.6
Kidney	1.8	Kidney Cancer Clontech 8120607	11.4
Kidney (fetal)	7.8	Kidney NAT Clontech 8120608	7.1
Renal ca. 786-0	8.5	Kidney Cancer Clontech 8120613	8.2
Renal ca. A498	7.0	Kidney NAT Clontech 8120614	8.1
Renal ca. RXF 393	17.6	Kidney Cancer Clontech 9010320	18.3
Renal ca. ACHN	3.9	Kidney NAT Clontech 9010321	33.4

Renal ca. UO-31	12.8	Normal Uterus GENPAK 061018	11.8
Renal ca. TK-10	23.4	Uterus Cancer GENPAK 064011	30.1
Liver	1.4	Normal Thyroid Clontech A+ 6570-1	17.3
Liver (fetal)	1.0	Thyroid Cancer GENPAK 064010	39.2
Liver ca. (hepatoblast) HepG2	9.3	Thyroid Cancer INVITROGEN A302152	18.7
Lung	77.4	Thyroid NAT INVITROGEN A302153	18.7
Lung (fetal)	1.7	Normal Breast GENPAK 061019	32.3
Lung ca. (small cell) LX-1	57.5	84877 Breast Cancer (OD04566)	40.6
Lung ca. (small cell) NCI-H69	11.7	85975 Breast Cancer (OD04590-01)	100.0
Lung ca. (s.cell var.) SHP-77	100.0	85976 Breast Cancer Mets (OD04590-03)	76.3
Lung ca. (large cell)NCI-H460	6.3	87070 Breast Cancer Metastasis (OD04655-05)	73.2
Lung ca. (non-sm. cell) A549	28.7	GENPAK Breast Cancer 064006	46.0
Lung ca. (non-s.cell) NCI-H23	4.8	Breast Cancer Res. Gen. 1024	31.2
Lung ca (non-s.cell) HOP-62	3.1	Breast Cancer Clontech 9100266	41.5
Lung ca. (non-s.cl) NCI-H522	31.7	Breast NAT Clontech 9100265	13.4
Lung ca. (squam.) SW 900	19.4	Breast Cancer INVITROGEN A209073	39.2
Lung ca. (squam.) NCI-H596	27.4	Breast NAT INVITROGEN A2090734	39.8
Mammary gland	3.7	Normal Liver GENPAK 061009	20.9
Breast ca.* (pl. effusion) MCF-7	10.6	Liver Cancer GENPAK 064003	15.6
Breast ca.* (pl.ef) MDA-MB-231	6.6	Liver Cancer Research Genetics RNA 1025	17.2
Breast ca.* (pl. effusion) T47D	17.8	Liver Cancer Research Genetics RNA 1026	9.6
Breast ca. BT-549	15.0	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	42.9
Breast ca. MDA-N	5.6	Paired Liver Tissue Research Genetics RNA 6004-N	18.6

Ovary	1.4	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	12.2
Ovarian ca. OVCAR-3	8.4	Paired Liver Tissue Research Genetics RNA 6005-N	8.1
Ovarian ca. OVCAR-4	2.6	Normal Bladder GENPAK 061001	33.7
Ovarian ca. OVCAR-5	44.9	Bladder Cancer Research Genetics RNA 1023	5.7
Ovarian ca. OVCAR-8	5.0	Bladder Cancer INVITROGEN A302173	23.5
Ovarian ca. IGROV-1	5.2	87071 Bladder Cancer (OD04718-01)	69.7
Ovarian ca.* (ascites) SK-OV-3	50.1	87072 Bladder Normal Adjacent (OD04718-03)	20.6
Uterus	0.7	Normal Ovary Res. Gen.	2.9
Plancenta	0.0	Ovarian Cancer GENPAK 064008	18.6
Prostate	0.4	87492 Ovary Cancer (OD04768-07)	53.2
Prostate ca.* (bone met)PC-3	1.9	87493 Ovary NAT (OD04768-08)	13.5
Testis	0.3	Normal Stomach GENPAK 061017	15.0
Melanoma Hs688(A).T	2.1	Gastric Cancer Clontech 9060358	2.5
Melanoma* (met) Hs688(B).T	2.3	NAT Stomach Clontech 9060359	8.3
Melanoma UACC-62	5.7	Gastric Cancer Clontech 9060395	19.1
Melanoma M14	5.6	NAT Stomach Clontech 9060394	4.6
Melanoma LOX IMVI	12.5	Gastric Cancer Clontech 9060397	29.5
Melanoma* (met) SK-MEL-5	11.3	NAT Stomach Clontech 9060396	3.7
Adipose	3.2	Gastric Cancer GENPAK 064005	9.9

Table 31. Panels 3D and 4D

PANEL 3D		PANEL 4D	
Tissue Name	Rel. Expr., % 3dx4tm5137f_ag673_b1	Tissue Name	Rel. Expr., % 4dtm4833f_ag673

94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	13.6	93768_Secondary Th1_anti-CD28/anti-CD3	11.9
94906_TE671_Medulloblastom/Cerebellum_sscDNA	11.6	93769_Secondary Th2_anti-CD28/anti-CD3	8.2
94907_D283 Med_Medulloblastoma/Cerebellum_sscDNA	53.3	93770_Secondary Tr1_anti-CD28/anti-CD3	6.6
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	9.3	93573_Secondary Th1_resting day 4-6 in IL-2	0.0
94909_XF-498_CNS_sscDNA	7.8	93572_Secondary Th2_resting day 4-6 in IL-2	0.8
94910_SNB-78_CNS/glioma_sscDNA	8.6	93571_Secondary Tr1_resting day 4-6 in IL-2	0.5
94911_SF-268_CNS/glioblastoma_sscDNA	14.1	93568_primary Th1_anti-CD28/anti-CD3	17.7
94912_T98G_Glioblastoma_sscDNA	15.3	93569_primary Th2_anti-CD28/anti-CD3	9.1
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	15.1	93570_primary Tr1_anti-CD28/anti-CD3	16.3
94913_SF-295_CNS/glioblastoma_sscDNA	13.6	93565_primary Th1_resting dy 4-6 in IL-2	7.9
94914_Cerebellum_sscDNA	5.5	93566_primary Th2_resting dy 4-6 in IL-2	2.6
96777_Cerebellum_sscDNA	0.9	93567_primary Tr1_resting dy 4-6 in IL-2	4.3
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	36.5	93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	13.4
94917_DMS-114_Small cell lung cancer_sscDNA	8.1	93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	8.9
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	100.0	93251_CD8 Lymphocytes_anti-CD28/anti-CD3	12.9
94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	32.1	93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	10.5
94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	30.0	93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	5.2
94921_NCI-N417_Small cell	30.6	93354_CD4_none	1.4

lung cancer/neuroendocrine_sscDNA			
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	22.6	93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.8
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	67.1	93103_LAK cells_resting	18.0
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	19.8	93788_LAK cells_IL-2	7.8
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	36.3	93787_LAK cells_IL-2+IL-12	8.1
94927_NCI-H727_Lung carcinoid_sscDNA	20.2	93789_LAK cells_IL-2+IFN gamma	13.6
94928_NCI-UMC-11_Lung carcinoid_sscDNA	73.3	93790_LAK cells_IL-2+ IL-18	10.9
94929_LX-1_Small cell lung cancer_sscDNA	20.2	93104_LAK cells_PMA/ionomycin and IL-18	4.8
94930_Colo-205_Colon cancer_sscDNA	11.6	93578_NK Cells IL-2_resting	1.7
94931_KM12_Colon cancer_sscDNA	31.6	93109_Mixed Lymphocyte Reaction_Two Way MLR	13.0
94932_KM20L2_Colon cancer_sscDNA	8.5	93110_Mixed Lymphocyte Reaction_Two Way MLR	11.4
94933_NCI-H716_Colon cancer_sscDNA	36.9	93111_Mixed Lymphocyte Reaction_Two Way MLR	3.2
94935_SW-48_Colon adenocarcinoma_sscDNA	12.5	93112_Mononuclear Cells (PBMCs)_resting	1.4
94936_SW1116_Colon adenocarcinoma_sscDNA	9.0	93113_Mononuclear Cells (PBMCs)_PWM	23.7
94937_LS 174T_Colon adenocarcinoma_sscDNA	32.6	93114_Mononuclear Cells (PBMCs)_PHA-L	8.7
94938_SW-948_Colon adenocarcinoma_sscDNA	1.5	93249_Ramos (B cell)_none	19.9
94939_SW-480_Colon adenocarcinoma_sscDNA	6.7	93250_Ramos (B cell)_ionomycin	100.0
94940_NCI-SNU-5_Gastric carcinoma_sscDNA	12.4	93349_B lymphocytes_PWM	65.1
94941_KATO III_Gastric carcinoma_sscDNA	55.9	93350_B lymphoytes_CD40L and IL-4	6.0
94943_NCI-SNU-16_Gastric	12.2	92665_EOL-1	12.5

carcinoma_sscDNA		(Eosinophil)_dbcAMP differentiated	
94944_NCI-SNU-1_Gastric carcinoma_sscDNA	58.1	93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	4.4
94946_RF-1_Gastric adenocarcinoma_sscDNA	11.4	93356_Dendritic Cells_none	9.5
94947_RF-48_Gastric adenocarcinoma_sscDNA	15.3	93355_Dendritic Cells_LPS 100 ng/ml	8.7
96778_MKN-45_Gastric carcinoma_sscDNA	33.2	93775_Dendritic Cells_anti-CD40	12.2
94949_NCI-N87_Gastric carcinoma_sscDNA	16.7	93774_Monocytes_resting	14.8
94951_OVCAR-5_Ovarian carcinoma_sscDNA	10.0	93776_Monocytes_LPS 50 ng/ml	15.5
94952_RL95-2_Uterine carcinoma_sscDNA	7.6	93581_Macrophages_resting	35.4
94953_HelaS3_Cervical adenocarcinoma_sscDNA	11.1	93582_Macrophages_LPS 100 ng/ml	4.4
94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	28.9	93098_HUVEC (Endothelial)_none	27.0
94955_ES-2_Ovarian clear cell carcinoma_sscDNA	15.5	93099_HUVEC (Endothelial)_starved	39.2
94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	15.8	93100_HUVEC (Endothelial)_IL-1b	12.7
94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	12.4	93779_HUVEC (Endothelial)_IFN gamma	17.1
94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	25.5	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	14.0
94963_Raji_Burkitt's lymphoma_sscDNA	8.4	93101_HUVEC (Endothelial)_TNF alpha + IL4	22.4
94964_Daudi_Burkitt's lymphoma_sscDNA	29.1	93781_HUVEC (Endothelial)_IL-11	11.7
94965_U266_B-cell plasmacytoma/myeloma_sscDNA	8.0	93583_Lung Microvascular Endothelial Cells_none	14.7
94968_CA46_Burkitt's lymphoma_sscDNA	7.2	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	19.2
94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	10.7	92662_Microvascular Dermal endothelium_none	26.8
94972_JM1_pre-B-cell lymphoma/leukemia_sscDN	5.5	92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml)	18.2

A		and IL1b (1 ng/ml)	
94973_Jurkat_T cell leukemia_sscDNA	15.5	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	2.4
94974_TF-1_Erythroleukemia_sscDNA	33.9	93347_Small Airway Epithelium_none	8.7
94975_HUT 78_T-cell lymphoma_sscDNA	23.7	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	37.9
94977_U937_Histiocytic lymphoma_sscDNA	29.4	92668_Coronery Artery SMC_resting	17.4
94980_KU-812_Myelogenous leukemia_sscDNA	27.2	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	7.4
94981_769-P_Clear cell renal carcinoma_sscDNA	17.3	93107_astrocytes_resting	13.1
94983_Caki-2_Clear cell renal carcinoma_sscDNA	19.9	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	9.3
94984_SW 839_Clear cell renal carcinoma_sscDNA	15.4	92666_KU-812 (Basophil)_resting	13.0
94986_G401_Wilms' tumor_sscDNA	19.5	92667_KU-812 (Basophil)_PMA/ionoycin	26.8
94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	12.7	93579_CCD1106 (Keratinocytes)_none	14.9
94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	11.1	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	1.4
94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	38.5	93791_Liver Cirrhosis	2.3
94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	8.2	93792_Lupus Kidney	1.0
94991_HPAC_Pancreatic adenocarcinoma_sscDNA	24.3	93577_NCI-H292	12.3
94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	5.6	93358_NCI-H292_IL-4	20.0
94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	32.2	93360_NCI-H292_IL-9	31.4
94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	29.0	93359_NCI-H292_IL-13	13.7
94996_T24_Bladder carcinma (transitional cell)_sscDNA	13.0	93357_NCI-H292_IFN gamma	15.2

94997_5637_Bladder carcinoma_sscDNA	18.4	93777_HPAEC_-	14.7
94998_HT-1197_Bladder carcinoma_sscDNA	25.1	93778_HPAEC_IL-1 beta/TNA alpha	12.7
94999_UM-UC-3_Bladder carcinma (transitional cell)_sscDNA	3.3	93254_Normal Human Lung Fibroblast_none	8.0
95000_A204_Rhabdomyosarcoma_sscDNA	16.1	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	3.6
95001_HT-1080_Fibrosarcoma_sscDNA	16.7	93257_Normal Human Lung Fibroblast_IL-4	18.7
95002_MG-63_Osteosarcoma (bone)_sscDNA	12.9	93256_Normal Human Lung Fibroblast_IL-9	13.5
95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	34.7	93255_Normal Human Lung Fibroblast_IL-13	10.2
95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	16.9	93258_Normal Human Lung Fibroblast_IFN gamma	17.2
95005_A431_Epidermoid carcinoma_sscDNA	9.4	93106_Dermal Fibroblasts CCD1070_resting	39.0
95007_WM266-4_Melanoma_sscDNA	6.9	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	47.0
95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	0.3	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	15.7
95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	13.4	93772_dermal fibroblast_IFN gamma	5.6
95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	0.1	93771_dermal fibroblast_IL-4	11.7
95014_SCC-9_Squamous cell carcinoma of tongue_sscDNA	0.2	93259_IBD Colitis 1**	0.1
95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0.8	93260_IBD Colitis 2	0.3
95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	29.0	93261_IBD Crohns	0.5
		735010_Colon_normal	3.1
		735019_Lung_none	7.1
		64028-1_Thymus_none	9.4

		64030-1_Kidney_none	3.0

Panel 1.3D description: The gene MOL9a is expressed in a number of tissues, including the central nervous system, lung, mammary gland and kidney. Moreover, its expression seems to be enhanced in tumor cell lines as compared to normal tissue in most cases with a good therapeutic window.

Panel 2D description: Tissue distribution of this gene MOL9a in panel 2D confirms the results obtained in panel 1.3 D. There is enhanced expression of this gene MOL9a in tumor tissue as against the normal adjacent tissue, particularly in lung and kidney cancer, but also in cases of colon cancer, ovarian cancer, breast cancer, gastric cancer, bladder cancer, liver cancer and thyroid cancer. Some metastases, particularly the lung and those from melanoma express high levels of MOL9a. Corroborative information about the expression of this molecule is available in the form of ESTs, mostly from endothelial cells, colon, ovarian tumors, pancreas and brain regions. Panel 3D demonstrates increased expression of this gene MOL9a in a variety of carcinomas, supporting the results of panels 1.3D and 2D thus demonstrating utility for this protein as an antibody target. Therefore antibodies specific to this protein may be used as a therapeutic in the treatment of various types of cancer.

Panel 4D Description: This gene MOL9a is upregulated in endothelium, and epithelium regardless of stimulus. There is also high level expression of this protein in ionomycin-treated B cell line and mitogen (pokeweed mitogen, PWM) treated B cells. Consistent with this finding Peripheral blood mononuclear cells (PBMC) treated with PWM also demonstrate increased expression of this molecule. Further, induction of MOL9a is seen in activated T cells. In PBMC the T cell specific mitogen (Phytohemagglutinin, PHA) induces the expression of this transcript and in acute and chronically activated T cells the expression of this transcript is increased as compared to untreated or resting T cells.

The MOL9a is induced in activated B and T lymphocytes and may thus have a potential role in inflammation by regulating lymphocyte trafficking, or activation, or increasing tissue destruction. This molecule may also serve as a marker for activated T or B cells.

Impact of Therapeutic Targeting of MOL9a: Small molecule or antibody therapies to the molecule encoded by MOL9a may inhibit tissue damage due to T or B cell activation and the bioactive molecules produced by these cell types. These diseases would include asthma/allergy, colitis, Crohn's disease, lupus, and arthritis. Alternatively, protein therapeutics based on this molecule could serve as an adjuvant and help boost the effectiveness of vaccines or regulate immune status during organ transplant. 19506719_B_EXT may also serve as a marker for activated T cells and serve as a diagnostic tool in determining the extent of inflammation in autoimmune diseases such as asthma/allergy, colitis, Crohn's disease, lupus, and arthritis.

MOL9b

Expression of gene MOL9b was assessed using the primer-probe set Ag2458, described in Table 32. Results of the RTQ-PCR runs are shown in Tables 33 and 34.

Table 32. Probe name: Ag2458

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-GTTGGTGGTTCCAGGATTTT-3'	58.7	20	58	100
Probe	TET-5'-TGATGTCTCCTCTTCAGGCAATGTCT-3'-TAMRA	66.6	26	104	101
Reverse	5'-CTGCCAGCCACAGTATAGGA-3'	58.9	20	130	102

Table 33. Panels 1.3D and 2D

PANEL 1.3D			PANEL 2D	
Tissue Name	Rel. Expr., % 1.3dtm4270t_ag2458	Rel. Expr., % 1.3dx4tm5407t_ag2458_a2	Tissue Name	Rel. Expr., % 2dtm4271t_ag2458
Liver adenocarcinoma	33.9	41.4	Normal Colon GENPAK 061003	62.4
Pancreas	1.3	0.8	83219 CC Well to Mod Diff (ODO3866)	16.8

Pancreatic ca. CAPAN 2	6.9	44.3	83220 CC NAT (ODO3866)	11.7
Adrenal gland	0.7	1.1	83221 CC Gr.2 rectosigmoid (ODO3868)	18.6
Thyroid	2.8	3.3	83222 CC NAT (ODO3868)	8.4
Salivary gland	0.6	2.0	83235 CC Mod Diff (ODO3920)	34.2
Pituitary gland	1.6	0.4	83236 CC NAT (ODO3920)	11.3
Brain (fetal)	9.2	19.7	83237 CC Gr.2 ascend colon (ODO3921)	74.7
Brain (whole)	5.4	17.7	83238 CC NAT (ODO3921)	9.6
Brain (amygdala)	6.7	9.0	83241 CC from Partial Hepatectomy (ODO4309)	35.6
Brain (cerebellum)	2.7	10.2	83242 Liver NAT (ODO4309)	32.3
Brain (hippocampus)	23.0	13.1	87472 Colon mets to lung (OD04451-01)	29.7
Brain (substantia nigra)	1.6	7.2	87473 Lung NAT (OD04451-02)	6.4
Brain (thalamus)	4.9	16.6	Normal Prostate Clontech A+ 6546-1	8.8
Cerebral Cortex	26.2	8.2	84140 Prostate Cancer (OD04410)	25.9
Spinal cord	2.4	9.8	84141 Prostate NAT (OD04410)	27.9
CNS ca. (glio/astro) U87-MG	11.0	19.7	87073 Prostate Cancer (OD04720-01)	15.8
CNS ca. (glio/astro) U-118-MG	45.1	82.4	87074 Prostate NAT (OD04720-02)	28.1
CNS ca. (astro) SW1783	21.9	46.0	Normal Lung GENPAK 061010	24.8
CNS ca.* (neuro; met) SK-N-AS	73.7	40.2	83239 Lung Met to Muscle (ODO4286)	100.0
CNS ca. (astro) SF-539	9.9	12.0	83240 Muscle NAT (ODO4286)	31.9
CNS ca. (astro) SNB-75	22.5	71.5	84136 Lung Malignant Cancer (OD03126)	29.5
CNS ca. (glio) SNB-19	6.2	18.1	84137 Lung NAT (OD03126)	27.9
CNS ca. (glio) U251	5.9	45.0	84871 Lung Cancer (OD04404)	71.7
CNS ca. (glio) SF-295	13.0	26.4	84872 Lung NAT (OD04404)	15.1
Heart (fetal)	1.7	0.0	84875 Lung Cancer (OD04565)	28.5

Heart	1.2	4.4	84876 Lung NAT (OD04565)	13.1
Fetal Skeletal	11.4	1.2	85950 Lung Cancer (OD04237-01)	90.1
Skeletal muscle	3.8	41.7	85970 Lung NAT (OD04237-02)	16.8
Bone marrow	1.5	2.2	83255 Ocular Mel Met to Liver (ODO4310)	76.3
Thymus	0.8	0.4	83256 Liver NAT (ODO4310)	26.8
Spleen	0.9	0.8	84139 Melanoma Mets to Lung (OD04321)	36.3
Lymph node	1.3	10.4	84138 Lung NAT (OD04321)	22.5
Colorectal	4.8	3.1	Normal Kidney GENPAK 061008	33.7
Stomach	0.0	3.1	83786 Kidney Ca, Nuclear grade 2 (OD04338)	68.8
Small intestine	1.1	2.3	83787 Kidney NAT (OD04338)	33.4
Colon ca. SW480	19.5	18.9	83788 Kidney Ca Nuclear grade 1/2 (OD04339)	30.6
Colon ca.* (SW480 met)SW620	29.9	29.8	83789 Kidney NAT (OD04339)	27.2
Colon ca. HT29	17.7	9.7	83790 Kidney Ca, Clear cell type (OD04340)	49.3
Colon ca. HCT-116	22.1	43.8	83791 Kidney NAT (OD04340)	32.1
Colon ca. CaCo-2	13.5	18.4	83792 Kidney Ca, Nuclear grade 3 (OD04348)	16.0
83219 CC Well to Mod Diff (ODO3866)	10.6	7.0	83793 Kidney NAT (OD04348)	35.4
Colon ca. HCC-2998	45.7	21.1	87474 Kidney Cancer (OD04622-01)	13.2
Gastric ca.* (liver met) NCI-N87	38.4	69.5	87475 Kidney NAT (OD04622-03)	4.0
Bladder	7.4	13.6	85973 Kidney Cancer (OD04450-01)	48.6
Trachea	2.9	3.0	85974 Kidney NAT (OD04450-03)	30.4
Kidney	1.3	3.5	Kidney Cancer Clontech 8120607	20.4
Kidney (fetal)	3.6	3.9	Kidney NAT Clontech 8120608	7.3
Renal ca. 786-0	10.0	19.0	Kidney Cancer Clontech 8120613	14.4

Renal ca. A498	29.7	28.6	Kidney NAT Clontech 8120614	8.8
Renal ca. RXF 393	5.6	53.0	Kidney Cancer Clontech 9010320	12.2
Renal ca. ACHN	5.5	13.3	Kidney NAT Clontech 9010321	22.1
Renal ca. UO-31	21.6	45.5	Normal Uterus GENPAK 061018	8.3
Renal ca. TK-10	20.4	27.0	Uterus Cancer GENPAK 064011	15.3
Liver	2.9	2.4	Normal Thyroid Clontech A+ 6570-1	15.1
Liver (fetal)	3.8	5.0	Thyroid Cancer GENPAK 064010	33.0
Liver ca. (hepatoblast) HepG2	17.3	28.2	Thyroid Cancer INVITROGEN A302152	21.6
Lung	1.9	2.5	Thyroid NAT INVITROGEN A302153	14.4
Lung (fetal)	1.4	5.6	Normal Breast GENPAK 061019	33.2
Lung ca. (small cell) LX-1	11.8	40.6	84877 Breast Cancer (OD04566)	44.8
Lung ca. (small cell) NCI-H69	31.4	44.0	85975 Breast Cancer (OD04590-01)	95.9
Lung ca. (s.cell var.) SHP-77	69.3	90.5	85976 Breast Cancer Mets (OD04590-03)	61.1
Lung ca. (large cell)NCI-H460	9.9	63.6	87070 Breast Cancer Metastasis (OD04655-05)	38.4
Lung ca. (non-sm. cell) A549	20.9	25.9	GENPAK Breast Cancer 064006	33.2
Lung ca. (non-s.cell) NCI-H23	11.3	10.7	Breast Cancer Res. Gen. 1024	23.0
Lung ca (non-s.cell) HOP-62	4.1	9.1	Breast Cancer Clontech 9100266	33.4
Lung ca. (non-s.cl) NCI-H522	29.1	30.0	Breast NAT Clontech 9100265	19.5
Lung ca. (squam.) SW 900	9.7	20.1	Breast Cancer INVITROGEN A209073	47.0
Lung ca. (squam.) NCI-H596	9.5	43.2	Breast NAT INVITROGEN A2090734	37.6
Mammary gland	5.3	9.0	Normal Liver GENPAK 061009	15.5
Breast ca.* (pl. effusion) MCF-7	14.3	30.8	Liver Cancer GENPAK 064003	14.0
Breast ca.* (pl.ef) MDA-MB-231	42.3	41.1	Liver Cancer Research Genetics RNA 1025	20.4

Breast ca.* (pl. effusion) T47D	9.6	13.8	Liver Cancer Research Genetics RNA 1026	7.1
Breast ca. BT-549	100.0	100.0	Paired Liver Cancer Tissue Research Genetics RNA 6004-T	24.8
Breast ca. MDA-N	17.2	8.8	Paired Liver Tissue Research Genetics RNA 6004-N	18.0
Ovary	4.8	0.9	Paired Liver Cancer Tissue Research Genetics RNA 6005-T	13.4
Ovarian ca. OVCAR-3	11.3	20.9	Paired Liver Tissue Research Genetics RNA 6005-N	7.3
Ovarian ca. OVCAR-4	2.5	10.6	Normal Bladder GENPAK 061001	59.9
Ovarian ca. OVCAR-5	20.0	26.3	Bladder Cancer Research Genetics RNA 1023	5.2
Ovarian ca. OVCAR-8	18.6	16.5	Bladder Cancer INVITROGEN A302173	30.1
Ovarian ca. IGROV-1	6.9	6.8	87071 Bladder Cancer (OD04718-01)	65.5
Ovarian ca.* (ascites) SK-OV-3	32.3	64.3	87072 Bladder Normal Adjacent (OD04718-03)	18.4
Uterus	1.8	4.3	Normal Ovary Res. Gen.	5.1
Plancenta	2.2	1.1	Ovarian Cancer GENPAK 064008	29.1
Prostate	2.0	2.4	87492 Ovary Cancer (OD04768-07)	66.0
Prostate ca.* (bone met)PC-3	3.1	3.2	87493 Ovary NAT (OD04768-08)	7.7
Testis	2.0	1.5	Normal Stomach GENPAK 061017	16.4
Melanoma Hs688(A).T	4.6	5.4	Gastric Cancer Clontech 9060358	3.5
Melanoma* (met) Hs688(B).T	2.4	6.9	NAT Stomach Clontech 9060359	10.5
Melanoma UACC-62	1.3	12.6	Gastric Cancer Clontech 9060395	29.9
Melanoma M14	5.9	56.2	NAT Stomach Clontech 9060394	12.9
Melanoma LOX IMVI	14.7	8.1	Gastric Cancer Clontech 9060397	42.3
Melanoma* (met) SK-MEL-5	16.2	24.7	NAT Stomach Clontech 9060396	6.2
Adipose	4.4	3.4	Gastric Cancer GENPAK 064005	31.0

Table 34. Panels 3D and 4D

PANEL 3D		PANEL 4D	
Tissue Name	Rel. Expr., % 3dx4tm5121t_ag2458_b2	Tissue Name	Rel. Expr., % 4dtm4272t_ag2458
94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	13.6	93768_Secondary Th1_anti-CD28/anti-CD3	14.5
94906_TE671_Medulloblastom/Cerebellum_sscDNA	7.4	93769_Secondary Th2_anti-CD28/anti-CD3	7.4
94907_D283 Med_Medulloblastoma/Cerebellum_sscDNA	53.0	93770_Secondary Tr1_anti-CD28/anti-CD3	9.5
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	6.5	93573_Secondary Th1_resting day 4-6 in IL-2	0.2
94909_XF-498_CNS_sscDNA	6.8	93572_Secondary Th2_resting day 4-6 in IL-2	0.6
94910_SNB-78_CNS/glioma_sscDNA	9.8	93571_Secondary Tr1_resting day 4-6 in IL-2	0.8
94911_SF-268_CNS/glioblastoma_sscDNA	10.2	93568_primary Th1_anti-CD28/anti-CD3	19.8
94912_T98G_Glioblastoma_sscDNA	15.7	93569_primary Th2_anti-CD28/anti-CD3	13.0
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	16.5	93570_primary Tr1_anti-CD28/anti-CD3	19.2
94913_SF-295_CNS/glioblastoma_sscDNA	7.4	93565_primary Th1_resting dy 4-6 in IL-2	8.8
94914_Cerebellum_sscDNA	3.9	93566_primary Th2_resting dy 4-6 in IL-2	2.2
96777_Cerebellum_sscDNA	0.8	93567_primary Tr1_resting dy 4-6 in IL-2	3.6
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	46.9	93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	19.5
94917_DMS-114_Small cell lung cancer_sscDNA	10.9	93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	17.7
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	100.0	93251_CD8 Lymphocytes_anti-CD28/anti-CD3	9.3
94919_NCI-H146_Small cell lung	33.4	93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	11.0

cancer/neuroendocrine_sscDNA			
94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	30.2	93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	5.5
94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	26.1	93354_CD4_none	0.7
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	28.4	93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0.9
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	88.0	93103_LAK cells_resting	15.8
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	31.3	93788_LAK cells_IL-2	6.1
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	32.4	93787_LAK cells_IL-2+IL-12	8.8
94927_NCI-H727_Lung carcinoid_sscDNA	23.0	93789_LAK cells_IL-2+IFN gamma	11.7
94928_NCI-UMC-11_Lung carcinoid_sscDNA	75.0	93790_LAK cells_IL-2+ IL-18	13.2
94929_LX-1_Small cell lung cancer_sscDNA	17.0	93104_LAK cells_PMA/ionomycin and IL-18	8.5
94930_Colo-205_Colon cancer_sscDNA	11.1	93578_NK Cells IL-2_resting	2.5
94931_KM12_Colon cancer_sscDNA	37.3	93109_Mixed Lymphocyte Reaction_Two Way MLR	17.0
94932_KM20L2_Colon cancer_sscDNA	7.8	93110_Mixed Lymphocyte Reaction_Two Way MLR	10.2
94933_NCI-H716_Colon cancer_sscDNA	32.3	93111_Mixed Lymphocyte Reaction_Two Way MLR	7.4
94935_SW-48_Colon adenocarcinoma_sscDNA	7.8	93112_Mononuclear Cells (PBMCs)_resting	2.4
94936_SW1116_Colon adenocarcinoma_sscDNA	10.9	93113_Mononuclear Cells (PBMCs)_PWM	23.7
94937_LS 174T_Colon adenocarcinoma_sscDNA	29.3	93114_Mononuclear Cells (PBMCs)_PHA-L	9.6
94938_SW-948_Colon	1.9	93249_Ramos (B cell)_none	30.4

adenocarcinoma_sscDNA			
94939_SW-480_Colon adenocarcinoma_sscDNA	4.9	93250_Ramos (B cell)_ionomycin	100.0
94940_NCI-SNU-5_Gastric carcinoma_sscDNA	8.3	93349_B lymphocytes_PWM	70.2
94941 KATO III_Gastric carcinoma_sscDNA	53.1	93350_B lymphoytes_CD40L and IL-4	5.5
94943_NCI-SNU-16_Gastric carcinoma_sscDNA	7.3	92665_EOL-1 (Eosinophil)_dbcAMP differentiated	11.7
94944_NCI-SNU-1_Gastric carcinoma_sscDNA	64.4	93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	6.3
94946_RF-1_Gastric adenocarcinoma_sscDNA	11.4	93356_Dendritic Cells_none	12.4
94947_RF-48_Gastric adenocarcinoma_sscDNA	15.4	93355_Dendritic Cells_LPS 100 ng/ml	9.0
96778_MKN-45_Gastric carcinoma_sscDNA	28.8	93775_Dendritic Cells_anti-CD40	12.5
94949_NCI-N87_Gastric carcinoma_sscDNA	19.5	93774_Monocytes_resting	15.2
94951_OVCAR-5_Ovarian carcinoma_sscDNA	11.7	93776_Monocytes_LPS 50 ng/ml	11.7
94952_RL95-2_Uterine carcinoma_sscDNA	4.5	93581_Macrophages_resting	41.8
94953_HelaS3_Cervical adenocarcinoma_sscDNA	11.3	93582_Macrophages_LPS 100 ng/ml	6.8
94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	24.3	93098_HUVEC (Endothelial)_none	35.8
94955_ES-2_Ovarian clear cell carcinoma_sscDNA	16.1	93099_HUVEC (Endothelial)_starved	58.2
94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	8.7	93100_HUVEC (Endothelial)_IL-1b	16.5
94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	8.3	93779_HUVEC (Endothelial)_IFN gamma	26.1
94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	22.1	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	16.0
94963_Raji_Burkitt's lymphoma_sscDNA	8.3	93101_HUVEC (Endothelial)_TNF alpha + IL4	23.2
94964_Daudi_Burkitt's lymphoma_sscDNA	19.8	93781_HUVEC (Endothelial)_IL-11	13.6

94965_U266_B-cell plasmacytoma/myeloma_sscDNA	6.4	93583_Lung Microvascular Endothelial Cells_none	21.0
94968_CA46_Burkitt's lymphoma_sscDNA	6.5	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	18.3
94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	9.0	92662_Microvascular Dermal endothelium_none	35.4
94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	4.1	92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	20.0
94973_Jurkat_T cell leukemia_sscDNA	9.8	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	14.9
94974_TF-1_Erythroleukemia_sscDNA	31.5	93347_Small Airway Epithelium_none	7.2
94975_HUT 78_T-cell lymphoma_sscDNA	15.7	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	45.4
94977_U937_Histiocytic lymphoma_sscDNA	30.5	92668_Coronery Artery SMC_resting	17.7
94980_KU-812_Myelogenous leukemia_sscDNA	21.7	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	10.8
94981_769-P_Clear cell renal carcinoma_sscDNA	16.6	93107_astrocytes_resting	11.1
94983_Caki-2_Clear cell renal carcinoma_sscDNA	16.8	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	10.5
94984_SW 839_Clear cell renal carcinoma_sscDNA	11.8	92666_KU-812 (Basophil)_resting	18.8
94986_G401_Wilms' tumor_sscDNA	16.5	92667_KU-812 (Basophil)_PMA/ionoycin	27.9
94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	12.9	93579_CCD1106 (Keratinocytes)_none	20.9
94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	12.0	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	7.4
94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	32.6	93791_Liver Cirrhosis	3.7
94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	4.0	93792_Lupus Kidney	1.9
94991_HPAC_Pancreatic adenocarcinoma_sscDNA	26.4	93577_NCI-H292	18.6
94992_MIA PaCa-	8.2	93358_NCI-H292_IL-4	33.7

2_Pancreatic carcinoma_sscDNA			
94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	30.3	93360_NCI-H292_IL-9	36.9
94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	26.7	93359_NCI-H292_IL-13	20.0
94996_T24_Bladder carcinma (transitional cell)_sscDNA	8.2	93357_NCI-H292_IFN gamma	20.4
94997_5637_Bladder carcinoma_sscDNA	20.5	93777_HPAEC_-	18.8
94998_HT-1197_Bladder carcinoma_sscDNA	18.0	93778_HPAEC_IL-1 beta/TNA alpha	18.9
94999_UM-UC-3_Bladder carcinma (transitional cell)_sscDNA	4.6	93254_Normal Human Lung Fibroblast_none	9.5
95000_A204_Rhabdomyosarcoma_sscDNA	20.0	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	3.7
95001_HT-1080_Fibrosarcoma_sscDNA	15.4	93257_Normal Human Lung Fibroblast_IL-4	24.7
95002_MG-63_Osteosarcoma (bone)_sscDNA	16.2	93256_Normal Human Lung Fibroblast_IL-9	19.2
95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	27.5	93255_Normal Human Lung Fibroblast_IL-13	14.3
95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	12.5	93258_Normal Human Lung Fibroblast_IFN gamma	23.2
95005_A431_Epidermoid carcinoma_sscDNA	6.9	93106_Dermal Fibroblasts CCD1070_resting	47.0
95007_WM266-4_Melanoma_sscDNA	7.5	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	42.3
95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	0.1	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	20.2
95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	13.5	93772_dermal fibroblast_IFN gamma	9.2
95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	1.3	93771_dermal fibroblast_IL-4	22.1
95014_SCC-9_Squamous cell carcinoma of	0.3	93259_IBD Colitis 1**	1.4

tongue_sscDNA			
95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0.3	93260_IBD Colitis 2	1.1
95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	24.5	93261_IBD Crohns	1.0
		735010_Colon_normal	4.1
		735019_Lung_none	8.9
		64028-1_Thymus_none	10.5
		64030-1_Kidney_none	3.6

Panel 1.3D description: The gene MOL9b is expressed in a number of tissues, including the central nervous system, lung, mammary gland and kidney. Moreover, its expression seems to be enhanced in tumor cell lines relative to normal tissue in most cases with a good therapeutic window.

Panel 2D description: Tissue distribution of the gene MOL9b in panel 2D confirms the results obtained in panel 1.3 D. There is enhanced expression of this gene (MOL9b) in tumor tissue relative to normal adjacent tissue, particularly in lung and kidney cancers, but also in cancers of colon, ovary, breast, gastric, bladder, liver and thyroid. Some metastases, particularly lung metastases and those from melanoma express this gene MOL9b at particularly high levels. Corroborative information about the expression of this molecule is available in the form of ESTs, mostly from endothelial cells, colon, ovarian tumors, pancreas and brain regions. Panel 3D for the gene MOL9b shows high level of expression in a variety of carcinomas, supporting results from panels 1.3D and 2D, and demonstrating utility for this protein as an antibody target. Therefore antibodies specific to this protein may be used as a therapeutic in the treatment of various types of cancer.

Panel 4D Description: The gene MOL9b is upregulated in endothelium, and epithelium regardless of stimulus. There is up regulation of this molecule in an ionomycin treated B cell line and it is highly expressed in mitogen (PWM) treated B cells. Consistent with this finding, PBMCs treated with PWM also up regulate this molecule. Induction of this gene MOL9b is also seen in activated T cells. In PBMC the T cell specific mitogen PHA induces the expression of this transcript and in acute and chronically activated T cells the expression of this transcript is increased as compared to untreated or resting T cells. This transcript is also expressed in resting macrophages.

Potential Role(s) of in Inflammation: The molecule MOL9b is induced by B and T lymphocytes and may potentiate inflammation by regulating lymphocyte trafficking, or activation, or increasing tissue destruction. This molecule may also serve as a marker for activated T or B cells and may also be involved in the differentiation of monocytes into macrophages (see reference). Macrophages also participate in inflammation by producing multiple biologically active proteins like cytokines, activating other cells within the local microenvironment, and ingesting dead and dying cells.

Impact of Therapeutic Targeting of MOL9b: Small molecule or antibody therapies to the molecule encoded for by MOL9b may reduce or eliminate inflammation and tissue damage due to T or B cell activation or macrophages and the bioactive molecules produced by these cell types. These diseases would include asthma/allergy, colitis, Crohn's disease, lupus, and arthritis. Alternatively, protein therapeutics based on this molecule could serve as an adjuvant and help boost the effectiveness of vaccines or regulate immune status during organ transplant. MOL9b also serves as a marker for activated T and B cells and serve as a diagnostic tool for determining indirectly measuring the extent of inflammation due to autoimmune diseases which induce T or B cells activation such as asthma/allergy, colitis, Crohn's disease, lupus, and arthritis. Elevated expression of the gene MOL9b in macrophages may help in distinguishing resting macrophages from monocytes , dendritic cells.

MOL10a

Expression of gene MOL10a was assessed using the primer-probe set Ag1129, described in Table 35. Results of the RTQ-PCR runs are shown in Table 36.

Table 35. Probe name: Ag1129

Primers	Sequences	Tm	Length	Start Position	SEQ ID NO:
Forward	5'-CTAGACCAGCAGCTGGATGAT-3'	59.5	21	1518	103
Probe	TET-5'-CTACAGACCAAGTTTGCTCGCCTCCT-3'-TAMRA	68.7	26	1539	104
Reverse	5'-CAATGCGGTAAGCAATCTTAAG-3'	59	22	1587	105

Table 36. Panels 1.3D and 4D

PANEL 1.3D		PANEL 4D	
Tissue Name	Rel. Expr., % 1.3dx4tm5771t_ag1129_a2	Tissue Name	Rel. Expr., % 4Dtm1984t_ag1129
Liver adenocarcinoma	3.9	93768_Secondary Th1_anti-CD28/anti-CD3	0.0
Pancreas	3.7	93769_Secondary Th2_anti-CD28/anti-CD3	9.0
Pancreatic ca. CAPAN 2	2.8	93770_Secondary Tr1_anti-CD28/anti-CD3	9.0
Adrenal gland	1.8	93573_Secondary Th1_resting day 4-6 in IL-2	0.0
Thyroid	3.2	93572_Secondary Th2_resting day 4-6 in IL-2	0.0
Salivary gland	3.8	93571_Secondary Tr1_resting day 4-6 in IL-2	0.0
Pituitary gland	2.6	93568_primary Th1_anti-CD28/anti-CD3	0.0
Brain (fetal)	21.9	93569_primary Th2_anti-CD28/anti-CD3	0.0
Brain (whole)	14.6	93570_primary Tr1_anti-CD28/anti-CD3	8.9
Brain (amygdala)	13.0	93565_primary Th1_resting dy 4-6 in IL-2	6.8
Brain (cerebellum)	1.8	93566_primary Th2_resting dy 4-6 in IL-2	14.6
Brain (hippocampus)	13.7	93567_primary Tr1_resting dy 4-6 in IL-2	0.0
Brain (substantia nigra)	21.4	93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	5.9
Brain (thalamus)	10.3	93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	14.3
Cerebral Cortex	10.5	93251_CD8 Lymphocytes_anti-CD28/anti-CD3	33.0
Spinal cord	8.1	93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	4.2
CNS ca. (glio/astro) U87-MG	6.0	93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.0
CNS ca. (glio/astro) U-118-MG	0.0	93354_CD4_none	1.4
CNS ca. (astro)	3.5	93252_Secondary Th1/Th2/Tr1_anti-	20.2

SW1783		CD95 CH11	
CNS ca.* (neuro; met) SK-N-AS	0.0	93103_LAK cells_resting	8.7
CNS ca. (astro) SF-539	1.7	93788_LAK cells_IL-2	30.8
CNS ca. (astro) SNB-75	0.0	93787_LAK cells_IL-2+IL-12	15.6
CNS ca. (glio) SNB-19	0.9	93789_LAK cells_IL-2+IFN gamma	53.2
CNS ca. (glio) U251	1.4	93790_LAK cells_IL-2+ IL-18	20.6
CNS ca. (glio) SF-295	0.0	93104_LAK cells_PMA/ionomycin and IL-18	0.0
Heart (fetal)	0.0	93578_NK Cells IL-2_resting	5.9
Heart	3.3	93109_Mixed Lymphocyte Reaction_Two Way MLR	12.9
Fetal Skeletal	2.0	93110_Mixed Lymphocyte Reaction_Two Way MLR	3.5
Skeletal muscle	2.3	93111_Mixed Lymphocyte Reaction_Two Way MLR	6.8
Bone marrow	4.0	93112_Mononuclear Cells (PBMCs)_resting	17.2
Thymus	3.9	93113_Mononuclear Cells (PBMCs)_PWM	32.5
Spleen	0.0	93114_Mononuclear Cells (PBMCs)_PHA-L	20.3
Lymph node	1.7	93249_Ramos (B cell)_none	22.2
Colorectal	1.4	93250_Ramos (B cell)_ionomycin	68.3
Stomach	0.0	93349_B lymphocytes_PWM	33.7
Small intestine	0.0	93350_B lymphoytes_CD40L and IL-4	9.4
Colon ca. SW480	1.5	92665_EOL-1 (Eosinophil)_dbcAMP differentiated	15.3
Colon ca.* (SW480 met)SW620	2.0	93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0.0
Colon ca. HT29	2.2	93356_Dendritic Cells_none	0.0
Colon ca. HCT-116	3.7	93355_Dendritic Cells_LPS 100 ng/ml	6.7
Colon ca. CaCo-2	0.6	93775_Dendritic Cells_anti-CD40	0.0
83219 CC Well to Mod Diff (ODO3866)	5.2	93774_Monocytes_resting	20.6
Colon ca. HCC-2998	5.1	93776_Monocytes_LPS 50 ng/ml	15.8

Gastric ca.* (liver met) NCI-N87	10.0	93581_Macrophages_resting	15.9
Bladder	4.6	93582_Macrophages_LPS 100 ng/ml	64.2
Trachea	30.4	93098_HUVEC (Endothelial)_none	3.0
Kidney	3.3	93099_HUVEC (Endothelial)_starved	0.0
Kidney (fetal)	7.3	93100_HUVEC (Endothelial)_IL-1b	3.5
Renal ca. 786-0	0.0	93779_HUVEC (Endothelial)_IFN gamma	6.7
Renal ca. A498	0.0	93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.0
Renal ca. RXF 393	4.4	93101_HUVEC (Endothelial)_TNF alpha + IL4	8.1
Renal ca. ACHN	0.0	93781_HUVEC (Endothelial)_IL-11	0.0
Renal ca. UO-31	0.0	93583_Lung Microvascular Endothelial Cells_none	24.0
Renal ca. TK-10	5.9	93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	17.8
Liver	3.4	92662_Microvascular Dermal endothelium_none	5.2
Liver (fetal)	0.0	92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
Liver ca. (hepatoblast) HepG2	0.0	93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	79.6
Lung	30.2	93347_Small Airway Epithelium_none	0.0
Lung (fetal)	100.0	93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	53.6
Lung ca. (small cell) LX-1	1.9	92668_Coronery Artery SMC_resting	0.0
Lung ca. (small cell) NCI-H69	9.8	92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.0
Lung ca. (s.cell var.) SHP-77	9.5	93107_astrocytes_resting	0.0
Lung ca. (large cell)NCI-H460	0.0	93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	19.6
Lung ca. (non-sm. cell) A549	1.5	92666_KU-812 (Basophil)_resting	0.0
Lung ca. (non-s.cell) NCI-H23	1.8	92667_KU-812 (Basophil)_PMA/ionoycin	15.1
Lung ca (non-s.cell) HOP-62	0.8	93579_CCD1106 (Keratinocytes)_none	0.0
Lung ca. (non-s.cl) NCI-H522	8.7	93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	4.7

Lung ca. (squam.) SW 900	1.8	93791_Liver Cirrhosis	47.6
Lung ca. (squam.) NCI-H596	6.7	93792_Lupus Kidney	25.0
Mammary gland	8.0	93577_NCI-H292	17.0
Breast ca.* (pl. effusion) MCF-7	0.0	93358_NCI-H292_IL-4	4.8
Breast ca.* (pl.ef) MDA-MB-231	0.0	93360_NCI-H292_IL-9	12.9
Breast ca.* (pl. effusion) T47D	0.0	93359_NCI-H292_IL-13	0.0
Breast ca. BT-549	0.0	93357_NCI-H292_IFN gamma	4.4
Breast ca. MDA-N	0.0	93777_HPAEC_-	0.0
Ovary	2.3	93778_HPAEC_IL-1 beta/TNA alpha	6.9
Ovarian ca. OVCAR-3	0.0	93254_Normal Human Lung Fibroblast_none	0.0
Ovarian ca. OVCAR-4	1.2	93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	6.2
Ovarian ca. OVCAR-5	7.7	93257_Normal Human Lung Fibroblast_IL-4	6.9
Ovarian ca. OVCAR-8	0.0	93256_Normal Human Lung Fibroblast_IL-9	0.0
Ovarian ca. IGROV-1	0.0	93255_Normal Human Lung Fibroblast_IL-13	0.0
Ovarian ca.* (ascites) SK-OV-3	0.0	93258_Normal Human Lung Fibroblast_IFN gamma	0.0
Uterus	1.9	93106_Dermal Fibroblasts CCD1070_resting	12.9
Plancenta	0.0	93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	28.5
Prostate	4.9	93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0.0
Prostate ca.* (bone met)PC-3	4.4	93772_dermal fibroblast_IFN gamma	9.8
Testis	57.0	93771_dermal fibroblast_IL-4	2.6
Melanoma Hs688(A).T	0.0	93259_IBD Colitis 1**	88.3
Melanoma* (met) Hs688(B).T	0.0	93260_IBD Colitis 2	0.0
Melanoma UACC-62	0.0	93261_IBD Crohns	0.0
Melanoma M14	0.0	735010_Colon_normal	20.2

Melanoma LOX IMVI	3.6	735019_Lung_none	29.7
Melanoma* (met) SK-MEL-5	3.3	64028-1_Thymus_none	100.0
Adipose	3.2	64030-1_Kidney_none	10.0

The gene MOL10a shows high levels in the testis and in fetal lung in panel 1.3D. This indicates that this gene may be used for regeneration therapy in the lung and may also play a role in male fertility. The profile in panel 4D shows high expression in thymus with low to undetectable expression in other tissues and cell lines (Ct values >35). Therefore this gene may be involved in T-cell development and may be a marker for immature T cells.

EXAMPLE 2: SNP ANALYSIS OF MOL6A

Variant sequences are included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, however, in the case that a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern for example, alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, stability of transcribed message.

Method of novel SNP Identification: SNPs are identified by analyzing sequence assemblies using CuraGen's proprietary SNPTool algorithm. SNPTool identifies variation in assemblies with the following criteria: SNPs are not analyzed within 10 base pairs on both ends of an alignment; Window size (number of bases in a view) is 10; The allowed number of mismatches in a window is 2; Minimum SNP base quality (PHRED score) is 23; Minimum number of changes to score an SNP is 2/assembly position. SNPTool analyzes the assembly and displays SNP positions, associated individual variant sequences in the assembly, the depth of the assembly at that given position, the putative assembly allele frequency, and the SNP sequence variation. Sequence traces are then selected and brought into view for manual validation. The consensus assembly sequence is imported into CuraTools along with variant sequence changes to identify potential amino acid changes resulting from the SNP sequence variation. Comprehensive SNP data analysis is then exported into the SNPCalling database.

Method of novel SNP Confirmation: SNPs are confirmed employing a validated method know as Pyrosequencing (See Alderborn et al. Determination of Single Nucleotide Polymorphisms by Real-time Pyrophosphate DNA Sequencing. (2000). *Genome Research.* 10, Issue 8, August. 1249-1265). In brief, Pyrosequencing is a real time primer extension process of genotyping. This protocol takes double-stranded, biotinylated PCR products from genomic DNA samples and binds them to streptavidin beads. These beads are then denatured producing single stranded bound DNA. SNPs are characterized utilizing a technique based on an indirect bioluminometric assay of pyrophosphate (PP_i) that is released from each dNTP upon DNA chain elongation. Following Klenow polymerase-mediated base incorporation, PP_i is released and used as a substrate, together with adenosine 5'-phosphosulfate (APS), for ATP sulfurylase, which results in the formation of ATP. Subsequently, the ATP accomplishes the conversion of luciferin to its oxi-derivative by the action of luciferase. The ensuing light output becomes proportional to the number of added bases, up to about four bases. To allow processivity of the method dNTP excess is degraded by apyrase, which is also present in the starting reaction mixture, so that only dNTPs are added to the template during the sequencing. The process has been fully automated and adapted to a 96-well format, which allows rapid screening of large SNP panels.

The DNA and protein sequences for the novel single nucleotide polymorphic variants of the Trypsin -like gene of MOL6a (GM87760758_A) are reported in Table 37. Variants are reported individually but any combination of all or a select subset of variants are also included. In Table 37, the positions of the variant bases and the variant amino acid residues are underlined.

Table 37.

A. Variant 13373750 of MOL6a nucleotide sequence (SEQ ID NO. 11).

C toA at position 360.

B. Nucleotide sequence of variant at position 360.

1TACCATGAAATATGTCTTCTATTTGGGTGTCCTCGCTGGGACATTTTTCTTTGCTGACTCATCTGTCCAGAAAGAAGACC
81CTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAACCCAGCTGGGTGCTGGCC
161CCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGAGTCAGAGACGGTACTGAACAGAC
241AATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCACAGGATGACCTCATGCTCATCAAGCTGG
321CTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTACCCTCGCCACCACCAATGTCAGGCCAGGCACTGTCTGTCTA
401CTCTCAGGTTTGGACTGGAGCCAAGAAAACAGTGGCCGACACCCTGACTTGCGGCAGAACCTGGAGGCCCCCGTGATGTC
481TGATCGAGAATGCCAAAAAAACAGAACAAGGAAAAAGCCACAGGAATTCCTTATGTGTGAAATTTGTGAAAGTATTCAGC
561CGAATTTTTGGGGAGGTGGCCGTTGCTACTGTCATCTGCAAAGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGG
641AGGGGACGTCGGCATCTACACCAATGTTTACAAATATGTATCCTGGATTGAGAACACTGCTAAGGACAAGTGAGACCCTA
721A (SEQ ID NO.106)

C. Protein Sequence of variant at position 119.

1MKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGTEQT
I

81NPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLTLATTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVM
SD
161RECQKNRTRKKPQEFLMCEICESIQPNFWGGGRCYCHLQRQAPGNRGGALHGRGRRHLHQCLQICILD (SEQ ID
NO.107)

D. Effect of variant on amino acid residue

Pro to Thr

Example 3.: Method of Cloning of a MOL21 (CG54656-05) nucleic acid.

The sequence of MOL21 (Acc. No. CG54656-05) was derived by laboratory cloning of cDNA fragments, by *in silico* prediction of the sequence. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, were cloned. In silico prediction was based on sequences available in Curagen's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory cloning was performed using one or more of the methods summarized below:

SeqCalling^{TM} Technology: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Exon Linking: The cDNA coding for the CG54656-05 sequence was cloned by the polymerase chain reaction (PCR) using the primers:

CAGCTCGCTGTCTTGGTGGTC (SEQ ID NO.: 247) and

TCACAGGATGATGACACAAGCTCC (SEQ ID NO.: 248).

Primers were designed based on in silico predictions of the full length or some portion (one or more exons) of the cDNA/protein sequence of the invention. These primers were used to amplify a cDNA from a pool containing expressed human sequences derived from the following tissues: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea and uterus.

Multiple clones were sequenced and these fragments were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Physical clone: The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clone GM38019075_A.698002.B7.

Example 4 Expression profiling of MOL13 (CG53063-01 or 94115520_EXT).

Panel 1.3 (Table 38A): The profile was generated from a panel of 37 normal human tissues and 59 human cancer cell lines using specific gene probe and primer sets (Ag809). This gene is highly expressed in normal fetal heart and adult spleen and to a lesser extent in normal testes, prostate, ovary, mammary gland, trachea stomach, colorectal tissue, brain, pituitary gland and salivary gland.

Panel 4D (Tables 39A and 54A): The profile was generated from a panel of several human cell lines that were either untreated or treated with a wide variety factors which modulate the immune response. This panel shows that the normal colon expresses high levels of this transcript whereas three different inflammatory bowel disease tissues did not.

Panels 1.2 (Table 50A), 1.3 (Table 51A): The profiles were generated from panels of normal human tissues and human cancer cell lines using specific gene probe and primer sets (Ag809). This gene is highly expressed in normal fetal heart and adult spleen and to a lesser extent in normal testes, prostate, ovary, mammary gland, trachea stomach, colorectal tissue, brain, pituitary gland and salivary gland.

Panels 2D (Table 52A) and 3 (Table 53A): The profiles were generated from 2 control wells and 94 test samples composed of RNA or cDNA isolated from malignant human tissue and/or malignant tissues with "matched margins" obtained from noncancerous tissue just adjacent to the tumor, procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI).

Probe Name: Ag809
Forward 5'-ATGTGATCTTTGGCTGTGAAGT-3' (SEQ ID NO.: 249)
Probe FAM-5'-CTACCCCATGGCCTCCATCGAGT-3'-TAMRA (SEQ ID NO.: 250)
Reverse 5'-GGATGTCCAAGCCATCCTT-3' (SEQ ID NO.: 251)

Table 38A.

panel 1.3 ag809 1.3Dtm3313f_ag809

Adipose	1.14
Adrenal gland	0.45
Bladder	0.72
Bone marrow	0.7
Brain (amygdala)	0.46
Brain (cerebellum)	0
Brain (fetal)	0
Brain (hippocampus)	2.52
Cerebral Cortex	0.44
Brain (substantia nigra)	0.16
Brain (thalamus)	0.58
Brain (whole)	0.58
Colorectal	2.3
Heart (fetal)	8.48
Liver adenocarcinoma	15.39
Heart	2.68
Kidney	0.34
Kidney (fetal)	0.36
Liver	0.16
Liver (fetal)	0.21
Lung	0.75
Lung (fetal)	1.73
Lymph node	0.64
Mammary gland	1.92
Fetal Skeletal	28.32
Ovary	2.34
Pancreas	0.41
Pituitary gland	1.69
Plancenta	0.9
Prostate	3.04
Salivary gland	2.38
Skeletal muscle	0.63
Small intestine	0.88
Spinal cord	0.51
Spleen	11.91
Stomach	5.48
Testis	2.82
Thymus	0.81
Thyroid	1.25
Trachea	4.54
Uterus	1.33
Breast ca.* (pl. effusion) MCF-7	1.09
Breast ca.* (pl.ef) MDA-MB-231	4.12
Breast ca. BT-549	1.48
Breast ca.* (pl. effusion) T47D	12.76
Breast ca. MDA-N	3.61
Ovarian ca. OVCAR-3	0.68
Ovarian ca.* (ascites) SK-OV-3	0.08
Ovarian ca. OVCAR-4	0.78
Ovarian ca. OVCAR-5	1.76
Ovarian ca. IGROV-1	1.9
Ovarian ca. OVCAR-8	2.45
CNS ca. (glio/astro) U87-MG	2.34

CNS ca. (astro)	SW1783	1.26
CNS ca. (glio/astro)	U-118-MG	19.34
CNS ca.* (neuro; met)	SK-N-AS	10.08
CNS ca. (astro)	SF-539	2.43
CNS ca. (astro)	SNB-75	2.3
CNS ca. (glio)	SNB-19	0
CNS ca. (glio)	U251	0.17
CNS ca. (glio)	SF-295	2.43
Colon ca.	SW480	9.02
Colon ca.* (SW480 met)	SW620	3.67
Colon ca.	HT29	1.02
Colon ca.	HCT-116	0.97
Colon ca.	CaCo-2	9.54
Gastric ca.* (liver met)	NCI-N87	2.03
83219 CC Well to Mod Diff (ODO3866)		0.58
Colon ca.	HCC-2998	5.37
Renal ca.	786-0	1.35
Renal ca.	A498	1.32
Renal ca.	RXF 393	0.9
Renal ca.	ACHN	1.9
Renal ca.	UO-31	0.25
Renal ca.	TK-10	0.11
Liver ca. (hepatoblast)	HepG2	10.44
Lung ca. (small cell)	LX-1	6.65
Lung ca. (small cell)	NCI-H69	0.57
Lung ca. (s.cell var.)	SHP-77	2.52
Lung ca. (non-sm. cell)	A549	0.67
Lung ca. (squam.)	SW 900	0.91
Lung ca. (squam.)	NCI-H596	0.13
Lung ca. (non-s.cell)	NCI-H23	6.65
Lung ca. (large cell)	NCI-H460	1.32
Lung ca (non-s.cell)	HOP-62	2.03
Lung ca. (non-s.cl)	NCI-H522	9.21
Pancreatic ca.	CAPAN 2	0.9
Prostate ca.* (bone met)	PC-3	6.93
Melanoma	Hs688(A).T	2.61
Melanoma* (met)	Hs688(B).T	13.77
Melanoma	UACC-62	0.33
Melanoma	M14	1.83
Melanoma	LOX IMVI	0.46
Melanoma* (met)	SK-MEL-5	0.65
genomic DNA control		100
Chemistry Control		96.59

Table 39A.

panel 4D ag809	4Dtm3315f_ag809
93768_Secondary Th1_anti-CD28/anti-CD3	2.01
93769_Secondary Th2_anti-CD28/anti-CD3	1.5
93770_Secondary Tr1_anti-CD28/anti-CD3	2.45
93573_Secondary Th1_resting day 4-6 in IL-2	0.99
93572_Secondary Th2_resting day 4-6 in IL-2	2.96
93571_Secondary Tr1_resting day 4-6 in IL-2	1.69

93568_primary Th1_anti-CD28/anti-CD3	0.41
93569_primary Th2_anti-CD28/anti-CD3	1.47
93570_primary Tr1_anti-CD28/anti-CD3	1.96
93565_primary Th1_resting dy 4-6 in IL-2	5.37
93566_primary Th2_resting dy 4-6 in IL-2	3.12
93567_primary Tr1_resting dy 4-6 in IL-2	0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	11.19
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	1.15
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.91
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.63
93354_CD4_none	1.08
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0
93103_LAK cells_resting	0.49
93788_LAK cells_IL-2	0
93787_LAK cells_IL-2+IL-12	0.69
93789_LAK cells_IL-2+IFN gamma	1.05
93790_LAK cells_IL-2+ IL-18	0.29
93104_LAK cells_PMA/ionomycin and IL-18	0
93578_NK Cells IL-2_resting	1.34
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.54
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.47
93111_Mixed Lymphocyte Reaction_Two Way MLR	2.65
93112_Mononuclear Cells (PBMCs)_resting	0
93113_Mononuclear Cells (PBMCs)_PWM	1.32
93114_Mononuclear Cells (PBMCs)_PHA-L	1.02
93249_Ramos (B cell)_none	1.21
93250_Ramos (B cell)_ionomycin	2.26
93349_B lymphocytes_PWM	4.27
93350_B lymphoytes_CD40L and IL-4	1.36
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	7.23
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	3.02
93356_Dendritic Cells_none	1.48
93355_Dendritic Cells_LPS 100 ng/ml	0.69
93775_Dendritic Cells_anti-CD40	0.5
93774_Monocytes_resting	0.52
93776_Monocytes_LPS 50 ng/ml	0
93581_Macrophages_resting	1.29
93582_Macrophages_LPS 100 ng/ml	1.75
93098_HUVEC (Endothelial)_none	2.29
93099_HUVEC (Endothelial)_starved	9.02
93100_HUVEC (Endothelial)_IL-1b	1.16
93779_HUVEC (Endothelial)_IFN gamma	1.41
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.83
93101_HUVEC (Endothelial)_TNF alpha + IL4	1.12
93781_HUVEC (Endothelial)_IL-11	3
93583_Lung Microvascular Endothelial Cells_none	0.77
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.53
92662_Microvascular Dermal endothelium_none	1.14
92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1.03
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0

93347_Small Airway Epithelium_none	0.39
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.53
92668_Coronery Artery SMC_resting	5.75
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	2.32
93107_astrocytes_resting	2.74
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
92666_KU-812 (Basophil)_resting	6.79
92667_KU-812 (Basophil)_PMA/ionoycin	8.42
93579_CCD1106 (Keratinocytes)_none	1.58
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	1.44
93791_Liver Cirrhosis	4.18
93792_Lupus Kidney	1.85
93577_NCI-H292	39.5
93358_NCI-H292_IL-4	38.96
93360_NCI-H292_IL-9	65.52
93359_NCI-H292_IL-13	37.11
93357_NCI-H292_IFN gamma	31.86
93777_HPAEC_-	0.48
93778_HPAEC_IL-1 beta/TNA alpha	1.23
93254_Normal Human Lung Fibroblast_none	42.34
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	17.8
93257_Normal Human Lung Fibroblast_IL-4	100
93256_Normal Human Lung Fibroblast_IL-9	72.7
93255_Normal Human Lung Fibroblast_IL-13	60.71
93258_Normal Human Lung Fibroblast_IFN gamma	81.79
93106_Dermal Fibroblasts CCD1070_resting	76.84
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	30.15
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	38.16
93772_dermal fibroblast_IFN gamma	34.15
93771_dermal fibroblast_IL-4	80.66
93259_IBD Colitis 1**	0
93260_IBD Colitis 2	0.29
93261_IBD Crohns	1.41
735010_Colon_normal	35.6
735019_Lung_none	11.03
64028-1_Thymus_none	5.75
64030-1_Kidney_none	9.67

Table 50A.

Tissue Name	Rel. Expr., % 1.2tm955f_ag809	Rel. Expr., % 1.2tm1128f_ag809
Endothelial cells	0	0
Endothelial cells (treated)	15.1	34.6
Pancreas	7.4	0.2
Pancreatic ca. CAPAN 2	1.9	4.1
Adrenal Gland (new lot*)	3.1	6.7
Thyroid	6.7	1
Salavary gland	40.3	63.3
Pituitary gland	16.4	14.1
Brain (fetal)	0.7	0

Brain (whole)	2.1	3.4
Brain (amygdala)	1	1.6
Brain (cerebellum)	0.3	0.7
Brain (hippocampus)	2.7	6.5
Brain (thalamus)	1.1	0.8
Cerebral Cortex	3.4	8.8
Spinal cord	0.7	0.7
CNS ca. (glio/astro) U87-MG	11.4	8.2
CNS ca. (glio/astro) U-118-MG	21.2	24.1
CNS ca. (astro) SW1783	1.6	1.7
CNS ca.* (neuro; met) SK-N-AS	65.1	46.7
CNS ca. (astro) SF-539	5.6	9.2
CNS ca. (astro) SNB-75	0.5	0
CNS ca. (glio) SNB-19	2.4	2.9
CNS ca. (glio) U251	1.1	0.9
CNS ca. (glio) SF-295	2.7	0.5
Heart	39.2	77.4
Skeletal Muscle (new lot*)	52.1	36.3
Bone marrow	0	1.2
Thymus	0.3	0
Spleen	19.5	21.9
Lymph node	0.3	6.9
Colorectal	0	1.1
Stomach	18.9	27.7
Small intestine	3.1	8.4
Colon ca. SW480	5.2	8.3
Colon ca.* (SW480 met)SW620	19.2	20.4
Colon ca. HT29	4.1	2.5
Colon ca. HCT-116	2	1.4
Colon ca. CaCo-2	35.1	24.5
83219 CC Well to Mod Diff (ODO3866)	0.6	3.8
Colon ca. HCC-2998	36.9	54
Gastric ca.* (liver met) NCI-N87	11.9	14.9
Bladder	7	13.8
Trachea	6	9.3
Kidney	2.7	6
Kidney (fetal)	6.5	28.5
Renal ca. 786-0	5	6.7
Renal ca. A498	7.7	12
Renal ca. RXF 393	0.7	0.7
Renal ca. ACHN	5.1	7.2
Renal ca. UO-31	0	0
Renal ca. TK-10	0.1	0
Liver	1.1	1.3
Liver (fetal)	0.8	1.7
Liver ca. (hepatoblast) HepG2	16.2	49
Lung	0.5	1.6
Lung (fetal)	3.1	1.9
Lung ca. (small cell) LX-1	44.4	33.4
Lung ca. (small cell) NCI-H69	1.8	0.3
Lung ca. (s.cell var.) SHP-77	4.3	4.3

Lung ca. (large cell)NCI-H460	13.1	45.7
Lung ca. (non-sm. cell) A549	9.4	15.6
Lung ca. (non-s.cell) NCI-H23	11	12.9
Lung ca (non-s.cell) HOP-62	6.2	2.7
Lung ca. (non-s.cl) NCI-H522	81.2	62.4
Lung ca. (squam.) SW 900	6.6	13.8
Lung ca. (squam.) NCI-H596	2	0.1
Mammary gland	5.3	4.6
Breast ca.* (pl. effusion) MCF-7	4.2	6.4
Breast ca.* (pl.ef) MDA-MB-231	2	6
Breast ca.* (pl. effusion) T47D	100	100
Breast ca. BT-549	3	5.7
Breast ca. MDA-N	17.4	20.4
Ovary	2.1	3.8
Ovarian ca. OVCAR-3	8.4	4.3
Ovarian ca. OVCAR-4	2.3	3.1
Ovarian ca. OVCAR-5	8.9	7
Ovarian ca. OVCAR-8	4.9	13.1
Ovarian ca. IGROV-1	7	7.7
Ovarian ca.* (ascites) SK-OV-3	0	0
Uterus	3.8	8.7
Plancenta	1.9	3.2
Prostate	13.4	33
Prostate ca.* (bone met)PC-3	42.9	76.3
Testis	8.1	9.4
Melanoma Hs688(A).T	5.3	6
Melanoma* (met) Hs688(B).T	3.5	3.4
Melanoma UACC-62	2.9	3.7
Melanoma M14	11.5	21.9
Melanoma LOX IMVI	2.6	1.8
Melanoma* (met) SK-MEL-5	1.7	3.2
Adipose	3.2	52.1

Table 51A:

Tissue Name	Rel. Expr., % 1.3Dtm3313f_ag809
Liver adenocarcinoma	54.3
Pancreas	1.4
Pancreatic ca. CAPAN 2	3.2
Adrenal gland	1.6
Thyroid	4.4
Salivary gland	8.4
Pituitary gland	6
Brain (fetal)	0
Brain (whole)	2
Brain (amygdala)	1.6
Brain (cerebellum)	0
Brain (hippocampus)	8.9
Brain (substantia nigra)	0.6
Brain (thalamus)	2
Cerebral Cortex	1.6

Spinal cord		1.8
CNS ca. (glio/astro)	U87-MG	8.2
CNS ca. (glio/astro)	U-118-MG	68.3
CNS ca. (astro)	SW1783	4.4
CNS ca.* (neuro; met)	SK-N-AS	35.6
CNS ca. (astro)	SF-539	8.6
CNS ca. (astro)	SNB-75	8.1
CNS ca. (glio)	SNB-19	0
CNS ca. (glio)	U251	0.6
CNS ca. (glio)	SF-295	8.6
Heart (fetal)		29.9
Heart		9.5
Fetal Skeletal		100
Skeletal muscle		2.2
Bone marrow		2.5
Thymus		2.9
Spleen		42
Lymph node		2.3
Colorectal		8.1
Stomach		19.3
Small intestine		3.1
Colon ca.	SW480	31.9
Colon ca.* (SW480 met)	SW620	12.9
Colon ca.	HT29	3.6
Colon ca.	HCT-116	3.4
Colon ca.	CaCo-2	33.7
83219 CC Well to Mod Diff (ODO3866)		2
Colon ca.	HCC-2998	18.9
Gastric ca.* (liver met)	NCI-N87	7.2
Bladder		2.5
Trachea		16
Kidney		1.2
Kidney (fetal)		1.3
Renal ca.	786-0	4.8
Renal ca.	A498	4.7
Renal ca.	RXF 393	3.2
Renal ca.	ACHN	6.7
Renal ca.	UO-31	0.9
Renal ca.	TK-10	0.4
Liver		0.6
Liver (fetal)		0.7
Liver ca. (hepatoblast)	HepG2	36.9
Lung		2.7
Lung (fetal)		6.1
Lung ca. (small cell)	LX-1	23.5
Lung ca. (small cell)	NCI-H69	2
Lung ca. (s.cell var.)	SHP-77	8.9
Lung ca. (large cell)	NCI-H460	4.7
Lung ca. (non-sm. cell)	A549	2.4
Lung ca. (non-s.cell)	NCI-H23	23.5
Lung ca (non-s.cell)	HOP-62	7.2

Lung ca. (non-s.cl) NCI-H522	32.5
Lung ca. (squam.) SW 900	3.2
Lung ca. (squam.) NCI-H596	0.5
Mammary gland	6.8
Breast ca.* (pl. effusion) MCF-7	3.8
Breast ca.* (pl.ef) MDA-MB-231	14.6
Breast ca.* (pl. effusion) T47D	45.1
Breast ca. BT-549	5.2
Breast ca. MDA-N	12.8
Ovary	8.2
Ovarian ca. OVCAR-3	2.4
Ovarian ca. OVCAR-4	2.7
Ovarian ca. OVCAR-5	6.2
Ovarian ca. OVCAR-8	8.7
Ovarian ca. IGROV-1	6.7
Ovarian ca.* (ascites) SK-OV-3	0.3
Uterus	4.7
Plancenta	3.2
Prostate	10.7
Prostate ca.* (bone met)PC-3	24.5
Testis	9.9
Melanoma Hs688(A).T	9.2
Melanoma* (met) Hs688(B).T	48.6
Melanoma UACC-62	1.2
Melanoma M14	6.5
Melanoma LOX IMVI	1.6
Melanoma* (met) SK-MEL-5	2.3
Adipose	4

<u>Table 52A:</u>

Tissue Name	Rel. Expr., % 2Dtm3314f_ag809
Normal Colon GENPAK 061003	6.8
83219 CC Well to Mod Diff (ODO3866)	6.1
83220 CC NAT (ODO3866)	2.5
83221 CC Gr.2 rectosigmoid (ODO3868)	0.9
83222 CC NAT (ODO3868)	1.2
83235 CC Mod Diff (ODO3920)	3.8
83236 CC NAT (ODO3920)	1.3
83237 CC Gr.2 ascend colon (ODO3921)	6.9
83238 CC NAT (ODO3921)	4
83241 CC from Partial Hepatectomy (ODO4309)	1.2
83242 Liver NAT (ODO4309)	0.6
87472 Colon mets to lung (OD04451-01)	4.4
87473 Lung NAT (OD04451-02)	1.2
Normal Prostate Clontech A+ 6546-1	10.2
84140 Prostate Cancer (OD04410)	41.8
84141 Prostate NAT (OD04410)	25.7
87073 Prostate Cancer (OD04720-01)	11
87074 Prostate NAT (OD04720-02)	10
Normal Lung GENPAK 061010	7.9

83239 Lung Met to Muscle (ODO4286)	6.5
83240 Muscle NAT (ODO4286)	2.6
84136 Lung Malignant Cancer (OD03126)	14.8
84137 Lung NAT (OD03126)	3.1
84871 Lung Cancer (OD04404)	2
84872 Lung NAT (OD04404)	1.9
84875 Lung Cancer (OD04565)	0.3
84876 Lung NAT (OD04565)	1.9
85950 Lung Cancer (OD04237-01)	1.3
85970 Lung NAT (OD04237-02)	2.6
83255 Ocular Mel Met to Liver (ODO4310)	0.1
83256 Liver NAT (ODO4310)	0.6
84139 Melanoma Mets to Lung (OD04321)	2.5
84138 Lung NAT (OD04321)	2.6
Normal Kidney GENPAK 061008	5.6
83786 Kidney Ca, Nuclear grade 2 (OD04338)	0.6
83787 Kidney NAT (OD04338)	3.7
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0.8
83789 Kidney NAT (OD04339)	3.1
83790 Kidney Ca, Clear cell type (OD04340)	1.5
83791 Kidney NAT (OD04340)	5.1
83792 Kidney Ca, Nuclear grade 3 (OD04348)	14.5
83793 Kidney NAT (OD04348)	2.5
87474 Kidney Cancer (OD04622-01)	1.7
87475 Kidney NAT (OD04622-03)	2
85973 Kidney Cancer (OD04450-01)	0.3
85974 Kidney NAT (OD04450-03)	2
Kidney Cancer Clontech 8120607	7
Kidney NAT Clontech 8120608	1.5
Kidney Cancer Clontech 8120613	2
Kidney NAT Clontech 8120614	4.1
Kidney Cancer Clontech 9010320	2.2
Kidney NAT Clontech 9010321	3.5
Normal Uterus GENPAK 061018	3.1
Uterus Cancer GENPAK 064011	17.6
Normal Thyroid Clontech A+ 6570-1	3.7
Thyroid Cancer GENPAK 064010	1.2
Thyroid Cancer INVITROGEN A302152	0.6
Thyroid NAT INVITROGEN A302153	2.6
Normal Breast GENPAK 061019	3.3
84877 Breast Cancer (OD04566)	0.9
85975 Breast Cancer (OD04590-01)	67.8
85976 Breast Cancer Mets (OD04590-03)	51
87070 Breast Cancer Metastasis (OD04655-05)	12.7
GENPAK Breast Cancer 064006	8.9
Breast Cancer Res. Gen. 1024	7.8
Breast Cancer Clontech 9100266	6.2
Breast NAT Clontech 9100265	3.3
Breast Cancer INVITROGEN A209073	3.4
Breast NAT INVITROGEN A2090734	8.7
Normal Liver GENPAK 061009	1.1

Liver Cancer GENPAK 064003	0.6
Liver Cancer Research Genetics RNA 1025	0.6
Liver Cancer Research Genetics RNA 1026	1.4
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	1.3
Paired Liver Tissue Research Genetics RNA 6004-N	1.3
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	1.1
Paired Liver Tissue Research Genetics RNA 6005-N	0.3
Normal Bladder GENPAK 061001	5.9
Bladder Cancer Research Genetics RNA 1023	1.7
Bladder Cancer INVITROGEN A302173	1.9
87071 Bladder Cancer (OD04718-01)	2
87072 Bladder Normal Adjacent (OD04718-03)	3.3
Normal Ovary Res. Gen.	2.2
Ovarian Cancer GENPAK 064008	29.1
87492 Ovary Cancer (OD04768-07)	100
87493 Ovary NAT (OD04768-08)	2.2
Normal Stomach GENPAK 061017	13.1
Gastric Cancer Clontech 9060358	1.3
NAT Stomach Clontech 9060359	8.8
Gastric Cancer Clontech 9060395	2.5
NAT Stomach Clontech 9060394	9.7
Gastric Cancer Clontech 9060397	15.9
NAT Stomach Clontech 9060396	12.9
Gastric Cancer GENPAK 064005	12.1

Table 53A:

Tissue Name	Rel. Expr., % 3dx4tm6102f_ag809_b2
94905_Daoy_Medulloblastoma/Cerebellum_sscDNA	1.4
94906_TE671_Medulloblastom/Cerebellum_sscDNA	18.5
94907_D283 Med_Medulloblastoma/Cerebellum_sscDNA	13.1
94908_PFSK-1_Primitive Neuroectodermal/Cerebellum_sscDNA	1.9
94909_XF-498_CNS_sscDNA	6.6
94910_SNB-78_CNS/glioma_sscDNA	9.3
94911_SF-268_CNS/glioblastoma_sscDNA	1.4
94912_T98G_Glioblastoma_sscDNA	1.5
96776_SK-N-SH_Neuroblastoma (metastasis)_sscDNA	0.9
94913_SF-295_CNS/glioblastoma_sscDNA	0.8
94914_Cerebellum_sscDNA	0
96777_Cerebellum_sscDNA	0.4
94916_NCI-H292_Mucoepidermoid lung carcinoma_sscDNA	13.9
94917_DMS-114_Small cell lung cancer_sscDNA	9
94918_DMS-79_Small cell lung cancer/neuroendocrine_sscDNA	45.9
94919_NCI-H146_Small cell lung cancer/neuroendocrine_sscDNA	3.7
94920_NCI-H526_Small cell lung cancer/neuroendocrine_sscDNA	4.2
94921_NCI-N417_Small cell lung cancer/neuroendocrine_sscDNA	3.3
94923_NCI-H82_Small cell lung cancer/neuroendocrine_sscDNA	0.6
94924_NCI-H157_Squamous cell lung cancer (metastasis)_sscDNA	0.7
94925_NCI-H1155_Large cell lung cancer/neuroendocrine_sscDNA	9
94926_NCI-H1299_Large cell lung cancer/neuroendocrine_sscDNA	10.9
94927_NCI-H727_Lung carcinoid_sscDNA	27.2

94928_NCI-UMC-11_Lung carcinoid_sscDNA	15.2
94929_LX-1_Small cell lung cancer_sscDNA	29.2
94930_Colo-205_Colon cancer_sscDNA	25.1
94931_KM12_Colon cancer_sscDNA	9.7
94932_KM20L2_Colon cancer_sscDNA	2.4
94933_NCI-H716_Colon cancer_sscDNA	100
94935_SW-48_Colon adenocarcinoma_sscDNA	5
94936_SW1116_Colon adenocarcinoma_sscDNA	6.5
94937_LS 174T_Colon adenocarcinoma_sscDNA	11.7
94938_SW-948_Colon adenocarcinoma_sscDNA	0
94939_SW-480_Colon adenocarcinoma_sscDNA	1.9
94940_NCI-SNU-5_Gastric carcinoma_sscDNA	7.5
94941_KATO III_Gastric carcinoma_sscDNA	8.2
94943_NCI-SNU-16_Gastric carcinoma_sscDNA	7.9
94944_NCI-SNU-1_Gastric carcinoma_sscDNA	13.4
94946_RF-1_Gastric adenocarcinoma_sscDNA	2.9
94947_RF-48_Gastric adenocarcinoma_sscDNA	3.6
96778_MKN-45_Gastric carcinoma_sscDNA	23.9
94949_NCI-N87_Gastric carcinoma_sscDNA	2.3
94951_OVCAR-5_Ovarian carcinoma_sscDNA	1.7
94952_RL95-2_Uterine carcinoma_sscDNA	6.9
94953_HelaS3_Cervical adenocarcinoma_sscDNA	12.1
94954_Ca Ski_Cervical epidermoid carcinoma (metastasis)_sscDNA	4.4
94955_ES-2_Ovarian clear cell carcinoma_sscDNA	1.7
94957_Ramos/6h stim_"; Stimulated with PMA/ionomycin 6h_sscDNA	1
94958_Ramos/14h stim_"; Stimulated with PMA/ionomycin 14h_sscDNA	1.2
94962_MEG-01_Chronic myelogenous leukemia (megokaryoblast)_sscDNA	2.6
94963_Raji_Burkitt's lymphoma_sscDNA	0.3
94964_Daudi_Burkitt's lymphoma_sscDNA	0.5
94965_U266_B-cell plasmacytoma/myeloma_sscDNA	2.4
94968_CA46_Burkitt's lymphoma_sscDNA	0
94970_RL_non-Hodgkin's B-cell lymphoma_sscDNA	0.8
94972_JM1_pre-B-cell lymphoma/leukemia_sscDNA	1.3
94973_Jurkat_T cell leukemia_sscDNA	3.8
94974_TF-1_Erythroleukemia_sscDNA	5.9
94975_HUT 78_T-cell lymphoma_sscDNA	0.5
94977_U937_Histiocytic lymphoma_sscDNA	9.3
94980_KU-812_Myelogenous leukemia_sscDNA	1.8
94981_769-P_Clear cell renal carcinoma_sscDNA	0
94983_Caki-2_Clear cell renal carcinoma_sscDNA	3.5
94984_SW 839_Clear cell renal carcinoma_sscDNA	0
94986_G401_Wilms' tumor_sscDNA	14.6
94987_Hs766T_Pancreatic carcinoma (LN metastasis)_sscDNA	19.3
94988_CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)_sscDNA	0.2
94989_SU86.86_Pancreatic carcinoma (liver metastasis)_sscDNA	5.3
94990_BxPC-3_Pancreatic adenocarcinoma_sscDNA	2.7
94991_HPAC_Pancreatic adenocarcinoma_sscDNA	1
94992_MIA PaCa-2_Pancreatic carcinoma_sscDNA	1.2
94993_CFPAC-1_Pancreatic ductal adenocarcinoma_sscDNA	9.2
94994_PANC-1_Pancreatic epithelioid ductal carcinoma_sscDNA	4.5
94996_T24_Bladder carcinma (transitional cell)_sscDNA	0.9

94997_5637_Bladder carcinoma_sscDNA	0.8
94998_HT-1197_Bladder carcinoma_sscDNA	4.6
94999_UM-UC-3_Bladder carcinma (transitional cell)_sscDNA	0.4
95000_A204_Rhabdomyosarcoma_sscDNA	46.9
95001_HT-1080_Fibrosarcoma_sscDNA	5.3
95002_MG-63_Osteosarcoma (bone)_sscDNA	22.8
95003_SK-LMS-1_Leiomyosarcoma (vulva)_sscDNA	11.2
95004_SJRH30_Rhabdomyosarcoma (met to bone marrow)_sscDNA	38.5
95005_A431_Epidermoid carcinoma_sscDNA	1.1
95007_WM266-4_Melanoma_sscDNA	11.9
95010_DU 145_Prostate carcinoma (brain metastasis)_sscDNA	0
95012_MDA-MB-468_Breast adenocarcinoma_sscDNA	7.1
95013_SCC-4_Squamous cell carcinoma of tongue_sscDNA	0
95014_SCC-9_Squamous cell carcinoma of tongue_sscDNA	0
95015_SCC-15_Squamous cell carcinoma of tongue_sscDNA	0
95017_CAL 27_Squamous cell carcinoma of tongue_sscDNA	1

Table 54A:

Tissue Name	Rel. Expr., % 4Dtm3315f_ag809
93768_Secondary Th1_anti-CD28/anti-CD3	2
93769_Secondary Th2_anti-CD28/anti-CD3	1.5
93770_Secondary Tr1_anti-CD28/anti-CD3	2.5
93573_Secondary Th1_resting day 4-6 in IL-2	1
93572_Secondary Th2_resting day 4-6 in IL-2	3
93571_Secondary Tr1_resting day 4-6 in IL-2	1.7
93568_primary Th1_anti-CD28/anti-CD3	0.4
93569_primary Th2_anti-CD28/anti-CD3	1.5
93570_primary Tr1_anti-CD28/anti-CD3	2
93565_primary Th1_resting dy 4-6 in IL-2	5.4
93566_primary Th2_resting dy 4-6 in IL-2	3.1
93567_primary Tr1_resting dy 4-6 in IL-2	0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	11.2
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	1.2
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0.9
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0.6
93354_CD4_none	1.1
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0
93103_LAK cells_resting	0.5
93788_LAK cells_IL-2	0
93787_LAK cells_IL-2+IL-12	0.7
93789_LAK cells_IL-2+IFN gamma	1.1
93790_LAK cells_IL-2+ IL-18	0.3
93104_LAK cells_PMA/ionomycin and IL-18	0
93578_NK Cells IL-2_resting	1.3
93109_Mixed Lymphocyte Reaction_Two Way MLR	0.5
93110_Mixed Lymphocyte Reaction_Two Way MLR	0.5
93111_Mixed Lymphocyte Reaction_Two Way MLR	2.6
93112_Mononuclear Cells (PBMCs)_resting	0
93113_Mononuclear Cells (PBMCs)_PWM	1.3

93114_Mononuclear Cells (PBMCs)_PHA-L	1
93249_Ramos (B cell)_none	1.2
93250_Ramos (B cell)_ionomycin	2.3
93349_B lymphocytes_PWM	4.3
93350_B lymphoytes_CD40L and IL-4	1.4
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	7.2
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	3
93356_Dendritic Cells_none	1.5
93355_Dendritic Cells_LPS 100 ng/ml	0.7
93775_Dendritic Cells_anti-CD40	0.5
93774_Monocytes_resting	0.5
93776_Monocytes_LPS 50 ng/ml	0
93581_Macrophages_resting	1.3
93582_Macrophages_LPS 100 ng/ml	1.7
93098_HUVEC (Endothelial)_none	2.3
93099_HUVEC (Endothelial)_starved	9
93100_HUVEC (Endothelial)_IL-1b	1.2
93779_HUVEC (Endothelial)_IFN gamma	1.4
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0.8
93101_HUVEC (Endothelial)_TNF alpha + IL4	1.1
93781_HUVEC (Endothelial)_IL-11	3
93583_Lung Microvascular Endothelial Cells_none	0.8
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.5
92662_Microvascular Dermal endothelium_none	1.1
92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	1
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0
93347_Small Airway Epithelium_none	0.4
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0.5
92668_Coronery Artery SMC_resting	5.8
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	2.3
93107_astrocytes_resting	2.7
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
92666_KU-812 (Basophil)_resting	6.8
92667_KU-812 (Basophil)_PMA/ionoycin	8.4
93579_CCD1106 (Keratinocytes)_none	1.6
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	1.4
93791_Liver Cirrhosis	4.2
93792_Lupus Kidney	1.8
93577_NCI-H292	39.5
93358_NCI-H292_IL-4	39
93360_NCI-H292_IL-9	65.5
93359_NCI-H292_IL-13	37.1
93357_NCI-H292_IFN gamma	31.9
93777_HPAEC_-	0.5
93778_HPAEC_IL-1 beta/TNA alpha	1.2
93254_Normal Human Lung Fibroblast_none	42.3
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	17.8
93257_Normal Human Lung Fibroblast_IL-4	100
93256_Normal Human Lung Fibroblast_IL-9	72.7
93255_Normal Human Lung Fibroblast_IL-13	60.7
93258_Normal Human Lung Fibroblast_IFN gamma	81.8

93106_Dermal Fibroblasts CCD1070_resting	76.8
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	30.1
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	38.2
93772_dermal fibroblast_IFN gamma	34.2
93771_dermal fibroblast_IL-4	80.7
93259_IBD Colitis 1**	0
93260_IBD Colitis 2	0.3
93261_IBD Crohns	1.4
735010_Colon_normal	35.6
735019_Lung_none	11
64028-1_Thymus_none	5.8
64030-1_Kidney_none	9.7

Example 5 Expression profiling of MOL16 (CG53980-01 or AL031704_A).

Panel 1.3 (Table 40A): The profile was generated from a panel of 37 normal human tissues and 59 human cancer cell lines using specific gene probe and primer sets (Ag547). This gene is highly expressed in normal testes, placenta and colorectal tissue.

Panel 4D (Table 41A): The profile was generated from a panel of several human cell lines that were either untreated or treated with a wide variety factors which modulate the immune response. This panel shows that the normal colon expresses high levels of this transcript whereas three different inflammatory bowel disease tissues did not.

Probe Name: Ag547
Primers Sequences TM Length Start Position
Forward 5'-TGACTGCTGCCCACTGCA-3' (SEQ ID NO.:252)
Probe TET-5'-CACCGACCCGTCCATCTACCGGAT-3'-TAMRA(SEQ ID NO.:253)
Reverse 5'-GAGATACACGTCCCCAGCGT-3' (SEQ ID NO.: 254)

TABLE 40A.

panel 1.3 ag547	
Liver adenocarcinoma	0
Heart (fetal)	0
Pancreas	0
Pancreatic ca. CAPAN 2	0
Adrenal gland	0
Thyroid	0
Salivary gland	0
Pituitary gland	0
Brain (fetal)	0
Brain (whole)	0
Brain (amygdala)	0
Brain (cerebellum)	0

Brain (hippocampus)	0
Brain (thalamus)	0
Cerebral Cortex	0
Spinal cord	0
CNS ca. (glio/astro) U87-MG	0
CNS ca. (glio/astro) U-118-MG	0
CNS ca. (astro) SW1783	0
CNS ca.* (neuro; met) SK-N-AS	0
CNS ca. (astro) SF-539	0
CNS ca. (astro) SNB-75	0
CNS ca. (glio) SNB-19	0
CNS ca. (glio) U251	0
CNS ca. (glio) SF-295	0
Heart	0
Skeletal muscle	0
Bone marrow	0
Thymus	0
Spleen	0
Lymph node	0
Colorectal	41.87
Stomach	0
Small intestine	0
Colon ca. SW480	0
Colon ca.* (SW480 met)SW620	0
Colon ca. HT29	28.93
Colon ca. HCT-116	0
Colon ca. CaCo-2	0
83219 CC Well to Mod Diff (ODO3866)	0
Colon ca. HCC-2998	0
Gastric ca.* (liver met) NCI-N87	0
Bladder	0
Trachea	0
Kidney	0
Kidney (fetal)	0
Renal ca. 786-0	0
Renal ca. A498	0
Renal ca. RXF 393	0
Renal ca. ACHN	0
Renal ca. UO-31	0
Renal ca. TK-10	0
Liver	0
Liver (fetal)	0
Liver ca. (hepatoblast) HepG2	0
Lung	0
Lung (fetal)	0
Lung ca. (small cell) LX-1	0
Lung ca. (small cell) NCI-H69	0
Lung ca. (s.cell var.) SHP-77	0
Lung ca. (large cell)NCI-H460	0
Lung ca. (non-sm. cell) A549	0
Lung ca. (non-s.cell) NCI-H23	0
Lung ca (non-s.cell) HOP-62	0
Lung ca. (non-s.cl) NCI-H522	0

Lung ca. (squam.)	SW 900	0
Lung ca. (squam.)	NCI-H596	0
Mammary gland		0
Breast ca.* (pl. effusion)	MCF-7	0
Breast ca.* (pl.ef)	MDA-MB-231	0
Breast ca.* (pl. effusion)	T47D	0
Breast ca.	BT-549	53.27
Breast ca.	MDA-N	0
Ovary		0
Ovarian ca.	OVCAR-3	0
Ovarian ca.	OVCAR-4	0
Ovarian ca.	OVCAR-5	0
Ovarian ca.	OVCAR-8	0
Ovarian ca.	IGROV-1	0
Ovarian ca.* (ascites)	SK-OV-3	0
Uterus		0
Plancenta		52.86
Prostate		0
Prostate ca.* (bone met)	PC-3	0
Testis		100
Melanoma	Hs688(A).T	0
Melanoma* (met)	Hs688(B).T	0
Melanoma	UACC-62	0
Melanoma	M14	0
Melanoma	LOX IMVI	0
Melanoma* (met)	SK-MEL-5	0
Adipose		0

TABLE 41A.

panel 4D ag547	
93768_Secondary Th1_anti-CD28/anti-CD3	0
93769_Secondary Th2_anti-CD28/anti-CD3	0
93770_Secondary Tr1_anti-CD28/anti-CD3	0
93573_Secondary Th1_resting day 4-6 in IL-2	0
93572_Secondary Th2_resting day 4-6 in IL-2	0
93571_Secondary Tr1_resting day 4-6 in IL-2	0
93568_primary Th1_anti-CD28/anti-CD3	0
93569_primary Th2_anti-CD28/anti-CD3	0
93570_primary Tr1_anti-CD28/anti-CD3	0
93565_primary Th1_resting dy 4-6 in IL-2	0
93566_primary Th2_resting dy 4-6 in IL-2	0
93567_primary Tr1_resting dy 4-6 in IL-2	0
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	0
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0
93354_CD4_none	0
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0
93103_LAK cells_resting	0
93788_LAK cells_IL-2	0
93787_LAK cells_IL-2+IL-12	14.66

93789_LAK cells_IL-2+IFN gamma	0
93790_LAK cells_IL-2+ IL-18	0
93104_LAK cells_PMA/ionomycin and IL-18	0
93578_NK Cells IL-2_resting	*0*
93109_Mixed Lymphocyte Reaction_Two Way MLR	16.96
93110_Mixed Lymphocyte Reaction_Two Way MLR	0
93111_Mixed Lymphocyte Reaction_Two Way MLR	0
93112_Mononuclear Cells (PBMCs)_resting	0
93113_Mononuclear Cells (PBMCs)_PWM	0
93114_Mononuclear Cells (PBMCs)_PHA-L	0
93249_Ramos (B cell)_none	0
93250_Ramos (B cell)_ionomycin	0
93349_B lymphocytes_PWM	0
93350_B lymphoytes_CD40L and IL-4	*14.46*
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0
93356_Dendritic Cells_none	0
93355_Dendritic Cells_LPS 100 ng/ml	0
93775_Dendritic Cells_anti-CD40	17.8
93774_Monocytes_resting	0
93776_Monocytes_LPS 50 ng/ml	8.9
93581_Macrophages_resting	0
93582_Macrophages_LPS 100 ng/ml	0
93098_HUVEC (Endothelial)_none	0
93099_HUVEC (Endothelial)_starved	0
93100_HUVEC (Endothelial)_IL-1b	0
93779_HUVEC (Endothelial)_IFN gamma	0
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0
93101_HUVEC (Endothelial)_TNF alpha + IL4	0
93781_HUVEC (Endothelial)_IL-11	0
93583_Lung Microvascular Endothelial Cells_none	0
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
92662_Microvascular Dermal endothelium_none	0
92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0
93347_Small Airway Epithelium_none	0
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
92668_Coronery Artery SMC_resting	0
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
93107_astrocytes_resting	0
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0
92666_KU-812 (Basophil)_resting	0
92667_KU-812 (Basophil)_PMA/ionoycin	10.88
93579_CCD1106 (Keratinocytes)_none	0
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0
93791_Liver Cirrhosis	13.12
93792_Lupus Kidney	0
93577_NCI-H292	0
93358_NCI-H292_IL-4	0
93360_NCI-H292_IL-9	16.61
93359_NCI-H292_IL-13	0

93357_NCI-H292_IFN gamma	0
93777_HPAEC_-	10.37
93778_HPAEC_IL-1 beta/TNA alpha	0
93254_Normal Human Lung Fibroblast_none	0
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	0
93257_Normal Human Lung Fibroblast_IL-4	0
93256_Normal Human Lung Fibroblast_IL-9	0
93255_Normal Human Lung Fibroblast_IL-13	0
93258_Normal Human Lung Fibroblast_IFN gamma	0
93106_Dermal Fibroblasts CCD1070_resting	3.74
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0
93772_dermal fibroblast_IFN gamma	0
93771_dermal fibroblast_IL-4	0
93259_IBD Colitis 1**	0
93260_IBD Colitis 2	0
93261_IBD Crohns	0
735010_Colon_normal	100
735019_Lung_none	33.92
64028-1_Thymus_none	0
64030-1_Kidney_none	0

Example 6 Expression profiling of MOL21 (CG54565-05).

Panel 4D (Table 42A): The **CG54656-05** transcript is up regulated in three different epithelial cell types after treatment with inflammatory cytokines. Two cell lines originate from lung tissue, the NCI H292 airway cell line and lung microvascular endothelial cells. Human umbilical vein epithelial cells (HUVEC) also up regulate expression of this transcript upon activation.

Probe Name: Ag1599

Primers Sequences TM Length Start Position
Forward 5'-CTCAAGTACCACACGGTCTCAT-3' (SEQ ID NO.: 255)
Probe TET-5'-CCGCACCCGGAAAGTCATTGTAAGT-3'-TAMRA (SEQ ID NO.: 256
Reverse 5'-TCAGGAAGCAGGTGATGTAAAC-3' (SEQ ID NO.: 257)

TABLE 42A.

panel 4D	4dtm4722_ag1599
Secondary Th1 act	0
Secondary Th2 act	0
Secondary Tr1 act	0
Secondary Th1 rest	0
Secondary Th2 rest	0
Secondary Tr1 rest	0
Primary Th1 act	0
Primary Th2 act	0
Primary Tr1 act	0
Primary Th1 rest	0
Primary Th2 rest	0
Primary Tr1 rest	13.77

CD45RA CD4 lymphocyte act	0
CD45RO CD4 lymphocyte act	40.61
CD8 lymphocyte act	0
Secondary CD8 lymphocyte rest	0
Secondary CD8 lymphocyte act	0
CD4 lymphocyte none	0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0
LAK cells rest	0
LAK cells IL-2	0
LAK cells IL-2+IL-12	0
LAK cells IL-2+IFN gamma	0
LAK cells IL-2+ IL-18	0
LAK cells PMA/ionomycin	0
NK Cells IL-2 rest	0
Two Way MLR 3 day	0
Two Way MLR 5 day	0
Two Way MLR 7 day	0
PBMC rest	0
PBMC PWM	0
PBMC PHA-L	0
Ramos (B cell) none	0
Ramos (B cell) ionomycin	0
B lymphocytes PWM	0
B lymphocytes CD40L and IL-4	0
EOL-1 dbcAMP	0
EOL-1 dbcAMP PMA/ionomycin	0
Dendritic cells none	0
Dendritic cells LPS	0
Dendritic cells anti-CD40	0
Monocytes rest	0
Monocytes LPS	0
Macrophages rest	0
Macrophages LPS	0
HUVEC none	0
HUVEC starved	0
HUVEC IL-1beta	0
HUVEC IFN gamma	0
HUVEC TNF alpha + IFN gamma	30.35
HUVEC TNF alpha + IL4	0
HUVEC IL-11	0
Lung Microvascular EC none	0
Lung Microvascular EC TNFalpha + IL-1beta	27.93
Microvascular Dermal EC none	0
Microsvasular Dermal EC TNFalpha + IL-1beta	0
Bronchial epithelium TNFalpha + IL1beta	0
Small airway epithelium none	0
Small airway epithelium TNFalpha + IL-1beta	0
Coronery artery SMC rest	0
Coronery artery SMC TNFalpha + IL-1beta	0
Astrocytes rest	0
Astrocytes TNFalpha + IL-1beta	0
KU-812 (Basophil) rest	0
KU-812 (Basophil) PMA/ionomycin	0

CCD1106 (Keratinocytes) none	0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0
Liver cirrhosis	29.12
Lupus kidney	0
NCI-H292 none	0
NCI-H292 IL-4	0
NCI-H292 IL-9	0
NCI-H292 IL-13	0
NCI-H292 IFN gamma	12.85
HPAEC none	0
HPAEC TNF alpha + IL-1 beta	0
Lung fibroblast none	0
Lung fibroblast TNF alpha + IL-1 beta	0
Lung fibroblast IL-4	0
Lung fibroblast IL-9	0
Lung fibroblast IL-13	0
Lung fibroblast IFN gamma	0
Dermal fibroblast CCD1070 rest	100
Dermal fibroblast CCD1070 TNF alpha	0
Dermal fibroblast CCD1070 IL-1 beta	0
Dermal fibroblast IFN gamma	0
Dermal fibroblast IL-4	0
IBD Colitis 1	0
IBD Colitis 2	21.02
IBD Crohn's	0
Colon	17.19
Lung	0
Thymus	0
Kidney	0

Example 7 Expression profiling of MOL18 (CG58604 or 416_d_14_A).

TaqMan Expression profile of CG58604 transcript:

Panel 1.1 (Tables 43A and 45A): There is very low expression of this transcript in most normal tissues with the exception of the brain. The expression of this transcript in the normal lung is very low.

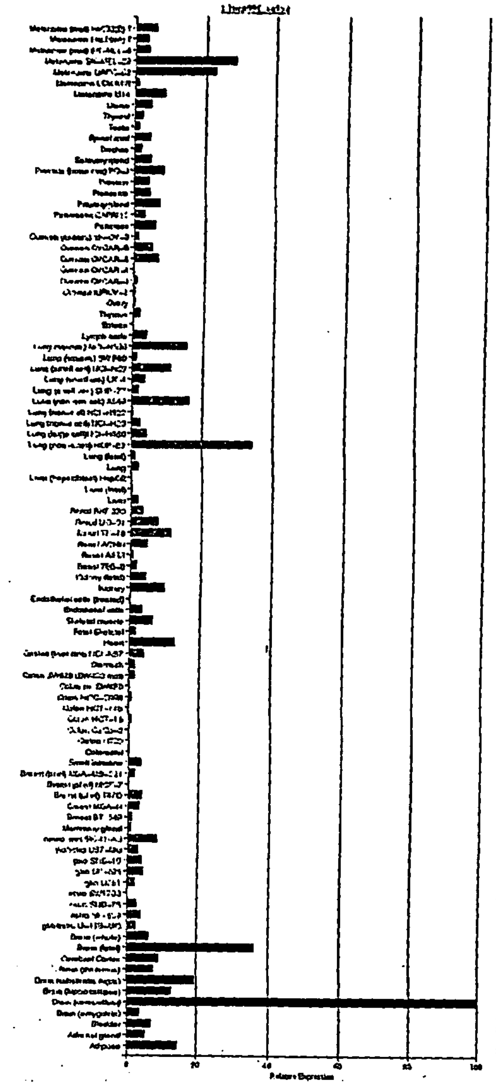
Panel 4D (Tables 44A and 46A): Lung fibroblast expression of **CG58604** is up highly regulated by IL-13. This transcript is also expressed on IL-4 treated dermal fibroblasts.

Probe Name: Ag552

Primers	Sequences
Forward	5'-GGAAGCTGACCGACCAGAAC-3' (SEQ ID NO.: 258)
Probe	FAM-5'-AGCCCATCCCTAGAGCCTTCATGTACTCA-3'-TAMRA (SEQ ID NO.: 259)
Reverse	5'-ATTTCCCACCTGCCTAGTGACA-3' (SEQ ID NO.: 260)

Table 43A (Panel 1.1)

Table 44A (Panel 4D)



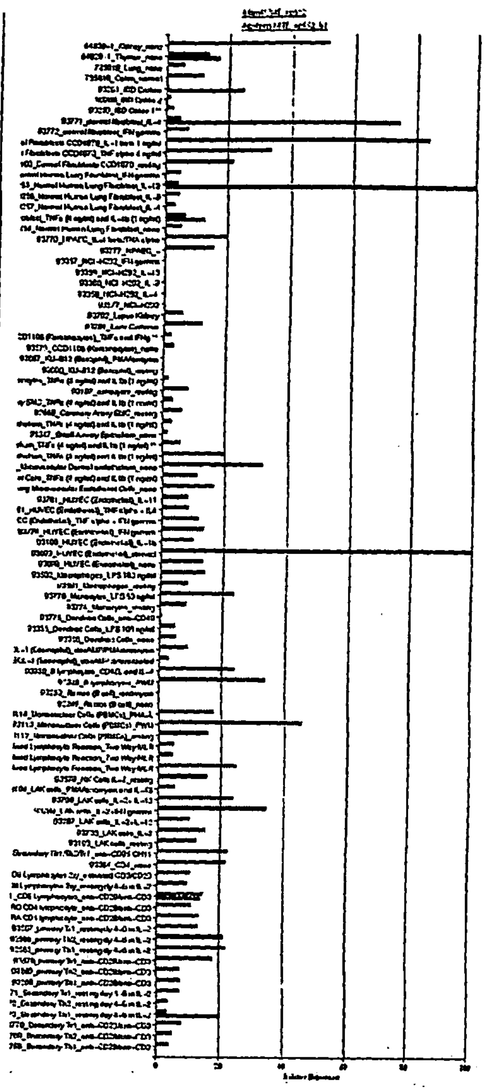


TABLE 45A.

Panel 1.1 ag552	1.1tm699f_ag552
Adipose	14.76
Adrenal gland	5.44
Bladder	6.93
Brain (amygdala)	3.79
Brain (cerebellum)	100
Brain (hippocampus)	12.94
Brain (substantia nigra)	19.75
Brain (thalamus)	7.86
Cerebral Cortex	9.34
Brain (fetal)	36.35
Brain (whole)	6.47
CNS ca. (glio/astro) U-118-MG	2.78
CNS ca. (astro) SF-539	4.09
CNS ca. (astro) SNB-75	2.94
CNS ca. (astro) SW1783	0.24
CNS ca. (glio) U251	2.37
CNS ca. (glio) SF-295	4.7

CNS ca. (glio)	SNB-19	4.36
CNS ca. (glio/astro)	U87-MG	3.19
CNS ca.* (neuro; met)	SK-N-AS	8.3
Mammary gland		1.15
Breast ca.	BT-549	1.41
Breast ca.	MDA-N	3.35
Breast ca.* (pl. effusion)	T47D	4.07
Breast ca.* (pl. effusion)	MCF-7	0
Breast ca.* (pl.ef)	MDA-MB-231	2.09
Small intestine		3.82
Colorectal		0.37
Colon ca.	HT29	0.36
Colon ca.	CaCo-2	0
Colon ca.	HCT-15	1.13
Colon ca.	HCT-116	0.21
Colon ca.	HCC-2998	1.1
Colon ca.	SW480	0.44
Colon ca.* (SW480 met)	SW620	1.81
Stomach		1.91
Gastric ca.* (liver met)	NCI-N87	4.48
Heart		13.21
Fetal Skeletal		2.01
Skeletal muscle		6.79
Endothelial cells		3.77
Endothelial cells (treated)		0
Kidney		9.88
Kidney (fetal)		4.74
Renal ca.	786-0	2.05
Renal ca.	A498	1.07
Renal ca.	ACHN	5.01
Renal ca.	TK-10	11.58
Renal ca.	UO-31	7.97
Renal ca.	RXF 393	3.77
Liver		2.26
Liver (fetal)		0.5
Liver ca. (hepatoblast)	HepG2	0
Lung		2.29
Lung (fetal)		1.49
Lung ca (non-s.cell)	HOP-62	34.87
Lung ca. (large cell)	NCI-H460	4.74
Lung ca. (non-s.cell)	NCI-H23	2.88
Lung ca. (non-s.cl)	NCI-H522	0.71
Lung ca. (non-sm. cell)	A549	16.49
Lung ca. (s.cell var.)	SHP-77	2.26
Lung ca. (small cell)	LX-1	4.07
Lung ca. (small cell)	NCI-H69	11.34
Lung ca. (squam.)	SW 900	1.63
Lung ca. (squam.)	NCI-H596	15.71
Lymph node		4.3
Spleen		0
Thymus		2.24
Ovary		0.62
Ovarian ca.	IGROV-1	0.68

Ovarian ca. OVCAR-3	1.17
Ovarian ca. OVCAR-4	0
Ovarian ca. OVCAR-5	7.13
Ovarian ca. OVCAR-8	5.63
Ovarian ca.* (ascites) SK-OV-3	1.58
Pancreas	6.29
Pancreatic ca. CAPAN 2	3.33
Pituitary gland	7.64
Plancenta	4.9
Prostate	4.45
Prostate ca.* (bone met)PC-3	8.84
Salavary gland	5.08
Trachea	2.3
Spinal cord	4.87
Testis	1.71
Thyroid	2.61
Uterus	5.11
Melanoma M14	9.02
Melanoma LOX IMVI	1.49
Melanoma UACC-62	23
Melanoma SK-MEL-28	28.92
Melanoma* (met) SK-MEL-5	4.33
Melanoma Hs688(A).T	3.98
Melanoma* (met) Hs688(B).T	6.29

TABLE 46A.

Panel 4D ag552	4dtm4830f_ag552	4dx4tm5143f_ag 552_b1
93768_Secondary Th1_anti-CD28/anti-CD3	0	4.42
93769_Secondary Th2_anti-CD28/anti-CD3	0	5.52
93770_Secondary Tr1_anti-CD28/anti-CD3	0	8.55
93573_Secondary Th1_resting day 4-6 in IL-2	19.75	3.74
93572_Secondary Th2_resting day 4-6 in IL-2	0	3.99
93571_Secondary Tr1_resting day 4-6 in IL-2	0	7.71
93568_primary Th1_anti-CD28/anti-CD3	0	8
93569_primary Th2_anti-CD28/anti-CD3	0	7.9
93570_primary Tr1_anti-CD28/anti-CD3	0	18.09
93565_primary Th1_resting dy 4-6 in IL-2	0	22.26
93566_primary Th2_resting dy 4-6 in IL-2	0	21.49
93567_primary Tr1_resting dy 4-6 in IL-2	0	13.65
93351_CD45RA CD4 lymphocyte_anti-CD28/anti-CD3	0	14.02
93352_CD45RO CD4 lymphocyte_anti-CD28/anti-CD3	0	11.44
93251_CD8 Lymphocytes_anti-CD28/anti-CD3	14.06	15.03
93353_chronic CD8 Lymphocytes 2ry_resting dy 4-6 in IL-2	0	10.1
93574_chronic CD8 Lymphocytes 2ry_activated CD3/CD28	0	11.13
93354_CD4_none	0	22
93252_Secondary Th1/Th2/Tr1_anti-CD95 CH11	0	22.66
93103_LAK cells_resting	0	12.75
93788_LAK cells_IL-2	0	15.64
93787_LAK cells_IL-2+IL-12	0	10.71
93789_LAK cells_IL-2+IFN gamma	0	34.75

93790_LAK cells_IL-2+ IL-18	0	24.21
93104_LAK cells_PMA/ionomycin and IL-18	0	5.46
93578_NK Cells IL-2_resting	0	15.92
93109_Mixed Lymphocyte Reaction_Two Way MLR	0	24.93
93110_Mixed Lymphocyte Reaction_Two Way MLR	0	4.72
93111_Mixed Lymphocyte Reaction_Two Way MLR	0	5.17
93112_Mononuclear Cells (PBMCs)_resting	0	16.01
93113_Mononuclear Cells (PBMCs)_PWM	0	45.74
93114_Mononuclear Cells (PBMCs)_PHA-L	0	17.56
93249_Ramos (B cell)_none	0	0
93250_Ramos (B cell)_ionomycin	0	0
93349_B lymphocytes_PWM	0	33.76
93350_B lymphoytes_CD40L and IL-4	0	24.37
92665_EOL-1 (Eosinophil)_dbcAMP differentiated	0	3.2
93248_EOL-1 (Eosinophil)_dbcAMP/PMAionomycin	0	9.34
93356_Dendritic Cells_none	0	5.54
93355_Dendritic Cells_LPS 100 ng/ml	0	5.13
93775_Dendritic Cells_anti-CD40	0	0.91
93774_Monocytes_resting	0	8.66
93776_Monocytes_LPS 50 ng/ml	0	23.67
93581_Macrophages_resting	0	9.01
93582_Macrophages_LPS 100 ng/ml	0	14.6
93098_HUVEC (Endothelial)_none	0	13.86
93099_HUVEC (Endothelial)_starved	0	100
93100_HUVEC (Endothelial)_IL-1b	0	10.46
93779_HUVEC (Endothelial)_IFN gamma	0	13.95
93102_HUVEC (Endothelial)_TNF alpha + IFN gamma	0	11.95
93101_HUVEC (Endothelial)_TNF alpha + IL4	0	8.99
93781_HUVEC (Endothelial)_IL-11	0	8.53
93583_Lung Microvascular Endothelial Cells_none	0	16.62
93584_Lung Microvascular Endothelial Cells_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0	11.25
92662_Microvascular Dermal endothelium_none	0	32.23
92663_Microsvasular Dermal endothelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0	19.86
93773_Bronchial epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml) **	0	6.14
93347_Small Airway Epithelium_none	0	1.75
93348_Small Airway Epithelium_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0	3.14
92668_Coronery Artery SMC_resting	0	6.27
92669_Coronery Artery SMC_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0	3.37
93107_astrocytes_resting	0	8.3
93108_astrocytes_TNFa (4 ng/ml) and IL1b (1 ng/ml)	0	2.09
92666_KU-812 (Basophil)_resting	0	0
92667_KU-812 (Basophil)_PMA/ionoycin	0	0.45
93579_CCD1106 (Keratinocytes)_none	0	3.61
93580_CCD1106 (Keratinocytes)_TNFa and IFNg **	0	2.71
93791_Liver Cirrhosis	0	12.68
93792_Lupus Kidney	0	6.27
93577_NCI-H292	0	0

93358_NCI-H292_IL-4	0	0.52
93360_NCI-H292_IL-9	0	0
93359_NCI-H292_IL-13	0	0
93357_NCI-H292_IFN gamma	0	0
93777_HPAEC_-	0	15.91
93778_HPAEC_IL-1 beta/TNA alpha	0	20.2
93254_Normal Human Lung Fibroblast_none	0	5.28
93253_Normal Human Lung Fibroblast_TNFa (4 ng/ml) and IL-1b (1 ng/ml)	12.85	6.62
93257_Normal Human Lung Fibroblast_IL-4	0	3.44
93256_Normal Human Lung Fibroblast_IL-9	0	4.77
93255_Normal Human Lung Fibroblast_IL-13	100	4.56
93258_Normal Human Lung Fibroblast_IFN gamma	0	5.17
93106_Dermal Fibroblasts CCD1070_resting	0	21.94
93361_Dermal Fibroblasts CCD1070_TNF alpha 4 ng/ml	0	33.7
93105_Dermal Fibroblasts CCD1070_IL-1 beta 1 ng/ml	0	84.47
93772_dermal fibroblast_IFN gamma	0	7.42
93771_dermal fibroblast_IL-4	74.74	4.83
93259_IBD Colitis 1**	0	2.52
93260_IBD Colitis 2	0	1.64
93261_IBD Crohns	24.83	0.62
735010_Colon_normal	0	11.96
735019_Lung_none	0	5.73
64028-1_Thymus_none	16.84	13.44
64030-1_Kidney_none	0	51.45

Example 8 Expression profiling of MOL20

Panel 1.2 (Table 47A): The profile was generated from a panel of 37 normal human tissues and 59 human cancer cell lines using specific gene probe and primer sets (Ag545). This gene is highly expressed in fetal brain and pituitary gland.

Panel 2D (Table 48A): The profile was generated from a panel of several human cell lines that were either untreated or treated with a wide variety factors which modulate the immune response. This panel shows that breast cancer and breast cancer metastases express high levels of this transcript whereas prostate cancer and lung cancer did not.

Probe Name: Ag545

Primers Sequences TM Length Start Position

Forward 5'-CGTCTCCGTGGCTACTCCA-3' (SEQ ID NO.: 261)

Probe TET-5'-ACCACCGCCATCTTGTTCACCATTACCT-3'-TAMRA (SEQ ID NO.: 262)

Reverse 5'-GCCCAAAGTGTGGCAAAGAT-3' (SEQ ID NO.: 263)

Panel 1.1D (Table 49A). The profile was generated from a panel of 37 normal tissues and 59 human cancer cell lines using specific gene probe and primer sets (Ag517). This gene is highly expressed in normal fetal brain, substantia nigra and skeletal muscle.

```
Probe Name: Ag517
Forward 5'-CGCACCCGGAAAGTCATT-3  (SEQ ID NO.: 264)
Probe TET-5'-TAAGTGTTTACATCACCTGCTTCCTGACCAGC-3'-TAMRA (SEQ ID NO.: 265)
Reverse 5'-TGTTGGGCCACCAGTAATAGG-3' (SEQ ID NO.: 26)
```

TABLE 47A.

panel 1.2 ag545		1.2tm875t_ag545
Endothelial cells		0
Heart (fetal)		0
Pancreas		0
Pancreatic ca.	CAPAN 2	0
Adrenal Gland (new lot*)		0
Thyroid		0
Salavary gland		0.4
Pituitary gland		26.4
Brain (fetal)		100
Brain (whole)		2.6
Brain (amygdala)		1.5
Brain (cerebellum)		0
Brain (hippocampus)		2
Brain (thalamus)		7.2
Cerebral Cortex		0.5
Spinal cord		0.8
CNS ca. (glio/astro)	U87-MG	0
CNS ca. (glio/astro)	U-118-MG	0
CNS ca. (astro)	SW1783	0
CNS ca.* (neuro; met)	SK-N-AS	0
CNS ca. (astro)	SF-539	0
CNS ca. (astro)	SNB-75	0
CNS ca. (glio)	SNB-19	0
CNS ca. (glio)	U251	0
CNS ca. (glio)	SF-295	0
Heart		0
Skeletal Muscle (new lot*)		0.2
Bone marrow		4.4
Thymus		0
Spleen		0
Lymph node		0
Colorectal		0.2
Stomach		0
Small intestine		0
Colon ca.	SW480	0
Colon ca.* (SW480 met)	SW620	0
Colon ca.	HT29	0.2

Colon ca. HCT-116	0
Colon ca. CaCo-2	0
83219 CC Well to Mod Diff (ODO3866)	2.1
Colon ca. HCC-2998	0
Gastric ca.* (liver met) NCI-N87	0
Bladder	4.2
Trachea	0
Kidney	0
Kidney (fetal)	0
Renal ca. 786-0	0
Renal ca. A498	0.6
Renal ca. RXF 393	0
Renal ca. ACHN	0
Renal ca. UO-31	0.3
Renal ca. TK-10	0.3
Liver	0
Liver (fetal)	0
Liver ca. (hepatoblast) HepG2	0
Lung	0
Lung (fetal)	0
Lung ca. (small cell) LX-1	0
Lung ca. (small cell) NCI-H69	17.4
Lung ca. (s.cell var.) SHP-77	0.1
Lung ca. (large cell)NCI-H460	0.5
Lung ca. (non-sm. cell) A549	3.4
Lung ca. (non-s.cell) NCI-H23	0
Lung ca (non-s.cell) HOP-62	0.2
Lung ca. (non-s.cl) NCI-H522	0
Lung ca. (squam.) SW 900	0
Lung ca. (squam.) NCI-H596	3.1
Mammary gland	0
Breast ca.* (pl. effusion) MCF-7	4.6
Breast ca.* (pl.ef) MDA-MB-231	0
Breast ca.* (pl. effusion) T47D	5.1
Breast ca. BT-549	0
Breast ca. MDA-N	1
Ovary	0
Ovarian ca. OVCAR-3	0
Ovarian ca. OVCAR-4	0
Ovarian ca. OVCAR-5	9
Ovarian ca. OVCAR-8	0
Ovarian ca. IGROV-1	0.6
Ovarian ca.* (ascites) SK-OV-3	0
Uterus	0
Placenta	0
Prostate	0
Prostate ca.* (bone met)PC-3	0.1
Testis	5
Melanoma Hs688(A).T	0.3
Melanoma* (met) Hs688(B).T	4.7
Melanoma UACC-62	0.1
Melanoma M14	2.1
Melanoma LOX IMVI	0.8

Melanoma* (met) SK-MEL-5	0.7
Adipose	13.6

TABLE 48A.

Panel 2D ag545	2dtm2421t_ag545	2Dtm2453t_ag545
Normal Colon GENPAK 061003	5	1.5
83219 CC Well to Mod Diff (ODO3866)	0	2.5
83220 CC NAT (ODO3866)	0.4	1
83221 CC Gr.2 rectosigmoid (ODO3868)	0	1.9
83222 CC NAT (ODO3868)	0	0
83235 CC Mod Diff (ODO3920)	3.8	1.9
83236 CC NAT (ODO3920)	0.4	0
83237 CC Gr.2 ascend colon (ODO3921)	0	3.1
83238 CC NAT (ODO3921)	0.9	2.2
83241 CC from Partial Hepatectomy (ODO4309)	0	0
83242 Liver NAT (ODO4309)	0	1
87472 Colon mets to lung (OD04451-01)	0.5	0
87473 Lung NAT (OD04451-02)	0	0
Normal Prostate Clontech A+ 6546-1	0	2.3
84140 Prostate Cancer (OD04410)	0	0
84141 Prostate NAT (OD04410)	0	0
87073 Prostate Cancer (OD04720-01)	0	0
87074 Prostate NAT (OD04720-02)	0	0
Normal Lung GENPAK 061010	2	0
83239 Lung Met to Muscle (ODO4286)	0	1.9
83240 Muscle NAT (ODO4286)	0	0
84136 Lung Malignant Cancer (OD03126)	0	1.8
84137 Lung NAT (OD03126)	0	0.7
84871 Lung Cancer (OD04404)	0.9	0
84872 Lung NAT (OD04404)	0	0
84875 Lung Cancer (OD04565)	0	0
84876 Lung NAT (OD04565)	0	0
85950 Lung Cancer (OD04237-01)	0	0
85970 Lung NAT (OD04237-02)	1.8	0
83255 Ocular Mel Met to Liver (ODO4310)	0	0
83256 Liver NAT (ODO4310)	0	3.5
84139 Melanoma Mets to Lung (OD04321)	0	1.4
84138 Lung NAT (OD04321)	1.7	0
Normal Kidney GENPAK 061008	0	0
83786 Kidney Ca, Nuclear grade 2 (OD04338)	0	0
83787 Kidney NAT (OD04338)	0	0
83788 Kidney Ca Nuclear grade 1/2 (OD04339)	0	0
83789 Kidney NAT (OD04339)	0	1.7
83790 Kidney Ca, Clear cell type (OD04340)	0	0
83791 Kidney NAT (OD04340)	0	0
83792 Kidney Ca, Nuclear grade 3 (OD04348)	0	1.9
83793 Kidney NAT (OD04348)	0	0
87474 Kidney Cancer (OD04622-01)	1	0
87475 Kidney NAT (OD04622-03)	0	0.8
85973 Kidney Cancer (OD04450-01)	0	1
85974 Kidney NAT (OD04450-03)	0	0
Kidney Cancer Clontech 8120607	2	0

Kidney NAT Clontech 8120608	0	0
Kidney Cancer Clontech 8120613	1.6	0
Kidney NAT Clontech 8120614	0	1.6
Kidney Cancer Clontech 9010320	0	0
Kidney NAT Clontech 9010321	0	0
Normal Uterus GENPAK 061018	0	0
Uterus Cancer GENPAK 064011	0	0
Normal Thyroid Clontech A+ 6570-1	0	0
Thyroid Cancer GENPAK 064010	0	1
Thyroid Cancer INVITROGEN A302152	1.9	0
Thyroid NAT INVITROGEN A302153	0	0
Normal Breast GENPAK 061019	0.9	0.7
84877 Breast Cancer (OD04566)	18.2	38.7
85975 Breast Cancer (OD04590-01)	100	85.9
85976 Breast Cancer Mets (OD04590-03)	48.6	46.7
87070 Breast Cancer Metastasis (OD04655-05)	84.1	100
GENPAK Breast Cancer 064006	0	0
Breast Cancer Res. Gen. 1024	0	0
Breast Cancer Clontech 9100266	6.5	2.6
Breast NAT Clontech 9100265	0	1.8
Breast Cancer INVITROGEN A209073	1.9	0.7
Breast NAT INVITROGEN A2090734	0.6	5.6
Normal Liver GENPAK 061009	0	0
Liver Cancer GENPAK 064003	1.7	0
Liver Cancer Research Genetics RNA 1025	0	0
Liver Cancer Research Genetics RNA 1026	0	0
Paired Liver Cancer Tissue Research Genetics RNA 6004-T	0	0
Paired Liver Tissue Research Genetics RNA 6004-N	1.7	1
Paired Liver Cancer Tissue Research Genetics RNA 6005-T	0	0
Paired Liver Tissue Research Genetics RNA 6005-N	0	0
Normal Bladder GENPAK 061001	0	1.9
Bladder Cancer Research Genetics RNA 1023	2.7	0.9
Bladder Cancer INVITROGEN A302173	1.1	2
87071 Bladder Cancer (OD04718-01)	0	0
87072 Bladder Normal Adjacent (OD04718-03)	0	3
Normal Ovary Res. Gen.	0	0
Ovarian Cancer GENPAK 064008	0.5	0
87492 Ovary Cancer (OD04768-07)	1.7	0
87493 Ovary NAT (OD04768-08)	0	2.1
Normal Stomach GENPAK 061017	2.1	0
Gastric Cancer Clontech 9060358	1.6	1.6
NAT Stomach Clontech 9060359	0	0
Gastric Cancer Clontech 9060395	0	0
NAT Stomach Clontech 9060394	0	0
Gastric Cancer Clontech 9060397	2	1.1
NAT Stomach Clontech 9060396	0	0
Gastric Cancer GENPAK 064005	1.8	0.8

TABLE 49A.

Panel 1.1D ag517	tm772t_ag517	1.1tm816f_ag686	1.1tm691t_ag517

Adipose	5.8	17.4	8.8
Adrenal gland	0	0	0
Bladder	0	0	0.2
Brain (amygdala)	0.7	0	0.7
Brain (cerebellum)	0	0	0.5
Brain (hippocampus)	0.4	0	0.7
Brain (substantia nigra)	17.1	40.9	23.7
Brain (thalamus)	3.7	4.6	3.1
Cerebral Cortex	0	0	0.6
Brain (fetal)	42.3	100	32.8
Brain (whole)	1.2	2.1	2.3
CNS ca. (glio/astro) U-118-MG	0	0	0.7
CNS ca. (astro) SF-539	0.8	0	0.2
CNS ca. (astro) SNB-75	0.3	0	0.4
CNS ca. (astro) SW1783	0.3	0	0.2
CNS ca. (glio) U251	0	0	1
CNS ca. (glio) SF-295	0	0	0.5
CNS ca. (glio) SNB-19	0	0	0.8
CNS ca. (glio/astro) U87-MG	0.6	0	0.6
CNS ca.* (neuro; met) SK-N-AS	0	0	0
Mammary gland	0.1	0	0.5
Breast ca. BT-549	0.1	0	0.8
Breast ca. MDA-N	0.2	0	1.3
Breast ca.* (pl. effusion) T47D	1.3	1.9	1.5
Breast ca.* (pl. effusion) MCF-7	3.9	8.2	4
Breast ca.* (pl.ef) MDA-MB-231	0	0	0
Small intestine	0	0	0.2
Colorectal	0	0	0.2
Colon ca. HT29	0.2	0	0.7
Colon ca. CaCo-2	0	0	0
Colon ca. HCT-15	2.4	0	1.3
Colon ca. HCT-116	0	0	0.1
Colon ca. HCC-2998	0.2	0	0.4
Colon ca. SW480	0	0	0
Colon ca.* (SW480 met)SW620	0	0	0
Stomach	0	0	0.3
Gastric ca.* (liver met) NCI-N87	0.1	0	1
Heart	0	0	0.8
Fetal Skeletal	0.8	0	5.3
Skeletal muscle	100	0	100
Endothelial cells	0	0	0.2
Heart (fetal)	0	0	0.1
Kidney	0	0	0
Kidney (fetal)	0.3	0	0.1
Renal ca. 786-0	0.2	0	0.5
Renal ca. A498	0.4	0	1.6
Renal ca. ACHN	0.4	0	0.4
Renal ca. TK-10	1.1	0	1.3
Renal ca. UO-31	0.6	0	0
Renal ca. RXF 393	0	0	0.4
Liver	0	0	0.1
Liver (fetal)	0	0	0.3
Liver ca. (hepatoblast) HepG2	0	0	0

Lung	0	0	0
Lung (fetal)	0	0	0
Lung ca (non-s.cell) HOP-62	0.2	0.2	2.9
Lung ca. (large cell)NCI-H460	0	0	1
Lung ca. (non-s.cell) NCI-H23	0.4	0	0.4
Lung ca. (non-s.cl) NCI-H522	0	0	1.2
Lung ca. (non-sm. cell) A549	1	0.7	2.9
Lung ca. (s.cell var.) SHP-77	0	0	0.4
Lung ca. (small cell) LX-1	0	0	0.2
Lung ca. (small cell) NCI-H69	10.1	13.8	4.3
Lung ca. (squam.) SW 900	0.6	0	0.2
Lung ca. (squam.) NCI-H596	2	0.3	3.5
Lymph node	0	0	0
Spleen	0	0	0
Thymus	0	0	0
Ovary	0	0	0
Ovarian ca. IGROV-1	0	0	0.8
Ovarian ca. OVCAR-3	0	0	0.1
Ovarian ca. OVCAR-4	0	0	0
Ovarian ca. OVCAR-5	7.1	9.5	5.5
Ovarian ca. OVCAR-8	0.2	0	0.5
Ovarian ca.* (ascites) SK-OV-3	0.6	0	2.3
Pancreas	0	0	0.2
Pancreatic ca. CAPAN 2	0	0	0.5
Pituitary gland	13.4	7.4	9.2
Placenta	0.8	0	0.7
Prostate	0	0	0.5
Prostate ca.* (bone met)PC-3	0	0	0.3
Salavary gland	0	0	2.1
Trachea	0	0	0.2
Spinal cord	2.5	0.2	1.4
Testis	6.5	0.1	2.3
Thyroid	0.2	0	0.7
Uterus	0.4	0	0.3
Melanoma M14	0.8	1	3.8
Melanoma LOX IMVI	0.2	0	0.2
Melanoma UACC-62	0	0	0
Melanoma SK-MEL-28	0	0	0.6
Melanoma* (met) SK-MEL-5	0	0	0.1
Melanoma Hs688(A).T	0.2	0	0.4
Melanoma* (met) Hs688(B).T	0.3	0	1.8

Example 9. Molecular Cloning of MOL 13 (CG53063-02)

The cDNA coding for the full-length (mature protein) of MOL13 (CG53063-02) from residue 1 to 274 was targeted for "in-frame" cloning by PCR. The PCR template is based on the previously identified plasmid, when available, or on human cDNA(s).

The following oligonucleotide primers were used to clone the target cDNA sequence:

F1: 5'-CACCGGATCC AGGCCATCCCCAGGCCCAGATTACCTGCGG-3' (SEQ ID NO: 267)

R1: 5'-GCCGTCGAC GTAGTAATCGTCATTCTCTTCACTCTCAGC-3' (SEQ ID NO: 268)

For downstream cloning purposes, the forward primer includes an in-frame BamH I restriction site and the reverse primer contains an in-frame Sal I restriction site.

FIS as template:

Two parallel PCR reactions were set up using a total of 0.5-1.0 ng human pooled cDNAs as template for each reaction. The pool is composed of 5 micrograms of each of the following human tissue cDNAs: adrenal gland, whole brain, amygdala, cerebellum, thalamus, bone marrow, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, liver, lymphoma, Burkitt's Raji cell line, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small Intestine, spleen, stomach, thyroid, trachea, uterus.

When the tissue of expression is known and available, the second PCR was performed using the above primers and 0.5ng-1.0 ng of one of the following human tissue cDNAs:

skeleton muscle, testis, mammary gland, adrenal gland, ovary, colon, normal cerebellum, normal adipose, normal skin, bone marrow, brain amygdala, brain hippocampus, brain substantia nigra, brain thalamus, thyroid, fetal lung, fetal liver, fetal brain, kidney, heart, spleen, uterus, pituitary gland, lymph node, salivary gland, small intestine, prostate, placenta, spinal cord, peripheral blood, trachea, stomach, pancreas, hypothalamus.

The reaction mixtures contained 2 microliters of each of the primers (original concentration: 5 pmol/ul), 1 microliter of 10mM dNTP (Clontech Laboratories, Palo Alto CA) and 1 microliter of Pfu DNA polymerase (Strategene) in 50 microliter-reaction volume. The following reaction conditions were used:

PCR condition 1:

a) 96°C 3 minutes
b) 96°C 30 seconds denaturation
c) 60°C 30 seconds, primer annealing
d) 72°C 6 minutes extension

Repeat steps b-d 15 times

e) 96°C 15 seconds denaturation
f) 60°C 30 seconds, primer annealing
g) 72°C 6 minutes extension

Repeat steps e-g 29 times

e) 72°C 10 minutes final extension

PCR condition 2:

a) 96°C 3 minutes

b) 96°C 15 seconds denaturation

c) 76°C 30 seconds, reducing the temperature by 1 °C per cycle

d) 72°C 4 minutes extension

Repeat steps b-d 34 times

e) 72°C 10 minutes final extension.

An amplified product was detected by agarose gel electrophoresis. The fragment was gel-purified and ligated into the pCR2.1-TOPO vector (Invitrogen, Carlsbad, CA) following the manufacturer's recommendation. Twelve clones per PCR reaction were picked and sequenced. The inserts were sequenced using vector-specific M13 Forward and M13 Reverse primers and the following gene-specific primers:

SF1: CTGTGTGCCTGTCGTTCGC (SEQ ID NO: 269)

SF2: ATGGCTTGGACATCCAGCTGCC (SEQ ID NO: 270)

SR1: GGTTCCGGCACCTCTCCG (SEQ ID NO: 271)

SR2: CCATCCTTCCTCCACTCGAT (SEQ ID NO: 272)

The insert assembly 277582085 was found to encode an open reading frame between residues 1 and 274 of the target sequence of CG53063-02. The cloned insert differs from the original sequence by three silent nucleotide changes.

Example 10. Molecular Cloning of MOL 21 (CG54656-05)

The cDNA coding for the domain of MOL 21 (CG54656-05) from residue 62 to 353 was targeted for "in-frame" cloning by PCR. The PCR template is based on the previously identified plasmid, when available, or on human cDNA(s).

The following oligonucleotide primers were used to clone the target cDNA sequence:

F3 5'-CGCGGTACC TCCTACAACTATCTCTTGGCACTCGCTGCT-3' (SEQ ID NO: 273)

R1 5'-CGCCTCGAG CGGGGATACTTTTATAGGTTTTCCATTTTT-3' (SEQ ID NO:274)

For downstream cloning purposes, the forward primer includes an in-frame *Kpn* I restriction site and the reverse primer contains an in-frame *Xho* I restriction site. Two PCR reactions were set up using a total of 1-5 ng of the plasmid that contains the insert for CG54656-05.

The reaction mixtures contained 2 microliters of each of the primers (original concentration: 5 pmol/ul), 1 microliter of 10mM dNTP (Clontech Laboratories, Palo Alto CA) and

1 microliter of 50xAdvantage-HF 2 polymerase (Clontech Laboratories) in 50 microliter-reaction volume. The following reaction conditions were used:

PCR condition 1:

a) 96°C 3 minutes
b) 96°C 30 seconds denaturation
c) 60°C 30 seconds, primer annealing
d) 72°C 6 minutes extension

Repeat steps b-d 15 times

e) 96°C 15 seconds denaturation
f) 60°C 30 seconds, primer annealing
g) 72°C 6 minutes extension

Repeat steps e-g 29 times

e) 72°C 10 minutes final extension

PCR condition 2:

a) 96°C 3 minutes
b) 96°C 15 seconds denaturation
c) 76°C 30 seconds, reducing the temperature by 1 °C per cycle
d) 72°C 4 minutes extension

Repeat steps b-d 34 times

e) 72°C 10 minutes final extension.

An amplified product was detected by agarose gel electrophoresis. The fragment was gel-purified and ligated into the pCR2.1TOPO vector (Invitrogen, Carlsbad, CA) following the manufacturer's recommendation. Twelve clones per PCR reaction were picked and sequenced. The inserts were sequenced using vector-specific M13 Forward and M13 Reverse primers and the following gene-specific primers:

F1 AGTAGAGGAAGAAGTTGATGGCTGT (SEQ ID NO: 276)
F2 ACGGTGAAGCAGTGGATCCAGATGAG (SEQ ID NO: 277)
R1 TGCTTCATCAGCAAGCGGTTC (SEQ ID NO: 278)
R2 CTACCTGGTGCCCTGCTCCATCT (SEQ ID NO: 279)

The insert assembly 253980583 was found to encode an open reading frame between residues 62 and 353 of the target sequence of CG54656-05. The cloned insert is 100% identical to the original sequence.

The cDNA coding for the domain of MOL21 (CG54656-05) from residue 47 to 353 was targeted for "in-frame" cloning by PCR. The PCR template is based on the previously identified plasmid, when available, or on human cDNA(s).

The following oligonucleotide primers were used to clone the target cDNA sequence:

F2 5'-CGCGGTACC GTGATCATCCTCTCCCAGCTGGTGGCAAGA-3' (SEQ ID NO: 280)

R1 5'-CGCCTCGAG CGGGGATACTTTTATAGGTTTTCCATTTTT-3' (SEQ ID NO: 281)

For downstream cloning purposes, the forward primer includes an in-frame *Kpn* I restriction site and the reverse primer contains an in-frame *Xho* I restriction site.

Two PCR reactions were set up as described above.

The inserts were sequenced using vector-specific M13 Forward and M13 Reverse primers and the following gene-specific primers:

F1 GGAACCGCTTGCTGATGAAGCAGTAG (SEQ ID NO: 282)

F2 ACGGTGAAGCAGTGGATCCAGATGAG (SEQ ID NO: 283)

R1 GCCACGCTCAAGGCTTTCTTC (SEQ ID NO: 284)

R2 GTCTACCTGGTGCCCTGCTCCATCTT (SEQ ID NO: 285)

The insert assembly 253980544 was found to encode an open reading frame between residues 47 and 353 of the target sequence of CG54656-05. The cloned insert is 100% identical to the original sequence.

The cDNA coding for the domain of MOL21 (CG54656-05) from residue 62 to 285 was targeted for "in-frame" cloning by PCR. The PCR template is based on the previously identified plasmid, when available, or on human cDNA(s).

The following oligonucleotide primers were used to clone the target cDNA sequence:

F3 5'-CGCGGTACC TCCTACAACTATCTCTTGGCACTCGCTGCT-3' (SEQ ID NO: 286)

R2 5'-CGCCTCGAG GTAGAGGAAGAAGTTGATGGCTGTGTTCAG-3' (SEQ ID NO: 287)

For downstream cloning purposes, the forward primer includes an in-frame *Kpn* I restriction site and the reverse primer contains an in-frame *Xho* I restriction site.

Two PCR reactions were set up as described above. The inserts were sequenced using vector-specific M13 Forward and M13 Reverse primers and the following gene-specific primers:

F1 GCTTCTGGCACTTGAAGAAAGCC (SEQ ID NO: 288)

F2 GGGCGCCCCATAGAGGTGGTAAAGAAT (SEQ ID NO: 289)

R1 GCAACCTGTACAGTTCTACACCAAT (SEQ ID NO: 290)

R2 CCGCTGGCTGGTACACATCAT (SEQ ID NO: 291).

The insert assembly 252514086 was found to encode an open reading frame between residues 62 and 285 of the target sequence of CG54656-05. The cloned insert is 100% identical to the original sequence.

The cDNA coding for the domain of MOL21 (CG54656-05) from residue 47 to 285 was targeted for "in-frame" cloning by PCR. The PCR template is based on the previously identified plasmid, when available, or on human cDNA(s).

The following oligonucleotide primers were used to clone the target cDNA sequence:

F2 5'-CGCGGTACC GTGATCATCCTCTCCCAGCTGGTGGCAAGA-3' (SEQ ID NO: 292)

R2 5'-CGCCTCGAG GTAGAGGAAGAAGTTGATGGCTGTGTTCAG-3' (SEQ ID NO: 293)

For downstream cloning purposes, the forward primer includes an in-frame *Kpn* I restriction site and the reverse primer contains an in-frame *Xho* I restriction site.

Two PCR reactions were set up as described above. The inserts were sequenced using vector-specific M13 Forward and M13 Reverse primers and the following gene-specific primers:

F1 ATTGGTGTAGAACTGTACAGGTTGCTTCTGG (SEQ ID NO: 294)

F2 GGGCGCCCCATAGAGGTGGTAAAGAAT (SEQ ID NO: 295)

R1 AACTTTTCCATAACAAGTAGCCCCT (SEQ ID NO: 296)

R2 CCGCTGGCTGGTACACATCAT (SEQ ID NO: 297)

The insert assembly 252417960 was found to encode an open reading frame between residues 47 and 285 of the target sequence of CG54656-05. The cloned insert is 100% identical to the original sequence.

The cDNA coding for the full length of MOL21 CG54656-05 from residue 1 to 353 was targeted for "in-frame" cloning by PCR. The PCR template is based on the previously identified plasmid, when available, or on human cDNA(s).

The following oligonucleotide primers were used to clone the target cDNA sequence:

F1 5'-CGCGGTACCACC ATGGAGCACACGCACGCCCACCTCGCAGCC-3' (SEQ ID NO: 298)

R1 5'-CGCCTCGAG CGGGGATACTTTTATAGGTTTTCCATTTTT-3' (SEQ ID NO: 299)

For downstream cloning purposes, the forward primer includes an in-frame *Kpn* I restriction site and the reverse primer contains an in-frame *Xho* I restriction site.

Two PCR reactions were set up as described above. The inserts were sequenced using vector-specific M13 Forward and M13 Reverse primers and the following gene-specific primers:

F1	CACTCTTAAGGAGAGCTGCTCAGCCA (SEQ ID NO: 300)
F2	TCCAGGGGCTACTTGTTATGGAA (SEQ ID NO: 301)
F3	TCGGACATGATGTGTACCAGCC (SEQ ID NO: 302)
F4	CACAATGATTGAGTTCAAGATGAAGAAGAT (SEQ ID NO: 303)
F5	GGTGAAGCAGTGGATCCAGATGAGGAC (SEQ ID NO: 304)
R1	CTAATCCGATTTCCTGTCTCCCG (SEQ ID NO: 305)
R2	GGCAAACTCACACTGCATCAAGA (SEQ ID NO: 306)
R3	ACATTGCCAACATGCTAGCCCTT (SEQ ID NO: 307)
R4	AGCTCAGGAGGAAGAGCAATTTTCG (SEQ ID NO: 308)
R5	GTGCCCTGCTCCATCTTCTTCAT (SEQ ID NO: 309)

The insert assembly 252417888 was found to encode an open reading frame between residues 1 and 353 of the target sequence of CG54656-05. The cloned insert is 100% identical to the original sequence.

EQUIVALENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims.

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:
   (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206;
   (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
   (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206; and
   (d) a variant of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence.

2 The polypeptide of claim 1, wherein said polypeptide comprises the amino acid sequence of a naturally-occurring allelic variant of an amino acid sequence selected from the group

consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206.

3. The polypeptide of claim 2, wherein said allelic variant comprises an amino acid sequence that is the translation of a nucleic acid sequence differing by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205.

4. The polypeptide of claim 1, wherein the amino acid sequence of said variant comprises a conservative amino acid substitution.

5. An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of:
   (a) a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206;
   (b) a variant of a mature form of an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of the amino acid residues from the amino acid sequence of said mature form;
   (c) an amino acid sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161,

163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206;

(d) a variant of an amino acid sequence selected from the group consisting SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence;

(e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising an amino acid sequence chosen from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or a variant of said polypeptide, wherein one or more amino acid residues in said variant differs from the amino acid sequence of said mature form, provided that said variant differs in no more than 15% of amino acid residues from said amino acid sequence; and

(f) a nucleic acid molecule comprising the complement of (a), (b), (c), (d) or (e).

6. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises the nucleotide sequence of a naturally-occurring allelic nucleic acid variant.

7. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule encodes a polypeptide comprising the amino acid sequence of a naturally-occurring polypeptide variant.

8. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205.

9. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
   (a) a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205;
   (b) a nucleotide sequence differing by one or more nucleotides from a nucleotide sequence selected from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205, provided that no more than 20% of the nucleotides differ from said nucleotide sequence;
   (c) a nucleic acid fragment of (a); and
   (d) a nucleic acid fragment of (b).

10. The nucleic acid molecule of claim 5, wherein said nucleic acid molecule hybridizes under stringent conditions to a nucleotide sequence chosen from the group consisting of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 114, 116, 118, 120, 123, 125, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, and 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203 and 205, or a complement of said nucleotide sequence.

11. The nucleic acid molecule of claim 5, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:
   (a) a first nucleotide sequence comprising a coding sequence differing by one or more nucleotide sequences from a coding sequence encoding said amino acid sequence, provided that no more than 20% of the nucleotides in the coding sequence in said first nucleotide sequence differ from said coding sequence;
   (b) an isolated second polynucleotide that is a complement of the first polynucleotide; and
   (c) a nucleic acid fragment of (a) or (b).

12. A vector comprising the nucleic acid molecule of claim 11.

13. The vector of claim 12, further comprising a promoter operably-linked to said nucleic acid molecule.

14. A cell comprising the vector of claim 12.

15. An antibody that binds immunospecifically to the polypeptide of claim 1.

16. The antibody of claim 15, wherein said antibody is a monoclonal antibody.

17. The antibody of claim 15, wherein the antibody is a humanized antibody.

18. A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:
    (a) providing the sample;
    (b) contacting the sample with an antibody that binds immunospecifically to the polypeptide; and
    (c) determining the presence or amount of antibody bound to said polypeptide,

thereby determining the presence or amount of polypeptide in said sample.

19. A method for determining the presence or amount of the nucleic acid molecule of claim 5 in a sample, the method comprising:
    (a) providing the sample;
    (b) contacting the sample with a probe that binds to said nucleic acid molecule; and
    (c) determining the presence or amount of the probe bound to said nucleic acid molecule,

thereby determining the presence or amount of the nucleic acid molecule in said sample.

20. The method of claim 19 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

21. The method of claim 20 wherein the cell or tissue type is cancerous.

22. A method of identifying an agent that binds to a polypeptide of claim 1, the method comprising:
    (a) contacting said polypeptide with said agent; and
    (b) determining whether said agent binds to said polypeptide.

23. The method of claim 22 wherein the agent is a cellular receptor or a downstream effector.

24. A method for identifying an agent that modulates the expression or activity of the polypeptide of claim 1, the method comprising:
    (a) providing a cell expressing said polypeptide;
    (b) contacting the cell with said agent, and
    (c) determining whether the agent modulates expression or activity of said polypeptide,

whereby an alteration in expression or activity of said peptide indicates said agent modulates expression or activity of said polypeptide.

25. A method for modulating the activity of the polypeptide of claim 1, the method comprising contacting a cell sample expressing the polypeptide of said claim with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptide.

26. A method of treating or preventing a MOLX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the polypeptide of claim 1 in an amount sufficient to treat or prevent said MOLX-associated disorder in said subject.

27. The method of claim 26 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.

28. The method of claim 26 wherein the disorder is related to cell signal processing and metabolic pathway modulation.

29. The method of claim 26, wherein said subject is a human.

30. A method of treating or preventing a MOLX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the nucleic acid of claim 5 in an amount sufficient to treat or prevent said MOLX-associated disorder in said subject.

31. The method of claim 30 wherein the disorder is selected from the group consisting of cardiomyopathy and atherosclerosis.

32. The method of claim 30 wherein the disorder is related to cell signal processing and metabolic pathway modulation.

33. The method of claim 30, wherein said subject is a human.

34. A method of treating or preventing a MOLX-associated disorder, said method comprising administering to a subject in which such treatment or prevention is desired the antibody of claim 15 in an amount sufficient to treat or prevent said MOLX-associated disorder in said subject.

35. The method of claim 34 wherein the disorder is diabetes.

36. The method of claim 34 wherein the disorder is related to cell signal processing and metabolic pathway modulation.

37. The method of claim 34, wherein the subject is a human.

38. A pharmaceutical composition comprising the polypeptide of claim 1 and a pharmaceutically-acceptable carrier.

39. A pharmaceutical composition comprising the nucleic acid molecule of claim 5 and a pharmaceutically-acceptable carrier.

40. A pharmaceutical composition comprising the antibody of claim 15 and a pharmaceutically-acceptable carrier.

41. A kit comprising in one or more containers, the pharmaceutical composition of claim 38.

42. A kit comprising in one or more containers, the pharmaceutical composition of claim 39.

43. A kit comprising in one or more containers, the pharmaceutical composition of claim 40.

44. A method for determining the presence of or predisposition to a disease associated with altered levels of the polypeptide of claim 1 in a first mammalian subject, the method comprising:

(a) measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and

(b) comparing the amount of said polypeptide in the sample of step (a) to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease;

wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.

45. The method of claim 44 wherein the predisposition is to a cancer.

46. A method for determining the presence of or predisposition to a disease associated with altered levels of the nucleic acid molecule of claim 5 in a first mammalian subject, the method comprising:

(a) measuring the amount of the nucleic acid in a sample from the first mammalian subject; and

(b) comparing the amount of said nucleic acid in the sample of step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;

wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

47. The method of claim 46 wherein the predisposition is to a cancer.

48. A method of treating a pathological state in a mammal, the method comprising administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide comprising an amino acid sequence of at least one of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or a biologically active fragment thereof.

49. A method of treating a pathological state in a mammal, the method comprising administering to the mammal the antibody of claim 15 in an amount sufficient to alleviate the pathological state.

50. A method for the screening of a candidate substance interacting with an olfactory receptor polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or fragments or variants thereof, comprises the following steps:

a) providing a polypeptide selected from the group consisting of the sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, or a peptide fragment or a variant thereof;

b) obtaining a candidate substance;

c) bringing into contact said polypeptide with said candidate substance; and

d) detecting the complexes formed between said polypeptide and said candidate substance.

51. A method for the screening of ligand molecules interacting with an olfactory receptor polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175,

177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, wherein said method comprises:

a) providing a recombinant eukaryotic host cell containing a nucleic acid encoding a polypeptide selected from the group consisting of the polypeptides comprising the amino acid sequences SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206;

b) preparing membrane extracts of said recombinant eukaryotic host cell;

c) bringing into contact the membrane extracts prepared at step b) with a selected ligand molecule; and

d) detecting the production level of second messengers metabolites.

52. A method for the screening of ligand molecules interacting with an olfactory receptor polypeptide selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206, wherein said method comprises:

a) providing an adenovirus containing a nucleic acid encoding a polypeptide selected from the group consisting of polypeptides comprising the amino acid sequences SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 115, 117, 119, 122, 124, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204 and 206;

b) infecting an olfactory epithelium with said adenovirus;

c) bringing into contact the olfactory epithelium b) with a selected ligand molecule; and

d) detecting the increase of the response to said ligand molecule.